

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2006, 19:06:58 ; Search time 7778 Seconds
(without alignment)
10646.941 Million cell updates/sec

Title: US-10-785-221-8

Perfect score: 1295

Sequence: 1 ccagaagttcaaggccccc.....ataaatatagcttgatattc 1295

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl.*

1: gb_env.*

2: gb_pat.*

3: gb_ph.*

4: gb_pl.*

5: gb_pr.*

6: gb_ro.*

7: gb_sts.*

8: gb_sv.*

9: gb_un.*

10: gb_vi.*

11: gb_ov.*

12: gb_htg.*

13: gb_in.*

14: gb_om.*

15: gb_da.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1295	100.0	1295	2	BD075420
2	1295	100.0	1295	2	BD172280
3	1295	100.0	1295	2	BD172599
4	1295	100.0	1295	2	BD172918
5	1295	100.0	1295	2	BD173237
6	1295	100.0	1295	2	BD175271
7	1295	100.0	1295	2	CQ957874
8	1295	100.0	1295	2	CQ957936
9	1295	100.0	1295	2	AR216160
10	1295	100.0	1295	2	AR410649
11	1295	100.0	1295	2	AR439013
12	1295	100.0	1295	2	AR473033
13	1295	100.0	1295	2	AR527019
14	1295	100.0	1295	2	AR566052
15	1295	100.0	1295	2	AR592070
16	1295	100.0	1295	2	AR604344
17	1295	100.0	1295	2	AR604930
18	1295	100.0	1295	2	AR613595

19	1295	100.0	1295	2	AR629922	Sequence
20	1295	100.0	1295	2	AR635766	Sequence
21	1295	100.0	1295	2	AR650495	Sequence
22	1295	100.0	1295	2	AR657436	Sequence
23	1295	100.0	1295	2	AR720388	Sequence
24	1295	100.0	1295	2	AR770947	Sequence
25	1295	100.0	1295	2	AR771314	Sequence
26	1295	100.0	1295	2	AX055378	Sequence
27	1295	100.0	1295	2	AX098375	Sequence
28	1295	100.0	1295	2	AX464202	Sequence
29	1295	100.0	1295	2	AX697472	Sequence
30	1295	100.0	1295	5	AY358361	Homo sapi
31	951.6	73.5	1246	5	AY077698	Homo sapi
32	951.6	73.5	1260	5	AF255910	Homo sapi
33	951.6	73.5	1397	2	DD210216	Methods o
34	951.6	73.5	1410	5	AY016009	Homo sapi
35	951.2	73.5	1076	5	BD106412	Secreted
36	950.2	73.4	1263	5	BC017779	Homo sapi
37	935.2	72.2	1389	2	DD164857	Human cDN
38	935.2	72.2	1389	2	AX772824	Sequence
39	922.4	71.2	1022	2	BD084186	28 human
40	922.4	71.2	1022	2	AR229209	Sequence
41	922.4	71.2	1022	2	AR650426	Sequence
42	922.4	71.2	1022	2	AR699658	Sequence
43	922.4	71.2	1022	2	AR723908	Sequence
44	922.4	71.2	1022	2	AX810711	Sequence
45	649	50.1	800	2	CQ731715	Sequence
46	616.2	47.6	920	7	BV180595	sqmml1044
47	614	47.4	905	2	AX083641	Sequence
48	609.4	47.1	4225	6	BC105305	Rattus no
49	603.8	46.6	1551	6	MMU291757	Mus muscu
50	602.2	46.5	1349	6	BC028778	Mus muscu
51	600.6	46.4	1082	6	AF255911	Mus muscu
52	594.2	45.9	1626	2	BD268817	Vascular
53	594.2	45.9	1631	2	AX036060	Sequence
54	383.2	29.6	413	2	CQ957893	Sequence
55	383.2	29.6	413	2	CQ957955	Sequence
56	383.2	29.6	413	2	AR216173	Sequence
57	383.2	29.6	413	2	AR629935	Sequence
58	343.6	26.5	75114	5	AF000226	Homo sapi
59	343.6	26.5	100000	5	AF000087	Homo sapi
60	343.6	26.5	100000	5	AF000139	Homo sapi
61	343.6	26.5	340000	5	AF001694	Homo sapi
62	332.6	25.7	484	2	CQ684447	Sequence
63	324.6	25.1	148196	5	BS000106	Pan trogl
64	302.6	23.4	343	2	BD071857	Secreted
65	231.4	17.9	135424	12	AC069040	Homo sapi
66	231.4	17.9	139931	5	AC078818	Homo sapi
67	223.8	17.3	176411	5	AC034139	Homo sapi
68	223.8	17.3	185440	12	AC015499	Homo sapi
69	222	17.1	174752	5	AC146075	Pan trogl
70	220.2	17.0	38096	5	EX901949	Human DNA
71	220.2	17.0	127867	5	HS694B14	Human DNA
72	219.6	17.0	98236	5	AC084824	Homo sapi
73	219.4	16.9	143145	5	AL591377	Human DNA
74	219.4	16.9	173854	12	AL137023	Homo sapi
75	219	16.9	135692	5	AC023315	Homo sapi
76	219	16.9	181991	5	AC025882	Homo sapi
77	218.6	16.9	61099	12	AC139421	Homo sapi
78	218.6	16.9	71260	12	AC139557	Homo sapi
79	218.6	16.9	71260	12	AC139557	Homo sapi
80	218.6	16.9	134506	12	AC146482	Homo sapi
81	218.6	16.9	139475	5	AC115992	Homo sapi
82	218.6	16.9	140152	5	AC027821	Homo sapi
83	218.6	16.9	180876	5	AC021317	Homo sapi
84	218.6	16.9	206040	12	AC132814	Homo sapi
85	218.4	16.9	89147	12	AC146857	Homo sapi
86	218.2	16.8	78693	5	AC114734	Homo sapi
87	218.2	16.8	110000	12	AC091528	Continuation (2 of
88	218.2	16.8	131378	5	AC112653	Continuation (2 of
89	218.2	16.8	135584	12	AC020749	Homo sapi
90	218	16.8	176539	5	AL354928	Human DNA
91	217.8	16.8	156525	12	AC040966	Homo sapi

C 92	217.8	16.8	162771	5	AC138781	Homo sapi	16.8	162771	5	AC138781	Homo sapi	213.8	16.5	146687	5	AC110592	Homo sapi	
C 93	217.8	16.8	167699	5	AC107050	Homo sapi	213.8	16.5	149916	5	AC145873	Pan trogl	213.8	16.5	149916	5	AC145873	Pan trogl
C 94	217.8	16.8	173251	5	AP002517	Homo sapi	213.8	16.5	159206	5	AC098584	Homo sapi	213.8	16.5	159206	5	AC098584	Homo sapi
C 95	217.8	16.8	179257	5	AC133529	Homo sapi	213.8	16.5	167757	5	AC116021	Homo sapi	213.8	16.5	167757	5	AC116021	Homo sapi
C 96	217.8	16.8	181262	5	AC110789	Homo sapi	213.8	16.5	181262	5	AC110789	Homo sapi	213.8	16.5	181262	5	AC110789	Homo sapi
C 97	217.8	16.8	187038	12	AC021179	Homo sapi	213.8	16.5	187038	12	AC021179	Homo sapi	213.8	16.5	187038	12	AC021179	Homo sapi
C 98	217.8	16.8	192985	12	AC021742	Homo sapi	213.8	16.5	192985	12	AC021742	Homo sapi	213.8	16.5	192985	12	AC021742	Homo sapi
C 99	217.4	16.8	147831	5	AC116037	Homo sapi	213.6	16.5	147831	5	AC116037	Homo sapi	213.6	16.5	147831	5	AC116037	Homo sapi
C 100	217.4	16.8	158242	5	AC146111	Pan trogl	213.6	16.5	158242	5	AC146111	Pan trogl	213.6	16.5	158242	5	AC146111	Pan trogl
C 101	217.4	16.8	192031	5	AC027129	Homo sapi	213.6	16.5	192031	5	AC027129	Homo sapi	213.6	16.5	192031	5	AC027129	Homo sapi
C 102	217	16.8	169687	12	AC146251	Pan trogl	213.6	16.5	169687	12	AC146251	Pan trogl	213.6	16.5	169687	12	AC146251	Pan trogl
C 103	216.8	16.7	165090	5	AC010655	Homo sapi	213.6	16.5	165090	5	AC010655	Homo sapi	213.6	16.5	165090	5	AC010655	Homo sapi
C 104	216.8	16.7	185363	5	CT573093	CH250-1K1	213.6	16.5	185363	5	CT573093	CH250-1K1	213.6	16.5	185363	5	CT573093	CH250-1K1
C 105	216.6	16.7	48289	5	AC067729	Homo sapi	213.6	16.5	48289	5	AC067729	Homo sapi	213.6	16.5	48289	5	AC067729	Homo sapi
C 106	216.6	16.7	123274	5	AC092979	Homo sapi	213.6	16.5	123274	5	AC092979	Homo sapi	213.6	16.5	123274	5	AC092979	Homo sapi
C 107	216.6	16.7	162337	12	AC025354	Homo sapi	213.6	16.5	162337	12	AC025354	Homo sapi	213.6	16.5	162337	12	AC025354	Homo sapi
C 108	216.4	16.7	150635	5	AL365185	Human DNA	213.6	16.5	150635	5	AL365185	Human DNA	213.6	16.5	150635	5	AL365185	Human DNA
C 109	216.2	16.7	145050	5	AC021078	Homo sapi	213.6	16.5	145050	5	AC021078	Homo sapi	213.6	16.5	145050	5	AC021078	Homo sapi
C 110	216.2	16.7	159787	12	AC016285	Homo sapi	213.6	16.5	159787	12	AC016285	Homo sapi	213.6	16.5	159787	12	AC016285	Homo sapi
C 111	216.2	16.7	161374	5	AC113603	Homo sapi	213.6	16.5	161374	5	AC113603	Homo sapi	213.6	16.5	161374	5	AC113603	Homo sapi
C 112	216.2	16.7	174742	5	AC068102	Homo sapi	213.6	16.5	174742	5	AC068102	Homo sapi	213.6	16.5	174742	5	AC068102	Homo sapi
C 113	216.2	16.7	207017	12	AC023373	Homo sapi	213.6	16.5	207017	12	AC023373	Homo sapi	213.6	16.5	207017	12	AC023373	Homo sapi
C 114	216	16.7	160760	5	AC091986	Homo sapi	213.6	16.5	160760	5	AC091986	Homo sapi	213.6	16.5	160760	5	AC091986	Homo sapi
C 115	215.8	16.7	36242	5	AL350228	Human DNA	213.6	16.5	36242	5	AL350228	Human DNA	213.6	16.5	36242	5	AL350228	Human DNA
C 116	215.8	16.7	40233	5	BX936346	Human DNA	213.6	16.5	40233	5	BX936346	Human DNA	213.6	16.5	40233	5	BX936346	Human DNA
C 117	215.8	16.7	107484	5	HS424L16	Human DNA	213.6	16.5	107484	5	HS424L16	Human DNA	213.6	16.5	107484	5	HS424L16	Human DNA
C 118	215.8	16.7	132433	5	HSX7210B1	Human DNA	213.6	16.5	132433	5	HSX7210B1	Human DNA	213.6	16.5	132433	5	HSX7210B1	Human DNA
C 119	215.8	16.7	142782	12	BM664737	Homo sapi	213.6	16.5	142782	12	BM664737	Homo sapi	213.6	16.5	142782	12	BM664737	Homo sapi
C 120	215.8	16.7	160855	12	AC009818	Homo sapi	213.6	16.5	160855	12	AC009818	Homo sapi	213.6	16.5	160855	12	AC009818	Homo sapi
C 121	215.8	16.7	168224	12	AC022876	Homo sapi	213.6	16.5	168224	12	AC022876	Homo sapi	213.6	16.5	168224	12	AC022876	Homo sapi
C 122	215.8	16.7	190727	5	AC068724	Homo sapi	213.6	16.5	190727	5	AC068724	Homo sapi	213.6	16.5	190727	5	AC068724	Homo sapi
C 123	215.8	16.7	201269	12	AP001849	Homo sapi	213.6	16.5	201269	12	AP001849	Homo sapi	213.6	16.5	201269	12	AP001849	Homo sapi
C 124	215.6	16.6	23353	2	CS138605	Sequence	213.6	16.5	23353	2	CS138605	Sequence	213.6	16.5	23353	2	CS138605	Sequence
C 125	215.6	16.6	24112	5	AY773965	Homo sapi	213.6	16.5	24112	5	AY773965	Homo sapi	213.6	16.5	24112	5	AY773965	Homo sapi
C 126	215.6	16.6	125823	5	HSJ561124	Human DNA	213.6	16.5	125823	5	HSJ561124	Human DNA	213.6	16.5	125823	5	HSJ561124	Human DNA
C 127	215.6	16.6	162644	5	AC078962	Homo sapi	213.6	16.5	162644	5	AC078962	Homo sapi	213.6	16.5	162644	5	AC078962	Homo sapi
C 128	215.6	16.6	169537	5	AC100814	Homo sapi	213.6	16.5	169537	5	AC100814	Homo sapi	213.6	16.5	169537	5	AC100814	Homo sapi
C 129	215.4	16.6	162877	5	AC018509	Homo sapi	213.6	16.5	162877	5	AC018509	Homo sapi	213.6	16.5	162877	5	AC018509	Homo sapi
C 130	215.4	16.6	190584	12	AC148540	Pan trogl	213.6	16.5	190584	12	AC148540	Pan trogl	213.6	16.5	190584	12	AC148540	Pan trogl
C 131	215.2	16.6	147052	5	AL590640	Human DNA	212.4	16.4	147052	5	AL590640	Human DNA	212.4	16.4	147052	5	AL590640	Human DNA
C 132	215.2	16.6	177531	2	AX706962	Sequence	212.4	16.4	177531	2	AX706962	Sequence	212.4	16.4	177531	2	AX706962	Sequence
C 133	215.2	16.6	177531	2	AX707892	Sequence	212.4	16.4	177531	2	AX707892	Sequence	212.4	16.4	177531	2	AX707892	Sequence
C 134	215.2	16.6	177531	2	AC005020	Homo sapi	212.4	16.4	177531	2	AC005020	Homo sapi	212.4	16.4	177531	2	AC005020	Homo sapi
C 135	215.2	16.6	232939	12	AC145881	Pan trogl	212.4	16.4	232939	12	AC145881	Pan trogl	212.4	16.4	232939	12	AC145881	Pan trogl
C 136	215.2	16.6	253389	12	AC008605	Homo sapi	212.4	16.4	253389	12	AC008605	Homo sapi	212.4	16.4	253389	12	AC008605	Homo sapi
C 137	215	16.6	37194	5	HSV210B9	Human DNA	212.4	16.4	37194	5	HSV210B9	Human DNA	212.4	16.4	37194	5	HSV210B9	Human DNA
C 138	215	16.6	40205	5	AF045450	Homo sapi	212.4	16.4	40205	5	AF045450	Homo sapi	212.4	16.4	40205	5	AF045450	Homo sapi
C 139	215	16.6	87387	5	AC062037	Homo sapi	212.4	16.4	87387	5	AC062037	Homo sapi	212.4	16.4	87387	5	AC062037	Homo sapi
C 140	215	16.6	154405	5	AC004990	Homo sapi	212.4	16.4	154405	5	AC004990	Homo sapi	212.4	16.4	154405	5	AC004990	Homo sapi
C 141	214.6	16.6	177322	12	AC024357	Mus muscu	212.4	16.4	177322	12	AC024357	Mus muscu	212.4	16.4	177322	12	AC024357	Mus muscu
C 142	214.6	16.6	180163	12	AC021510	Homo sapi	212.4	16.4	180163	12	AC021510	Homo sapi	212.4	16.4	180163	12	AC021510	Homo sapi
C 143	214.6	16.6	196806	5	AC104212	Homo sapi	212.4	16.4	196806	5	AC104212	Homo sapi	212.4	16.4	196806	5	AC104212	Homo sapi
C 144	214.6	16.6	207818	5	AC019206	Homo sapi	212.4	16.4	207818	5	AC019206	Homo sapi	212.4	16.4	207818	5	AC019206	Homo sapi
C 145	214.4	16.6	10511	5	AF097738	Homo sapi	212.4	16.4	10511	5	AF097738	Homo sapi	212.4	16.4	10511	5	AF097738	Homo sapi
C 146	214.4	16.6	132604	5	AC060226	Homo sapi	212.4	16.4	132604	5	AC060226	Homo sapi	212.4	16.4	132604	5	AC060226	Homo sapi
C 147	214.4	16.6	145477	12	AC010810	Homo sapi	212.4	16.4	145477	12	AC010810	Homo sapi	212.4	16.4	145477	12	AC010810	Homo sapi
C 148	214.4	16.6	161943	5	HS84M10	Homo sapi	212.4	16.4	161943	5	HS84M10	Homo sapi	212.4	16.4	161943	5	HS84M10	Homo sapi
C 149	214.4	16.6	164953	5	AC016252	Homo sapi	212.4	16.4	164953	5	AC016252	Homo sapi	212.4	16.4	164953	5	AC016252	Homo sapi
C 150	214.4	16.6	170944	5	AC093484	Homo sapi	212.4	16.4	170944	5	AC093484	Homo sapi	212.4	16.4	170944	5	AC093484	Homo sapi
C 151	214.4	16.6	181907	12	AC108731	Homo sapi	212.4	16.4	181907	12	AC108731	Homo sapi	212.4	16.4	181907	12	AC108731	Homo sapi
C 152	214.4	16.6	183925	12	AC078870	Homo sapi	212.4	16.4	183925	12	AC078870	Homo sapi	212.4	16.4	183925	12	AC078870	Homo sapi
C 153	214.4	16.6	186787	5	AC010267	Homo sapi	212.4	16.4	186787	5	AC010267	Homo sapi	212.4	16.4	186787	5	AC010267	Homo sapi
C 154	214.4	16.6	192307	5	AC005971	Homo sapi	212.4	16.4	192307	5	AC005971	Homo sapi	212.4	16.4	192307	5	AC005971	Homo sapi
C 155	214.4	16.6	202033	5	AC055822	Homo sapi	212.4	16.4	202033	5	AC055822	Homo sapi	212.4	16.4	202033	5	AC055822	Homo sapi
C 156	214.4	16.6	222871	12	AC108094	Homo sapi	212.4	16.4	222871	12	AC108094	Homo sapi	212.4	16.4	222871	12	AC108094	Homo sapi
C 157	214.2	16.5	37790	2	CQ760559	Sequence	212.2	16.4	37790	2	CQ760559	Sequence	212.2	16.4	37790	2	CQ760559	Sequence
C 158	214.2	16.5	38166	2	CQ760560	Sequence	212.2	16.4	38166	2	CQ760560	Sequence	212.2	16.4	38166	2	CQ760560	Sequence
C 159	214.2	16.5	97375	5	AL353898	Human DNA	212.2	16.4	97375	5	AL353898	Human DNA	212.2	16.4	97375	5	AL353898	Human DNA
C 160	214.2	16.5	162609	5	AC108022	Homo sapi	212.2	16.4	162609	5	AC108022							

c 238	c 212	16.4	173185	5	AP004606	AP004606 Homo sapi
c 239	c 212	16.4	176018	12	AC157755	AC157755 Pan trogl
c 240	c 212	16.4	179285	5	BS000229	BS000229 Pan trogl
c 241	c 212	16.4	190537	12	AC1010757	AC1010757 Homo sapi
c 242	c 212	16.4	192336	5	AL158155	AL158155 Human DNA
c 243	c 212	16.4	204662	5	CNS01RHQ	CNS01RHQ Human chr
c 244	c 212	16.4	216129	12	AC157530	AC157530 Pan trogl
c 245	c 211.8	16.4	38968	5	AC000075	AC000075 Homo sapi
c 246	c 211.8	16.4	145340	5	AL136525	AL136525 Human DNA
c 247	c 211.8	16.4	159704	5	AC106000	AC106000 Homo sapi
c 248	c 211.8	16.4	172256	12	AC051637	AC051637 Homo sapi
c 249	c 211.8	16.4	184523	5	AC087279	AC087279 Homo sapi
c 250	c 211.8	16.4	205463	5	AL355388	AL355388 Human DNA
c 251	c 211.6	16.3	109409	12	AC021869	AC021869 Homo sapi
c 252	c 211.6	16.3	156692	5	CNS05TBZ	CNS05TBZ Human chr
c 253	c 211.6	16.3	171951	5	CNS05TDA	CNS05TDA Human chr
c 254	c 211.6	16.3	181297	12	AC020675	AC020675 Homo sapi
c 255	c 211.6	16.3	181625	5	AC113211	AC113211 Homo sapi
c 256	c 211.6	16.3	192881	5	AC067923	AC067923 Homo sapi
c 257	c 211.4	16.3	830	7	BV468993	BV468993 G591P6062
c 258	c 211.4	16.3	3938	5	BC059174	BC059174 Homo sapi
c 259	c 211.4	16.3	37590	2	AX252460	AX252460 Sequence
c 260	c 211.4	16.3	50502	5	HS44940A6	HS44940A6 Human DNA
c 261	c 211.4	16.3	114491	5	AC010331	AC010331 Homo sapi
c 262	c 211.4	16.3	127590	5	AC002554	AC002554 Human Chr
c 263	c 211.4	16.3	127591	12	AC124062	AC124062 Homo sapi
c 264	c 211.4	16.3	134350	5	AC004905	AC004905 Homo sapi
c 265	c 211.4	16.3	156598	12	AC012040	AC012040 Homo sapi
c 266	c 211.4	16.3	163964	5	AL356214	AL356214 Human DNA
c 267	c 211.4	16.3	167924	12	AC067891	AC067891 Homo sapi
c 268	c 211.4	16.3	186617	5	AC006487	AC006487 Homo sapi
c 269	c 211.2	16.3	43390	5	AC007191	AC007191 Homo sapi
c 270	c 211.2	16.3	44676	5	HSU9266	HSU9266 Human DNA s
c 271	c 211.2	16.3	132755	5	AC092536	AC092536 Homo sapi
c 272	c 211.2	16.3	159849	12	AC021454	AC021454 Homo sapi
c 273	c 211.2	16.3	160848	12	AC009647	AC009647 Homo sapi
c 274	c 211.2	16.3	171530	5	AC083870	AC083870 Homo sapi
c 275	c 211.2	16.3	185685	12	AC024283	AC024283 Homo sapi
c 276	c 211.2	16.3	197676	12	AC022544	AC022544 Homo sapi
c 277	c 211.2	16.3	220173	5	AC012183	AC012183 Homo sapi
c 278	c 211	16.3	36921	5	AC004185	AC004185 Homo sapi
c 279	c 211	16.3	62732	5	HS414D7	HS414D7 Human DNA
c 280	c 211	16.3	69495	5	BA0022539	BA0022539 Human DNA
c 281	c 211	16.3	110000	5	BA000025_07	Continuation (8 of
c 282	c 211	16.3	121659	5	CR388229	CR388229 Human DNA
c 283	c 211	16.3	148841	5	AC011462	AC011462 Homo sapi
c 284	c 211	16.3	152113	5	AL592285	AL592285 Human DNA
c 285	c 211	16.3	156539	5	AC091736	AC091736 Homo sapi
c 286	c 211	16.3	168887	5	AL662833	AL662833 Human DNA
c 287	c 211	16.3	187624	5	AC093768	AC093768 Homo sapi
c 288	c 211	16.3	191752	5	AL513475	AL513475 Human DNA
c 289	c 211	16.3	219447	5	HUMFLNG6PD	L44140 Homo sapien
c 290	c 211	16.3	236822	5	D84394	D84394 Homo sapien
c 291	c 211	16.3	349980	2	CS039419	CS039419 Sequence
c 292	c 210.8	16.3	5191	2	AX926592	AX926592 Sequence
c 293	c 210.8	16.3	5191	2	AX926641	AX926641 Sequence
c 294	c 210.8	16.3	5906	5	AB011166	AB011166 Homo sapi
c 295	c 210.8	16.3	64000	5	AP002455	AP002455 Homo sapi
c 296	c 210.8	16.3	81490	5	AL590987	AL590987 Human DNA
c 297	c 210.8	16.3	94359	5	AP000974	AP000974 Homo sapi
c 298	c 210.8	16.3	117489	5	AC005628	AC005628 Homo sapi
c 299	c 210.8	16.3	121856	12	AC022575	AC022575 Homo sapi
c 300	c 210.8	16.3	135810	5	AC023992	AC023992 Homo sapi
c 301	c 210.8	16.3	136911	12	AL135843	AL135843 Homo sapi
c 302	c 210.8	16.3	141168	12	AC147432	AC147432 Pan trogl
c 303	c 210.8	16.3	161572	5	AC106897	AC106897 Homo sapi
c 304	c 210.8	16.3	165230	5	AL158067	AL158067 Human DNA
c 305	c 210.8	16.3	167631	12	AC016032	AC016032 Homo sapi
c 306	c 210.8	16.3	168113	5	BX664608	BX664608 Human DNA
c 307	c 210.8	16.3	168117	12	BX664620	BX664620 Homo sapi
c 308	c 210.8	16.3	169752	5	CR788261	CR788261 Human DNA
c 309	c 210.8	16.3	175120	5	AC004687	AC004687 Homo sapi
c 310	c 210.8	16.3	178657	12	AC022845	AC022845 Homo sapi
c 311	c 210.8	16.3	182427	5	AL162390	AL162390 Human DNA
c 312	c 210.8	16.3	195760	12	AC016486	AC016486 Homo sapi
c 313	c 210.6	16.3	22996	5	AC087175	AC087175 Homo sapi
c 314	c 210.6	16.3	63705	5	AF135419	AF135419 sHomo sap
c 315	c 210.6	16.3	110000	5	AB128049	AB128049 Macaca mu
c 316	c 210.6	16.3	134826	5	AL158210	AL158210 Human DNA
c 317	c 210.6	16.3	150647	12	AF311104	AF311104 Homo sapi
c 318	c 210.6	16.3	154179	5	AC087533	AC087533 Homo sapi
c 319	c 210.6	16.3	163997	5	AC022731	AC022731 Homo sapi
c 320	c 210.6	16.3	166310	5	AC171180	AC171180 Pan trogl
c 321	c 210.6	16.3	182504	12	AC019180	AC019180 Homo sapi
c 322	c 210.6	16.3	182826	5	AC148688	AC148688 Macaca mu
c 323	c 210.6	16.3	184511	12	AC011721	AC011721 Homo sapi
c 324	c 210.6	16.3	196349	12	AC022032	AC022032 Homo sapi
c 325	c 210.6	16.3	205638	5	AC009634	AC009634 Homo sapi
c 326	c 210.4	16.2	150401	12	AC079980	AC079980 Homo sapi
c 327	c 210.4	16.2	167259	12	AL591407	AL591407 Homo sapi
c 328	c 210.4	16.2	183914	12	AC069331	AC069331 Homo sapi
c 329	c 210.4	16.2	185323	12	AC009799	AC009799 Homo sapi
c 330	c 210.4	16.2	185644	5	AC087455	AC087455 Homo sapi
c 331	c 210.4	16.2	193319	5	AL158154	AL158154 Human DNA
c 332	c 210.4	16.2	193681	5	AC069382	AC069382 Homo sapi
c 333	c 210.4	16.2	194264	5	AL356956	AL356956 Human DNA
c 334	c 210.4	16.2	199289	5	AC012378	AC012378 Homo sapi
c 335	c 210.4	16.2	202563	5	AC021192	AC021192 Homo sapi
c 336	c 210.4	16.2	229379	5	AC010746	AC010746 Homo sapi
c 337	c 210.4	16.2	315681	12	AL355380	AL355380 Homo sapi
c 338	c 210.2	16.2	32289	5	HSU73628	HSU73628 Human chrom
c 339	c 210.2	16.2	56827	5	HSMHCA35	HSMHCA35 Homo sapien
c 340	c 210.2	16.2	83550	5	AF312912	AF312912 Homo sapi
c 341	c 210.2	16.2	102588	5	BX927239	BX927239 Human DNA
c 342	c 210.2	16.2	105104	5	HSJ47A17	HSJ47A17 Human DNA
c 343	c 210.2	16.2	110000	12	AC091528	AC091528 Homo sapi
c 344	c 210.2	16.2	128978	2	CQ861712	CQ861712 Sequence
c 345	c 210.2	16.2	128978	5	AC002073	AC002073 Human PAC
c 346	c 210.2	16.2	131870	12	CR933858	CR933858 Homo sapi
c 347	c 210.2	16.2	135934	12	AC018925	AC018925 Homo sapi
c 348	c 210.2	16.2	140489	12	AC023066	AC023066 Homo sapi
c 349	c 210.2	16.2	142726	5	AC104836	AC104836 Homo sapi
c 350	c 210.2	16.2	150140	12	AC005478	AC005478 Homo sapi
c 351	c 210.2	16.2	162274	12	AC013819	AC013819 Homo sapi
c 352	c 210.2	16.2	162603	12	AC073303	AC073303 Homo sapi
c 353	c 210.2	16.2	166563	5	AL358949	AL358949 Human DNA
c 354	c 210.2	16.2	172231	5	AC134775	AC134775 Homo sapi
c 355	c 210.2	16.2	172516	5	AC068457	AC068457 Homo sapi
c 356	c 210.2	16.2	174400	5	AC011603	AC011603 Homo sapi
c 357	c 210.2	16.2	184313	12	AC136509	AC136509 Pan trogl
c 358	c 210.2	16.2	193126	5	AC006045	AC006045 Homo sapi
c 359	c 210.2	16.2	349980	2	CS039422	CS039422 Sequence
c 360	c 210	16.2	64200	5	AC087691	AC087691 Homo sapi
c 361	c 210	16.2	77573	5	AY572796	AY572796 Homo sapi
c 362	c 210	16.2	94651	12	AL389882	AL389882 Homo sapi
c 363	c 210	16.2	149249	5	AC079945	AC079945 Homo sapi
c 364	c 210	16.2	152557	12	AC006078	AC006078 Homo sapi
c 365	c 210	16.2	153442	12	AC091101	AC091101 Homo sapi
c 366	c 210	16.2	167344	5	CNS01DSD	AL121769 Human Chr
c 367	c 210	16.2	170815	12	AC004127	AC004127 Homo sapi
c 368	c 210	16.2	174612	5	AC018494	AC018494 Homo sapi
c 369	c 210	16.2	177834	5	AC018811	AC018811 Homo sapi
c 370	c 210	16.2	178780	5	AC069302	AC069302 Homo sapi
c 371	c 210	16.2	185979	5	AC091296	AC091296 Pan trogl
c 372	c 210	16.2	188679	12	AC023121	AC023121 Homo sapi
c 373	c 210	16.2	203748	12	AC069250	AC069250 Homo sapi
c 374	c 210	16.2	211937	5	AP003064	AP003064 Homo sapi
c 375	c 210	16.2	215150	12	AC116438	AC116438 Pan trogl
c 376	c 209.8	16.2	26078	5	AF376770	AF376770 Homo sapi
c 377	c 209.8	16.2	29748	5	HSJ1908A	HSJ1908A s
c 378	c 209.8	16.2	53025	5	AC118458	AC118458 Homo sapi
c 379	c 209.8	16.2	137113	5	AC076966	AC076966 Homo sapi
c 380	c 209.8	16.2	140974	5	AC068533	AC068533 Homo sapi
c 381	c 209.8	16.2	148781	5	AC007114	AC007114 Homo sapi
c 382	c 209.8	16.2	152426	5	AC145724	AC145724 Pan trogl
c 383	c 209.8	16.2	156961	5	AC015592	AC015592 Homo sapi

384	209.8	16.2	177571	12	AC022567	AC022567 Homo sapi	C 457	209	16.1	31059	5	AC009005	AC009005 Homo sapi
385	209.8	16.2	178262	12	AC061974	AC061974 Homo sapi	C 458	209	16.1	32074	5	AC011556	AC011556 Homo sapi
386	209.8	16.2	179383	12	AC060789	AC060789 Homo sapi	C 459	209	16.1	61412	12	AC106026	AC106026 Homo sapi
387	209.8	16.2	194241	12	AC093324	AC093324 Homo sapi	460	209	16.1	65900	5	EX005209	EX005209 Human DNA
388	209.8	16.2	202540	5	AC002524	AC002524 Homo sapi	461	209	16.1	67519	5	AL138788	AL138788 Human DNA
389	209.8	16.2	216457	5	CNS01RG1	AL157689 Human chr	462	209	16.1	89817	5	AC005876	AC005876 citb.188
390	209.8	16.2	227079	12	AC138431	AC138431 Homo sapi	463	209	16.1	102782	5	CR759815	CR759815 Human DNA
391	209.6	16.2	59776	5	AC098831	AC098831 Homo sapi	C 464	209	16.1	104564	5	AC112502	AC112502 Homo sapi
392	209.6	16.2	100000	5	AP000151	AP000151 Homo sapi	C 465	209	16.1	111779	5	AL159988	AL159988 Human DNA
393	209.6	16.2	102247	5	AP001432	AP001432 Homo sapi	C 466	209	16.1	119184	5	EX248098	EX248098 Human DNA
394	209.6	16.2	138517	5	AC019288	AC019288 Homo sapi	C 467	209	16.1	145340	5	AL136525	AL136525 Human DNA
395	209.6	16.2	145050	5	AC021078	AC021078 Homo sapi	C 468	209	16.1	155643	5	AC104620	AC104620 Homo sapi
396	209.6	16.2	145456	5	AL513366	AL513366 Human DNA	C 469	209	16.1	157893	5	EX664609	EX664609 Human DNA
397	209.6	16.2	150482	2	CS086329	CS086329 Sequence	C 470	209	16.1	169173	5	AL627311	AL627311 Human DNA
398	209.6	16.2	152345	5	AP000009	AP000009 Homo sapi	C 471	209	16.1	171508	12	AC093007	AC093007 Homo sapi
399	209.6	16.2	155559	12	AL133336	AL133336 Homo sapi	C 472	209	16.1	172200	12	AC022626	AC022626 Homo sapi
400	209.6	16.2	169620	12	AC012674	AC012674 Homo sapi	C 473	209	16.1	182020	5	AC113170	AC113170 Homo sapi
401	209.6	16.2	170121	5	AF064860	AF064860 Homo sapi	C 474	209	16.1	191668	12	CR759969	CR759969 Homo sapi
402	209.6	16.2	171813	12	AC022722	AC022722 Homo sapi	C 475	209	16.1	194799	5	AC006430	AC006430 Homo sapi
403	209.6	16.2	176036	2	CS086330	CS086330 Sequence	C 476	209	16.1	200368	5	CNS01DUH	AL133244 BAC reque
404	209.6	16.2	177322	5	AC022168	AC022168 Homo sapi	C 477	209	16.1	292420	12	AC020873	AC020873 Mus muscu
405	209.6	16.2	177831	5	AP000925	AP000925 Homo sapi	C 478	209	16.1	321519	12	AL714004	AL714004 Homo sapi
406	209.6	16.2	181833	5	CNS05TEN	AL159236 Human chr	C 479	208.8	16.1	9912	5	AL159177	AL159177 Human DNA
407	209.6	16.2	183995	5	AC018463	AC018463 Homo sapi	C 480	208.8	16.1	43337	5	DQ196343	DQ196343 Homo sapi
408	209.6	16.2	184762	12	AC023500	AC023500 Homo sapi	C 481	208.8	16.1	102112	5	AC005231	AC005231 Homo sapi
409	209.6	16.2	191563	5	CNS01DXG	AL139300 Human chr	C 482	208.8	16.1	116503	5	CNS05TBS	AL163973 Human chr
410	209.6	16.2	193159	12	AP001282	AP001282 Homo sapi	C 483	208.8	16.1	146206	5	AC026800	AC026800 Homo sapi
411	209.6	16.2	340000	5	AP001728	AP001728 Homo sapi	C 484	208.8	16.1	152765	12	AC008566	AC008566 Homo sapi
412	209.6	16.2	340000	5	HS21C080	AL163280 Homo sapi	C 485	208.8	16.1	157481	5	AC093512	AC093512 Homo sapi
413	209.4	16.2	10276	5	AY766122	AY766122 Homo sapi	C 486	208.8	16.1	157722	5	AL356154	AL356154 Human DNA
414	209.4	16.2	51447	5	AL445567	AL445567 Human DNA	C 487	208.8	16.1	174913	5	AL158819	AL158819 Human DNA
415	209.4	16.2	55965	5	AC104653	AC104653 Homo sapi	C 488	208.8	16.1	175144	12	AC010415	AC010415 Homo sapi
416	209.4	16.2	64432	12	AL513183	AL513183 Homo sapi	C 489	208.8	16.1	175689	5	AC148703	AC148703 Macaca mu
417	209.4	16.2	100374	5	HS193B12	Z98744 Human DNA s	C 490	208.8	16.1	185061	12	AC062024	AC062024 Homo sapi
418	209.4	16.2	102008	12	AC016552	AC016552 Homo sapi	C 491	208.8	16.1	188967	5	AC087521	AC087521 Homo sapi
419	209.4	16.2	124940	5	HS162E17	AL160492 Homo sapi	C 492	208.8	16.1	191681	12	AC079210	AC079210 Homo sapi
420	209.4	16.2	134960	12	AP002337	AP002337 Homo sapi	C 493	208.8	16.1	192568	12	AC068289	AC068289 Homo sapi
421	209.4	16.2	137233	12	AC090271	AC090271 Homo sapi	C 494	208.8	16.1	202513	5	AC148702	AC148702 Macaca mu
422	209.4	16.2	149157	5	AC004448	AC004448 Homo sapi	C 495	208.8	16.1	217221	5	AC008682	AC008682 Homo sapi
423	209.4	16.2	153185	12	AC073228	AC073228 Homo sapi	C 496	208.6	16.1	682	5	HSU05037	HSU0537 Human BRCA2
424	209.4	16.2	158109	5	AC114321	AC114321 Homo sapi	C 497	208.6	16.1	9391	5	AP000306	AP000306 Homo sapi
425	209.4	16.2	159167	12	AC025745	AC025745 Homo sapi	C 498	208.6	16.1	34149	5	DQ007053	DQ007053 Homo sapi
426	209.4	16.2	162554	5	AC079354	AC079354 Homo sapi	C 499	208.6	16.1	50188	5	AP000047	AP000047 Homo sapi
427	209.4	16.2	162936	12	AL391359	AL391359 Homo sapi	C 500	208.6	16.1	86372	12	AC139423	AC139423 Homo sapi
428	209.4	16.2	168565	5	AP003419	AP003419 Homo sapi	C 501	208.6	16.1	88761	5	AL161643	AL161643 Human DNA
429	209.4	16.2	169144	12	AC005849	AC005849 Homo sapi	C 502	208.6	16.1	98305	12	AP000685	AP000685 Homo sapi
430	209.4	16.2	178653	12	AC090088	AC090088 Homo sapi	C 503	208.6	16.1	100000	5	AP000115	AP000115 Homo sapi
431	209.4	16.2	178982	5	AP001591	AP001591 Homo sapi	C 504	208.6	16.1	100000	5	AP000191	AP000191 Homo sapi
432	209.4	16.2	184057	5	AP000753	AP000753 Homo sapi	C 505	208.6	16.1	103327	5	AL662830	AL662830 Human DNA
433	209.4	16.2	184059	12	AC090382	AC090382 Homo sapi	C 506	208.6	16.1	112224	5	HS423B22	AL034379 Human DNA
434	209.4	16.2	195101	5	AC110615	AC110615 Homo sapi	C 507	208.6	16.1	134278	5	AP001822	AP001822 Homo sapi
435	209.4	16.2	197837	5	AC093107	AC093107 Homo sapi	C 508	208.6	16.1	143216	5	AC006358	AC006358 Homo sapi
436	209.4	16.2	199321	5	AP0000941	AP0000941 Homo sapi	C 509	208.6	16.1	147419	5	HS738P11	AL031736 Human DNA
437	209.4	16.2	204298	5	AL662844	AL662844 Human DNA	C 510	208.6	16.1	149843	5	AP0000892	AP0000892 Homo sapi
438	209.4	16.2	244525	5	AC008499	AC008499 Homo sapi	C 511	208.6	16.1	153023	12	AL355880	AL355880 Homo sapi
439	209.4	16.2	235808	12	AC151867	AC151867 Callithri	C 512	208.6	16.1	154179	5	AC087533	AC087533 Homo sapi
440	209.2	16.2	7350	5	AB209689	AB209689 Homo sapi	C 513	208.6	16.1	160169	12	AC051664	AC051664 Homo sapi
441	209.2	16.2	91672	5	AC006468	AC006468 Homo sapi	C 514	208.6	16.1	162510	12	AP000761	AP000761 Homo sapi
442	209.2	16.2	116236	5	AC099677	AC099677 Homo sapi	C 515	208.6	16.1	165576	12	AC084867	AC084867 Homo sapi
443	209.2	16.2	120038	5	AC020551	AC020551 Homo sapi	C 516	208.6	16.1	168867	5	AP003733	AP003733 Homo sapi
444	209.2	16.2	122103	5	HS291J10	Z93017 Human DNA s	C 517	208.6	16.1	168499	5	AC092037	AC092037 Homo sapi
445	209.2	16.2	139953	5	HSBA504H3	AL121585 Human DNA	C 518	208.6	16.1	173769	5	AC113933	AC113933 Homo sapi
446	209.2	16.2	142728	5	HSJD792G4	AL049636 Human DNA	C 519	208.6	16.1	184433	12	AC108479	AC108479 Homo sapi
447	209.2	16.2	156394	12	AC026558	AC026558 Homo sapi	C 520	208.6	16.1	190856	12	AC009160	AC009160 Homo sapi
448	209.2	16.2	158250	5	AC020781	AC020781 Homo sapi	C 521	208.6	16.1	199892	12	AC020997	AC020997 Homo sapi
449	209.2	16.2	170237	12	AC142285	AC142285 Pan trogl	C 522	208.6	16.1	205638	5	AC009634	AC009634 Homo sapi
450	209.2	16.2	170892	12	AC068438	AC068438 Homo sapi	C 523	208.6	16.1	213942	5	AC099790	AC099790 Homo sapi
451	209.2	16.2	174018	12	AL445311	AL445311 Homo sapi	C 524	208.6	16.1	340000	5	AP001717	AP001717 Homo sapi
452	209.2	16.2	190185	5	AC026464	AC026464 Homo sapi	C 525	208.4	16.1	1323	5	BC038742	BC038742 Homo sapi
453	209.2	16.2	219428	5	AC159020	AC159020 Pan trogl	C 526	208.4	16.1	19654	5	D86566	D86566 Homo sapien
454	209.2	16.2	230711	12	AC146492	AC146492 Gorilla g	C 527	208.4	16.1	36542	5	AC006117	AC006117 Homo sapi
455	209.2	16.2	249140	12	AC136952	AC136952 Danio rer	C 528	208.4	16.1	38852	5	AC006261	AC006261 Homo sapi
456	209	16.1	2822	5	AK055193	AK055193 Homo sapi	C 529	208.4	16.1	48217	5	AC073932	AC073932 Homo sapi

c 530	308.4	16.1	75663	5	AC068987	AC068987 Homo sapi	c 603	208	16.1	166164	12	CT009522	CT009522 Homo sapi
c 531	208.4	16.1	102907	5	CR933878	CR933878 Human DNA	c 604	208	16.1	169553	5	AL145821	AL145821 Papio anu
c 532	208.4	16.1	108822	5	AC004968	AC004968 Homo sapi	c 605	208	16.1	173828	5	AL592504	AL592504 Human DNA
c 533	208.4	16.1	108994	5	HS124K22	AL031176 Human DNA	c 606	208	16.1	174487	5	AC073896	AC073896 Homo sapi
c 534	208.4	16.1	126404	5	AL845509	AL845509 Human DNA	c 607	208	16.1	181140	5	AP002793	AP002793 Homo sapi
c 535	208.4	16.1	145476	12	AC044911	AC044911 Homo sapi	c 608	208	16.1	182197	12	AC022422	AC022422 Homo sapi
c 536	208.4	16.1	150213	12	AC013800	AC013800 Homo sapi	c 609	208	16.1	186011	12	AC079461	AC079461 Homo sapi
c 537	208.4	16.1	157244	5	AP005204	AP005204 Homo sapi	c 610	208	16.1	186210	5	AC007596	AC007596 Homo sapi
c 538	208.4	16.1	158256	5	AC009024	AC009024 Homo sapi	c 611	208	16.1	209355	12	AL645762	AL645762 Homo sapi
c 539	208.4	16.1	163816	5	AC012308	AC012308 Homo sapi	c 612	207.8	16.0	2086	5	AY181059	AY181059 Pongo pyg
c 540	208.4	16.1	169950	12	AC084049	AC084049 Homo sapi	c 613	207.8	16.0	63916	5	HS69811	AL021397 Human DNA
c 541	208.4	16.1	173738	12	AC069293	AC069293 Homo sapi	c 614	207.8	16.0	85151	5	AL596219	AL596219 Human DNA
c 542	208.4	16.1	174933	5	AC009087	AC009087 Homo sapi	c 615	207.8	16.0	99876	5	HS090108	AL078461 Human DNA
c 543	208.4	16.1	175982	12	AC113210	AC113210 Homo sapi	c 616	207.8	16.0	100580	5	BS000235	BS000235 Pan trogl
c 544	208.4	16.1	179040	12	AC022732	AC022732 Homo sapi	c 617	207.8	16.0	103343	5	AC108078	AC108078 Homo sapi
c 545	208.4	16.1	184945	5	AC099314	AC099314 Homo sapi	c 618	207.8	16.0	112846	5	AC004991	AC004991 Homo sapi
c 546	208.4	16.1	194578	12	AC007832	AC007832 Homo sapi	c 619	207.8	16.0	129592	12	AC170060	AC170060 Callicebu
c 547	208.4	16.1	197140	5	AC145966	AC145966 Pan trogl	c 620	207.8	16.0	136002	5	AL450426	AL450426 Human DNA
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c 549	208.4	16.1	210344	5	AC099850	AC099850 Homo sapi	c 622	207.8	16.0	148891	5	AL162274	AL162274 Human DNA
c 550	208.4	16.1	226147	5	AP002478	AP002478 Homo sapi	c 623	207.8	16.0	150294	5	AC091748	AC091748 Homo sapi
c 551	208.4	16.1	237855	12	AL391558	AL391558 Homo sapi	c 624	207.8	16.0	152918	12	AC153734	AC153734 Pan trogl
c 552	208.2	16.1	643	7	BV564665	BV564665 qpz69f06	c 625	207.8	16.0	155515	2	CS200161	CS200161 Sequence
c 553	208.2	16.1	716	7	BV593629	BV593629 G591P5583	c 626	207.8	16.0	156300	5	AC026620	AC026620 Homo sapi
c 554	208.2	16.1	958	7	BV574221	BV574221 G591P6033	c 627	207.8	16.0	157348	5	AC084757	AC084757 Homo sapi
c 555	208.2	16.1	22838	5	AL354792	AL354792 Human DNA	c 628	207.8	16.0	159497	2	CS200180	CS200180 Sequence
c 556	208.2	16.1	35475	5	AP003114	AP003114 Homo sapi	c 629	207.8	16.0	159660	2	CS200162	CS200162 Sequence
c 557	208.2	16.1	58846	5	BX470206	BX470206 Human DNA	c 630	207.8	16.0	160456	5	BS000236	BS000236 Pan trogl
c 558	208.2	16.1	80743	5	AL162402	AL162402 Human DNA	c 631	207.8	16.0	166914	5	AC127522	AC127522 Homo sapi
c 559	208.2	16.1	95388	12	CR762464	CR762464 Homo sapi	c 632	207.8	16.0	167686	12	AC149260	AC149260 Papio anu
c 560	208.2	16.1	95556	5	CR752645	CR752645 Human DNA	c 633	207.8	16.0	169598	5	AC087650	AC087650 Homo sapi
c 561	208.2	16.1	105118	5	AC019127	AC019127 Homo sapi	c 634	207.8	16.0	171976	5	AP003069	AP003069 Homo sapi
c 562	208.2	16.1	110000	12	AC055726_2	Continuation (3 of	c 635	207.8	16.0	172657	5	AC004386	AC004386 Homo sapi
c 563	208.2	16.1	112063	5	AC091485	AC091485 Homo sapi	c 636	207.8	16.0	172792	5	AL391684	AL391684 Human DNA
c 564	208.2	16.1	113681	5	HS1141E15	AL034422 Human DNA	c 637	207.8	16.0	173364	12	AC009807	AC009807 Homo sapi
c 565	208.2	16.1	122553	12	CR753417	CR753417 Homo sapi	c 638	207.8	16.0	174342	12	AC016901	AC016901 Homo sapi
c 566	208.2	16.1	126253	5	AP002023	AP002023 Homo sapi	c 639	207.8	16.0	174520	5	BS000234	BS000234 Pan trogl
c 567	208.2	16.1	127188	12	AC005063	AC005063 Homo sapi	c 640	207.8	16.0	176524	5	AC010726	AC010726 Homo sapi
c 568	208.2	16.1	149866	5	AC025627	AC025627 Homo sapi	c 641	207.8	16.0	176550	12	AC021852	AC021852 Homo sapi
c 569	208.2	16.1	150005	5	AL450344	AL450344 Human DNA	c 642	207.8	16.0	177623	2	CS200160	CS200160 Sequence
c 570	208.2	16.1	154413	5	AC021989	AC021989 Homo sapi	c 643	207.8	16.0	180835	5	AC009131	AC009131 Homo sapi
c 571	208.2	16.1	159123	5	AC007739	AC007739 Homo sapi	c 644	207.8	16.0	181948	12	AC169003	AC169003 Callicebu
c 572	208.2	16.1	161090	5	AC117415	AC117415 Homo sapi	c 645	207.8	16.0	184841	12	AC129486	AC129486 Homo sapi
c 573	208.2	16.1	163157	5	AC108670	AC108670 Homo sapi	c 646	207.8	16.0	186152	12	AC130358	AC130358 Homo sapi
c 574	208.2	16.1	165909	12	AC079152	AC079152 Homo sapi	c 647	207.8	16.0	190152	12	AC149183	AC149183 Papio anu
c 575	208.2	16.1	165982	12	AC163241	AC163241 Callicebu	c 648	207.8	16.0	192583	12	AC015941	AC015941 Homo sapi
c 576	208.2	16.1	170954	12	AC164658	AC164658 Pan trogl	c 649	207.8	16.0	194973	5	AC024474	AC024474 Homo sapi
c 577	208.2	16.1	171116	12	AC164943	AC164943 Callicebu	c 650	207.8	16.0	203518	12	AC149169	AC149169 Papio anu
c 578	208.2	16.1	173933	5	AP002022	AP002022 Homo sapi	c 651	207.8	16.0	209751	5	AC087645	AC087645 Homo sapi
c 579	208.2	16.1	175361	12	AL390843	AL390843 Homo sapi	c 652	207.8	16.0	270105	12	AC099650	AC099650 Homo sapi
c 580	208.2	16.1	186010	12	AC073083	AC073083 Homo sapi	c 653	207.6	16.0	748	7	BV595402	BV595402 S215P6101
c 581	208.2	16.1	186864	5	AC023050	AC023050 Homo sapi	c 654	207.6	16.0	1976	5	AK130645	AK130645 Homo sapi
c 582	208.2	16.1	188818	12	AC098674	AC098674 Homo sapi	c 655	207.6	16.0	39338	5	AC004644	AC004644 Homo sapi
c 583	208.2	16.1	193580	12	CR751222	CR751222 Homo sapi	c 656	207.6	16.0	68883	5	AL390242	AL390242 Human DNA
c 584	208.2	16.1	208642	5	HSAS08N32	AL117339 Human DNA	c 657	207.6	16.0	75335	5	HS107715	AL034394 Human DNA
c 585	208	16.1	53962	5	AC009246	AC009246 Homo sapi	c 658	207.6	16.0	77498	5	AL162505	AL162505 Human DNA
c 586	208	16.1	63601	5	AC080135	AC080135 Homo sapi	c 659	207.6	16.0	84495	2	AR366536	AR366536 Sequence
c 587	208	16.1	67131	5	CR752644	CR752644 Human DNA	c 660	207.6	16.0	93276	5	AL139124	AL139124 Human DNA
c 588	208	16.1	76850	5	AC003109	AC003109 Human DNA	c 661	207.6	16.0	93342	5	AC087245	AC087245 Homo sapi
c 589	208	16.1	83030	5	AC004814	AC004814 Homo sapi	c 662	207.6	16.0	98271	5	AL162590	AL162590 Human DNA
c 590	208	16.1	87424	5	AC006077	AC006077 Homo sapi	c 663	207.6	16.0	126039	5	AC012665	AC012665 Homo sapi
c 591	208	16.1	88698	12	AC009008	AC009008 Homo sapi	c 664	207.6	16.0	134357	12	AC074127	AC074127 Human DNA
c 592	208	16.1	102717	5	AC004079	AC004079 Homo sapi	c 665	207.6	16.0	135209	5	HS42616	AL020997 Human DNA
c 593	208	16.1	109699	5	AL359973	AL359973 Human DNA	c 666	207.6	16.0	144832	12	AC009555	AC009555 Homo sapi
c 594	208	16.1	128899	5	AL391139	AL391139 Human DNA	c 667	207.6	16.0	150192	5	AC008686	AC008686 Homo sapi
c 595	208	16.1	133925	5	AC011444	AC011444 Homo sapi	c 668	207.6	16.0	151834	5	AC005399	AC005399 Homo sapi
c 596	208	16.1	144429	12	AC032017	AC032017 Homo sapi	c 669	207.6	16.0	154839	5	AP002993	AP002993 Homo sapi
c 597	208	16.1	153997	5	AC073348	AC073348 Homo sapi	c 670	207.6	16.0	156345	12	AC023015	AC023015 Homo sapi
c 598	208	16.1	154898	5	AC012119	AC012119 Homo sapi	c 671	207.6	16.0	160623	5	AL670296	AL670296 Human DNA
c 599	208	16.1	157546	5	AL953854	AL953854 Human DNA	c 672	207.6	16.0	165432	5	AC104810	AC104810 Homo sapi
c 600	208	16.1	161695	12	AC079849	AC079849 Homo sapi	c 673	207.6	16.0	165622	12	AC022902	AC022902 Homo sapi
c 601	208	16.1	162472	5	CNS01DUW	AL133371 Human chr	c 674	207.6	16.0	167116	5	AC009305	AC009305 Homo sapi
c 602	208	16.1	163915	12	AC087451	AC087451 Homo sapi	c 675	207.6	16.0	173520	12	AC160883	AC160883 Papio anu

C 676	207.6	16.0	173893	5	AC010150	AC010150 Homo sapi	749	207.2	16.0	210359	5	HS4430K20	AL121898 Human DNA
C 677	207.6	16.0	174758	12	AC149552	AC149552 Papio anu	750	207	16.0	1175	2	BD223169	BD223169 98 human
C 678	207.6	16.0	187779	5	AC091231	AC091231 Homo sapi	751	207	16.0	1175	2	AR243867	AR243867 Sequence
C 679	207.6	16.0	190814	5	AC006111	AC006111 Homo sapi	752	207	16.0	2649	2	CQ714142	CQ714142 Sequence
C 680	207.6	16.0	194916	5	AL138921	AL138921 Human DNA	753	207	16.0	2669	5	HSTRAXGEN	X59073 H.sapiens m
C 681	207.6	16.0	199928	5	AL138581	AL138581 Pan trogl	754	207	16.0	24360	5	AF271267S3	AF271269 Homo sapi
C 682	207.6	16.0	202768	12	AC092345	AC092345 Homo sapi	755	207	16.0	37323	5	CR856018	CR856018 Human DNA
C 683	207.6	16.0	207516	5	AC097108	AC097108 Homo sapi	756	207	16.0	48610	5	AL606501	AL606501 Human DNA
C 684	207.6	16.0	220480	12	AC023973	AC023973 Homo sapi	C 757	207	16.0	69203	5	AL626763	AL626763 Human DNA
C 685	207.6	16.0	349980	2	CS039422	CS039422 Sequence	C 758	207	16.0	80796	5	AC073136	AC073136 Homo sapi
C 686	207.4	16.0	766	7	BV673576	BV673576 S215P6092	C 759	207	16.0	84731	12	AC068885	AC068885 Homo sapi
C 687	207.4	16.0	38679	5	AL390034	AL390034 Human DNA	C 760	207	16.0	109232	12	AL159157	AL159157 Homo sapi
C 688	207.4	16.0	93133	5	AC022140	AC022140 Homo sapi	C 761	207	16.0	900170	5	AL161743	AL161743 Human DNA
C 689	207.4	16.0	96075	5	AL590639	AL590639 Human DNA	C 762	207	16.0	107652	5	HSBJ259N9	AL078477 Human DNA
C 690	207.4	16.0	104895	12	AC093288	AC093288 Homo sapi	C 763	207	16.0	111864	12	AL1339687	AC139687 Homo sapi
C 691	207.4	16.0	110000	12	AC049982_1	Continuation (2 of	C 764	207	16.0	117890	5	AL133466	AL133466 Human DNA
C 692	207.4	16.0	117213	5	AC026779	AC026779 Homo sapi	C 765	207	16.0	128159	5	DQ314884	DQ314884 Homo sapi
C 693	207.4	16.0	123159	12	HSAC000384	AC000384 Homo sapi	C 766	207	16.0	137582	12	AC148726	AC148726 Pongo pyg
C 694	207.4	16.0	139484	5	AC040980	AC040980 Homo sapi	C 767	207	16.0	137883	5	CNS057DK	AL356802 Human chr
C 695	207.4	16.0	142085	12	AC036153	AC036153 Homo sapi	C 768	207	16.0	138391	12	AL357733	AL357733 Homo sapi
C 696	207.4	16.0	144771	12	AC018610	AC018610 Homo sapi	C 769	207	16.0	142067	5	BS3233860	BS3233860 Human DNA
C 697	207.4	16.0	144794	12	AP001182	AP001182 Homo sapi	C 770	207	16.0	146463	12	AC068306	AC068306 Homo sapi
C 698	207.4	16.0	155589	5	AC084879	AC084879 Homo sapi	C 771	207	16.0	153645	5	AC025426	AC025426 Homo sapi
C 699	207.4	16.0	157405	12	AP001315	AP001315 Homo sapi	C 772	207	16.0	153852	12	AC009694	AC009694 Homo sapi
C 700	207.4	16.0	158276	12	AC027709	AC027709 Homo sapi	C 773	207	16.0	158463	12	AC171645	AC171645 Macaca mu
C 701	207.4	16.0	161815	5	AC092015	AC092015 Homo sapi	C 774	207	16.0	161749	12	AL356745	AL356745 Homo sapi
C 702	207.4	16.0	162446	5	AC068776	AC068776 Homo sapi	C 775	207	16.0	163047	5	AP000889	AP000889 Homo sapi
C 703	207.4	16.0	164055	5	AC011387	AC011387 Homo sapi	C 776	207	16.0	163816	5	AC012308	AC012308 Homo sapi
C 704	207.4	16.0	164844	5	AC009058	AC009058 Homo sapi	C 777	207	16.0	167078	5	HSBJ139D8	AL096814 Human DNA
C 705	207.4	16.0	166870	5	CNS057BP	AL359238 Human chr	C 778	207	16.0	167587	5	AC108000	AC108000 Homo sapi
C 706	207.4	16.0	167473	12	AC148982	AC148982 Pan trogl	C 779	207	16.0	169125	5	AC126605	AC126605 Homo sapi
C 707	207.4	16.0	169250	5	AP002812	AP002812 Homo sapi	C 780	207	16.0	169612	12	AC027393	AC027393 Homo sapi
C 708	207.4	16.0	172004	5	AC008482	AC008482 Homo sapi	C 781	207	16.0	172437	12	AC022270	AC022270 Homo sapi
C 709	207.4	16.0	184521	5	AC164661	AC164661 Pan trogl	C 782	207	16.0	174028	12	AC087363	AC087363 Homo sapi
C 710	207.4	16.0	187824	5	AP001095	AP001095 Homo sapi	C 783	207	16.0	175106	12	AC011655	AC011655 Homo sapi
C 711	207.4	16.0	187824	5	AP001095	AP001095 Homo sapi	C 784	207	16.0	175310	5	AC135735	AC135735 Homo sapi
C 712	207.4	16.0	192203	5	AC034102	AC034102 Homo sapi	C 785	207	16.0	179544	5	AF015720	AF015720 Homo sapi
C 713	207.4	16.0	194615	12	AC024190	AC024190 Homo sapi	C 786	207	16.0	180430	5	AC096768	AC096768 Homo sapi
C 714	207.4	16.0	202041	12	AC007427	AC007427 Homo sapi	C 787	207	16.0	181714	12	AC090442	AC090442 Homo sapi
C 715	207.4	16.0	202041	12	AC007427	AC007427 Homo sapi	C 788	207	16.0	184050	12	AC087819	AC087819 Homo sapi
C 716	207.4	16.0	205954	5	AC008546	AC008546 Homo sapi	C 789	207	16.0	184444	12	AC090471	AC090471 Homo sapi
C 717	207.4	16.0	206777	12	AC153303	AC153303 Pan trogl	C 790	207	16.0	187712	5	AC027088	AC027088 Homo sapi
C 718	207.4	16.0	207785	5	AP001091	AP001091 Homo sapi	C 791	207	16.0	189036	12	AC019142	AC019142 Homo sapi
C 719	207.4	16.0	219122	5	AC080038	AC080038 Homo sapi	C 792	207	16.0	190015	5	AC087639	AC087639 Homo sapi
C 720	207.4	16.0	219574	5	AP002956	AP002956 Homo sapi	C 793	207	16.0	192197	12	AC145173	AC145173 Homo sapi
C 721	207.4	16.0	308232	12	AL392004	AL392004 Homo sapi	C 794	207	16.0	193680	5	AC127482	AC127482 Homo sapi
C 722	207.2	16.0	2303	5	AL138829	AL138829 Human DNA	C 795	207	16.0	215308	5	AC090469	AC090469 Homo sapi
C 723	207.2	16.0	35040	5	DQ086826	DQ086826 Homo sapi	C 796	207	16.0	218074	5	AC023283	AC023283 Homo sapi
C 724	207.2	16.0	62038	5	AC108469	AC108469 Homo sapi	C 797	207	16.0	228353	12	AL445283	AL445283 Homo sapi
C 725	207.2	16.0	104395	5	AC092469	AC092469 Homo sapi	C 798	207	16.0	248214	12	AL138811	AL138811 Homo sapi
C 726	207.2	16.0	111616	5	AL590652	AL590652 Human DNA	C 799	207	16.0	254112	12	CR762382	CR762382 Homo sapi
C 727	207.2	16.0	120166	5	AC091390	AC091390 Homo sapi	C 800	206.8	16.0	61528	5	AC114757	AC114757 Homo sapi
C 728	207.2	16.0	125108	5	AF030453	AF030453 Homo sapi	C 801	206.8	16.0	64271	12	AC025921	AC025921 Homo sapi
C 729	207.2	16.0	135734	12	AC002346	AC002346 Homo sapi	C 802	206.8	16.0	72000	5	AP002958	AP002958 Homo sapi
C 730	207.2	16.0	138675	5	HS1057820	AL109823 Human DNA	C 803	206.8	16.0	93119	5	AL451006	AL451006 Human DNA
C 731	207.2	16.0	139146	12	AC149227	AC149227 Pan trogl	C 804	206.8	16.0	102807	12	AP000674	AP000674 Homo sapi
C 732	207.2	16.0	141930	5	AC146389	AC146389 Pan trogl	C 805	206.8	16.0	104140	5	AC008122	AC008122 Homo sapi
C 733	207.2	16.0	143413	12	AC025979	AC025979 Homo sapi	C 806	206.8	16.0	106234	12	AY267352	AY267352 Homo sapi
C 734	207.2	16.0	146181	5	AP001269	AP001269 Homo sapi	C 807	206.8	16.0	110000	12	AC147308	AC147308 Pan trogl
C 735	207.2	16.0	158663	5	AC005088	AC005088 Homo sapi	C 808	206.8	16.0	111865	12	AL355883	AL355883 Homo sapi
C 736	207.2	16.0	164345	5	AC145994	AC145994 Pan trogl	C 809	206.8	16.0	119419	12	AP000666	AP000666 Homo sapi
C 737	207.2	16.0	165699	5	AL513023	AL513023 Human DNA	C 810	206.8	16.0	121450	12	AL355541	AL355541 Homo sapi
C 738	207.2	16.0	166802	12	AC016253	AC016253 Homo sapi	C 811	206.8	16.0	122228	5	AC000003	AC000003 Homo sapi
C 739	207.2	16.0	167627	5	AC079382	AC079382 Homo sapi	C 812	206.8	16.0	131664	12	AC018852	AC018852 Homo sapi
C 740	207.2	16.0	172931	5	AC006581	AC006581 Homo sapi	C 813	206.8	16.0	133814	12	AC027550	AC027550 Homo sapi
C 741	207.2	16.0	173239	5	AC016399	AC016399 Homo sapi	C 814	206.8	16.0	139493	12	AC018537	AC018537 Homo sapi
C 742	207.2	16.0	179673	5	AC026468	AC026468 Homo sapi	C 815	206.8	16.0	143039	5	AC016559	AC016559 Homo sapi
C 743	207.2	16.0	179993	12	AC015879	AC015879 Homo sapi	C 816	206.8	16.0	143516	5	AC083783	AC083783 Homo sapi
C 744	207.2	16.0	180157	5	AC015799	AC015799 Homo sapi	C 817	206.8	16.0	145100	12	AC024641	AC024641 Homo sapi
C 745	207.2	16.0	184144	5	AL451010	AL451010 Human DNA	C 818	206.8	16.0	145616	5	HS108K11	285986 Human DNA b
C 746	207.2	16.0	190430	12	AC118987	AC118987 Pan trogl	C 819	206.8	16.0	146096	12	AP001009	AP001009 Homo sapi
C 747	207.2	16.0	193456	12	AC149228	AC149228 Pan trogl	C 820	206.8	16.0	147434	12	AC027562	AC027562 Homo sapi
C 748	207.2	16.0	202874	5	AL389888	AL389888 Human DNA	C 821	206.8	16.0	148750	5	AL596225	AL596225 Human DNA

c 822	206.8	16.0	148833	5	AL159990	AL159990 Human DNA	895	206.6	16.0	139409	5	AC069181	Homo sapi
c 823	206.8	16.0	152395	5	AL161907	Human DNA	896	206.6	16.0	140092	5	AL162615	Human DNA
c 824	206.8	16.0	152709	5	AC027526	Homo sapi	897	206.6	16.0	145673	5	AC105755	Homo sapi
825	206.8	16.0	153367	12	AC011163	Homo sapi	898	206.6	16.0	150447	12	AL136222	Homo sapi
826	206.8	16.0	153733	12	AC011980	Homo sapi	899	206.6	16.0	150902	5	AC055736	Homo sapi
c 827	206.8	16.0	156591	12	AC024647	Homo sapi	900	206.6	16.0	151367	5	AC025750	Homo sapi
828	206.8	16.0	157677	12	AP002470	AP002470 Homo sapi	c 901	206.6	16.0	155537	5	AC130310	Homo sapi
c 829	206.8	16.0	158414	5	AC005940	Homo sapi	902	206.6	16.0	156100	12	AC011934	Homo sapi
c 830	206.8	16.0	159752	5	AC006480	Homo sapi	903	206.6	16.0	156312	5	AC138470	Homo sapi
c 831	206.8	16.0	159946	12	AC079194	Homo sapi	c 904	206.6	16.0	156321	2	CS162220	Sequence
c 832	206.8	16.0	161226	5	AP001619	AP001619 Homo sapi	c 905	206.6	16.0	156321	5	AC074331	Homo sapi
833	206.8	16.0	162081	5	AL139083	Human DNA	906	206.6	16.0	160854	5	AC110602	Homo sapi
834	206.8	16.0	163850	12	AC083785	Homo sapi	907	206.6	16.0	162617	5	AC007501	Homo sapi
835	206.8	16.0	164784	12	AP001384	Homo sapi	908	206.6	16.0	167132	5	AC069154	Homo sapi
836	206.8	16.0	165328	12	AC022185	Homo sapi	909	206.6	16.0	170723	5	AC013470	Homo sapi
837	206.8	16.0	165662	5	AC009930	Homo sapi	c 910	206.6	16.0	170769	5	AC009122	Homo sapi
838	206.8	16.0	166013	12	AC016328	Homo sapi	911	206.6	16.0	171962	12	AC013537	Homo sapi
c 839	206.8	16.0	167071	5	AC092380	Homo sapi	912	206.6	16.0	174656	12	AC019249	Homo sapi
c 840	206.8	16.0	168062	5	AL353768	Human DNA	913	206.6	16.0	175488	12	AC013556	Homo sapi
841	206.8	16.0	168367	5	AC104440	Homo sapi	c 914	206.6	16.0	176467	5	AC074349	Homo sapi
842	206.8	16.0	168420	12	AC096874	Pan trogl	c 915	206.6	16.0	176713	5	AP000751	Homo sapi
c 843	206.8	16.0	168738	5	AC012485	Homo sapi	916	206.6	16.0	176975	5	AC008050	Homo sapi
844	206.8	16.0	169770	5	AC027763	Homo sapi	c 917	206.6	16.0	178338	5	AL158068	Human DNA
c 845	206.8	16.0	170940	5	AC120042	Homo sapi	918	206.6	16.0	182878	12	AC169836	Macaca mu
846	206.8	16.0	172990	12	AC011973	Homo sapi	919	206.6	16.0	183607	5	AC066597	Homo sapi
847	206.8	16.0	173093	12	AC013579	Homo sapi	c 920	206.6	16.0	184116	5	AC181984	Pan trogl
848	206.8	16.0	173527	5	AC008756	Homo sapi	921	206.6	16.0	185708	5	AC108171	Homo sapi
c 849	206.8	16.0	174327	12	AL672191	Homo sapi	922	206.6	16.0	186330	5	AC007376	Homo sapi
c 850	206.8	16.0	174741	5	AC040977	Homo sapi	c 923	206.6	16.0	188065	12	AC018689	Homo sapi
851	206.8	16.0	179641	5	AC098591	Homo sapi	c 924	206.6	16.0	188741	5	AC002542	Homo sapi
c 852	206.8	16.0	180907	5	AL131157	Homo sapi	c 925	206.6	16.0	189048	5	AC090739	Homo sapi
853	206.8	16.0	182003	5	AL355987	Human DNA	c 926	206.6	16.0	190267	5	AP006285	Homo sapi
c 854	206.8	16.0	183099	12	AC034144	Homo sapi	c 927	206.6	16.0	191594	5	AC130462	Homo sapi
c 855	206.8	16.0	183451	5	AC005972	Homo sapi	c 928	206.6	16.0	192211	12	AC147239	Pan trogl
c 856	206.8	16.0	184402	12	AC158698	Pongo pyg	929	206.6	16.0	194832	5	AC025287	Homo sapi
857	206.8	16.0	185062	5	AC021231	Homo sapi	930	206.6	16.0	197168	12	AC055765	Homo sapi
858	206.8	16.0	185759	12	AC090201	Homo sapi	931	206.6	16.0	200771	12	AC133587	Homo sapi
c 859	206.8	16.0	185802	5	AC023881	Homo sapi	932	206.6	16.0	204182	12	AC097271	Pan trogl
c 860	206.8	16.0	185947	5	AC092630	Homo sapi	933	206.6	16.0	217456	5	AC068319	Homo sapi
c 861	206.8	16.0	187640	5	AC073840	Homo sapi	934	206.6	16.0	231260	12	AL160172	Homo sapi
862	206.8	16.0	190360	5	AP001924	Homo sapi	935	206.6	16.0	239333	12	AC090040	Homo sapi
c 863	206.8	16.0	190988	12	AC096876	Pan trogl	936	206.6	16.0	319064	12	CT009516	Homo sapi
c 864	206.8	16.0	191919	5	AC016770	Homo sapi	c 937	206.4	15.9	27740	2	AX695383	Sequence
c 865	206.8	16.0	191968	12	AC158414	Pongo pyg	c 938	206.4	15.9	37136	5	HSSRL9A13	Human DNA
c 866	206.8	16.0	194129	12	AC147063	Pan trogl	c 939	206.4	15.9	52550	5	CR759770	Human DNA
c 867	206.8	16.0	197811	12	AC009833	Homo sapi	c 940	206.4	15.9	55028	5	AC016473	Homo sapi
868	206.8	16.0	200207	12	AC007867	Homo sapi	c 941	206.4	15.9	77498	5	AL162505	Human DNA
c 869	206.8	16.0	202092	5	AL104946	Homo sapi	c 942	206.4	15.9	102684	5	BX000688	Human DNA
c 870	206.8	16.0	202565	5	AL354696	Human DNA	943	206.4	15.9	105335	5	AC107374	Homo sapi
c 871	206.8	16.0	203266	12	AC097006	Pan trogl	944	206.4	15.9	129806	5	AC006137	Homo sapi
c 872	206.8	16.0	207256	5	AC010321	Homo sapi	c 945	206.4	15.9	134292	5	HS271M21	Human DNA
873	206.8	16.0	210429	12	AC161100	Aotus nan	c 946	206.4	15.9	135325	5	AC073447	Homo sapi
c 874	206.8	16.0	211973	12	AP001163	Homo sapi	947	206.4	15.9	143104	5	AL606503	Human DNA
c 875	206.8	16.0	212357	12	AC009544	Homo sapi	c 948	206.4	15.9	145431	5	AL662826	Human DNA
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877	206.8	16.0	221535	5	AP001359	Homo sapi	950	206.4	15.9	151798	12	AC044819	Homo sapi
c 878	206.8	16.0	302921	12	AC090998	Homo sapi	c 951	206.4	15.9	153071	12	AC104155	Pan trogl
c 879	206.8	16.0	336578	5	AP001745	AP001745 Homo sapi	952	206.4	15.9	153454	12	AC122173	Pan trogl
880	206.6	16.0	710	7	BV631640	S215P6129	953	206.4	15.9	154904	5	AL162272	Human DNA
c 881	206.6	16.0	21111	5	AL592526	Human DNA	c 954	206.4	15.9	155874	5	AL645936	Human DNA
c 882	206.6	16.0	321178	5	AL606840	Human DNA	c 955	206.4	15.9	155948	5	BS000092	Pan trogl
883	206.6	16.0	60199	5	AC083883	Homo sapi	c 956	206.4	15.9	161053	5	AL356608	Human DNA
c 884	206.6	16.0	95571	5	AL354980	Human DNA	c 957	206.4	15.9	163332	5	AC004821	Homo sapi
885	206.6	16.0	107835	5	AL360298	Human DNA	c 958	206.4	15.9	163105	12	AC042420	Homo sapi
c 886	206.6	16.0	110000	12	AL831785 ⁴	Continuation (5 of	c 959	206.4	15.9	166684	5	AL161287	Pan trogl
887	206.6	16.0	110626	5	AC005541	Homo sapi	c 960	206.4	15.9	167292	5	AL157713	Human DNA
888	206.6	16.0	115932	5	HS1107	Human DNA	c 961	206.4	15.9	168863	5	AC011286	Homo sapi
c 889	206.6	16.0	118508	5	AL929236	Human DNA	c 962	206.4	15.9	170675	12	AC026094	Homo sapi
890	206.6	16.0	121132	5	AC006141	Homo sapi	c 963	206.4	15.9	172238	5	AC090942	Homo sapi
891	206.6	16.0	122457	5	AC104662	Homo sapi	c 964	206.4	15.9	180096	5	AC025483	Homo sapi
c 892	206.6	16.0	123162	5	AC130895	Homo sapi	c 965	206.4	15.9	182350	5	BS000243	Pan trogl
893	206.6	16.0	128960	5	HSJ919F19	Human DNA	966	206.4	15.9	188462	5	AL592301	Human DNA
894	206.6	16.0	129856	5	AC016620	Homo sapi	c 967	206.4	15.9	188571	5	AC107956	Homo sapi

C 968	206.4	15.9	207004	12	AL954141	AL954141 Homo sapi	C1041	15.9	55176	5	AC080153	AC080153 Homo sapi
C 969	206.4	15.9	208233	5	AL353791	AL353791 Human DNA	1042	15.9	59039	12	AC139533	AC139533 Homo sapi
C 970	206.4	15.9	208989	5	AC027124	AC027124 Homo sapi	C1043	15.9	59554	2	AX695587	AX695587 Sequence
C 971	206.4	15.9	214216	12	AC026609	AC026609 Homo sapi	1044	15.9	67050	5	AP001412	AP001412 Homo sapi
C 972	206.4	15.9	237931	5	AC022098	AC022098 Homo sapi	1045	15.9	72117	5	HSJ132F21	HSJ132F21 Human DNA
C 973	206.4	15.9	281622	12	AC117374	AC117374 Homo sapi	1046	15.9	81171	5	AC079858	AC079858 Homo sapi
C 974	206.4	15.9	349980	2	CS039413	CS039413 Sequence	C1047	15.9	86106	5	AC114546	AC114546 Homo sapi
C 975	206.2	15.9	588	7	BV510332	BV510332 qtm08b09.	1048	15.9	90705	5	AC010289	AC010289 Homo sapi
C 976	206.2	15.9	658	7	BV629760	BV629760 S217F6961	1049	15.9	98758	5	HS223H9	HS223H9 Human DNA
C 977	206.2	15.9	707	7	BV540338	BV540338 G591P6414	1050	15.9	100000	5	AP000010	AP000010 Homo sapi
C 978	206.2	15.9	6566	2	AX591967	AX591967 Sequence	1051	15.9	100000	5	AP000152	AP000152 Homo sapi
C 979	206.2	15.9	11224	5	AF538844	AF538844 Homo sapi	1052	15.9	108879	5	AC004804	AC004804 Homo sapi
C 980	206.2	15.9	11651	5	DQ194553	DQ194553 Homo sapi	1053	15.9	117824	5	AL389886	AL389886 Human DNA
C 981	206.2	15.9	12937	5	CR626870	CR626870 Human DNA	C1054	15.9	122972	12	AL694434	AL694434 Homo sapi
C 982	206.2	15.9	39641	5	AC016949	AC016949 Homo sapi	1055	15.9	124095	5	AC002477	AC002477 Human PAC
C 983	206.2	15.9	62309	5	AC110495	AC110495 Homo sapi	C1056	15.9	129884	5	AL355385	AL355385 Human DNA
C 984	206.2	15.9	63808	12	AC090554	AC090554 Homo sapi	C1057	15.9	131701	5	AC110583	AC110583 Homo sapi
C 985	206.2	15.9	97621	5	AL607089	AL607089 Human DNA	1058	15.9	135505	5	AC004477	AC004477 Homo sapi
C 986	206.2	15.9	107848	5	AC105030	AC105030 Homo sapi	C1059	15.9	140195	5	AC087163	AC087163 Homo sapi
C 987	206.2	15.9	108500	5	AP001624	AP001624 Homo sapi	C1060	15.9	144000	5	AC007621	AC007621 Homo sapi
C 988	206.2	15.9	114131	12	AC169861	AC169861 Macaca mu	1061	15.9	147876	12	AC144353	AC144353 Homo sapi
C 989	206.2	15.9	128611	5	AC083849	AC083849 Homo sapi	1062	15.9	150482	2	CS086329	CS086329 Sequence
C 990	206.2	15.9	132070	5	AC003663	AC003663 Homo sapi	C1063	15.9	151983	12	AC027178	AC027178 Homo sapi
C 991	206.2	15.9	132884	5	AL391845	AL391845 Human DNA	1064	15.9	152303	12	AC143335	AC143335 Homo sapi
C 992	206.2	15.9	135190	5	AC131945	AC131945 Homo sapi	C1065	15.9	155897	12	AP000823	AP000823 Homo sapi
C 993	206.2	15.9	135968	12	AC021707	AC021707 Homo sapi	1066	15.9	157897	12	AC016824	AC016824 Homo sapi
C 994	206.2	15.9	142280	12	CNS001RG2	AL160235 Homo sapi	C1067	15.9	162810	5	AC083923	AC083923 Homo sapi
C 995	206.2	15.9	144333	5	AC105036	AC105036 Homo sapi	C1068	15.9	163689	5	AL451065	AL451065 Human DNA
C 996	206.2	15.9	146621	5	AL928846	AL928846 Human DNA	1069	15.9	170520	5	AC012064	AC012064 Homo sapi
C 997	206.2	15.9	147545	5	AC126614	AC126614 Homo sapi	1070	15.9	171812	5	AC013399	AC013399 Homo sapi
C 998	206.2	15.9	148327	5	AC093214	AC093214 Homo sapi	C1071	15.9	172660	5	AC136968	AC136968 Pan trogl
C 999	206.2	15.9	150791	5	AL162458	AL162458 Human DNA	1072	15.9	176096	2	CS086330	CS086330 Sequence
C 1000	206.2	15.9	151894	12	AL389926	AL389926 Homo sapi	C1073	15.9	177322	12	AC024357	AC024357 Mus muscu
C1001	206.2	15.9	153830	5	AL513191	AL513191 Human DNA	1074	15.9	180523	12	AC135716	AC135716 Homo sapi
C1002	206.2	15.9	154604	12	AC104974	AC104974 Homo sapi	C1075	15.9	180523	5	CNS01DSH	AL121784 Human chr
C1003	206.2	15.9	157719	5	AP001623	AP001623 Homo sapi	1076	15.9	180631	12	AC177809	AC177809 Pan trogl
C1004	206.2	15.9	159122	12	AC025556	AC025556 Homo sapi	1077	15.9	185182	5	AC093423	AC093423 Homo sapi
C1005	206.2	15.9	161139	5	AC132812	AC132812 Homo sapi	C1078	15.9	185617	5	AL662848	AL662848 Human DNA
C1006	206.2	15.9	162070	12	AC013626	AC013626 Homo sapi	1079	15.9	189281	12	AC012458	AC012458 Homo sapi
C1007	206.2	15.9	163093	12	AC130428	AC130428 Homo sapi	C1080	15.9	190565	5	AC007374	AC007374 Homo sapi
C1008	206.2	15.9	164076	5	AC021059	AC021059 Homo sapi	1081	15.9	191434	5	AC087477	AC087477 Homo sapi
C1009	206.2	15.9	164576	5	CR954985	CR954985 Human DNA	1082	15.9	191971	5	AC146102	AC146102 Pan trogl
C1010	206.2	15.9	168613	5	AC091133	AC091133 Homo sapi	1083	15.9	193599	5	AC024382	AC024382 Homo sapi
C1011	206.2	15.9	168767	5	AC099562	AC099562 Homo sapi	1084	15.9	199636	12	AP001126	AP001126 Homo sapi
C1012	206.2	15.9	168779	5	AC026405	AC026405 Homo sapi	C1085	15.9	200606	5	AC099849	AC099849 Homo sapi
C1013	206.2	15.9	169074	12	AC148830	AC148830 Pan trogl	1086	15.9	208817	5	AC145992	AC145992 Pan trogl
C1014	206.2	15.9	169665	12	AC032042	AC032042 Homo sapi	1087	15.9	215867	12	AC145353	AC145353 Gorilla g
C1015	206.2	15.9	170189	2	CS200169	CS200169 Sequence	1088	15.9	230131	12	AC144361	AC144361 Gorilla g
C1016	206.2	15.9	171004	12	AC006286	AC006286 Homo sapi	C1089	15.9	233775	5	AC044860	AC044860 Homo sapi
C1017	206.2	15.9	171279	12	AC036185	AC036185 Homo sapi	1090	15.9	234053	5	AC002429	AC002429 Homo sapi
C1018	206.2	15.9	175081	5	AC021151	AC021151 Homo sapi	1091	15.9	340000	5	AP001728	AP001728 Homo sapi
C1019	206.2	15.9	175320	5	AC009283	AC009283 Homo sapi	205.8	15.9	25483	5	AL450431	AL450431 Human DNA
C1020	206.2	15.9	178152	5	AC096633	AC096633 Homo sapi	1093	15.9	38425	5	AL512372	AL512372 Human DNA
C1021	206.2	15.9	183037	5	AL390036	AL390036 Human DNA	C1094	15.9	39925	5	AC130897	AC130897 Homo sapi
C1022	206.2	15.9	183094	12	AC149436	AC149436 Pan trogl	C1095	15.9	55448	5	AC084353	AC084353 Homo sapi
C1023	206.2	15.9	183818	12	AC149455	AC149455 Papio anu	C1096	15.9	62893	5	AC140058	AC140058 Homo sapi
C1024	206.2	15.9	184841	12	AC129486	AC129486 Homo sapi	C1097	15.9	77849	12	AC067872	AC067872 Homo sapi
C1025	206.2	15.9	185030	5	AC008785	AC008785 Homo sapi	1098	15.9	78467	5	AC008078	AC008078 Homo sapi
C1026	206.2	15.9	185931	12	AL133554	AL133554 Homo sapi	C1099	15.9	87013	5	HS528L19	HS528L19 s
C1027	206.2	15.9	188460	5	AC010542	AC010542 Homo sapi	205.8	15.9	103577	5	AC009449	AC009449 Homo sapi
C1028	206.2	15.9	195917	5	AC005013	AC005013 Homo sapi	C1100	15.9	105582	12	AC139065	AC139065 Homo sapi
C1029	206.2	15.9	196753	5	AC008055	AC008055 Homo sapi	1102	15.9	110000	12	AC008576	Continuation (3 of
C1030	206.2	15.9	198052	5	AC019205	AC019205 Homo sapi	C1103	15.9	113879	5	AC011904	AC011904 Homo sapi
C1031	206.2	15.9	199706	12	AC097329	AC097329 Pan trogl	C1104	15.9	114526	5	HSJ1043F6	HSJ1043F6 Human DNA
C1032	206.2	15.9	210008	5	AC016885	AC016885 Homo sapi	C1105	15.9	116960	5	AL356362	AL356362 Human DNA
C1033	206.2	15.9	210204	5	AC007954	AC007954 Homo sapi	C1106	15.9	118150	5	HSJ800C24	HSJ800C24 Human DNA
C1034	206.2	15.9	262483	5	CT005239	CT005239 Pan trogl	1107	15.9	120187	5	AC005884	AC005884 Homo sapi
C1035	206.2	15.9	340000	5	AP001746	AP001746 Homo sapi	1108	15.9	121010	5	AL137860	AL137860 Human DNA
C1036	206.2	15.9	762	7	BV578234	BV578234 GS91P6095	C1109	15.9	123355	5	AL106754	AL106754 Homo sapi
C1037	206	15.9	2345	2	CS166927	CS166927 Sequence	C1110	15.9	124603	5	AC093119	AC093119 Homo sapi
C1038	206	15.9	2345	2	AX833048	AX833048 Sequence	C1111	15.9	127431	5	AC027796	AC027796 Homo sapi
C1039	206	15.9	2345	5	AK094446	AK094446 Homo sapi	1112	15.9	128668	5	AC119674	AC119674 Homo sapi
C1040	206	15.9	46387	12	UB2212	UB2212 Homo sapi	1113	15.9	129300	5	AC015815	AC015815 Homo sapi

c1114	205.8	15.9	133221	5	AC104841	AC104841 Homo sapi	1187	205.6	15.9	170559	12	AC026989	AC026989 Homo sapi
c1115	205.8	15.9	135640	5	AC036178	AC036178 Homo sapi	1188	205.6	15.9	170956	12	AC024973	AC024973 Homo sapi
c1116	205.8	15.9	136028	12	AC147036	Pan trogl	c1189	205.6	15.9	170970	5	AL354707	AL354707 Human DNA
c1117	205.8	15.9	137033	5	AC005280	AC005280 Homo sapi	1190	205.6	15.9	171092	5	AC093540	AC093540 Pan trogl
c1118	205.8	15.9	147514	5	AC008521	Homo sapi	c1191	205.6	15.9	171787	5	AC011598	AC011598 Homo sapi
c1119	205.8	15.9	148493	5	HS1061C18	Human DNA	1192	205.6	15.9	171994	5	AC060798	AC060798 Homo sapi
c1120	205.8	15.9	153148	12	AC017030	AC017030 Homo sapi	c1193	205.6	15.9	173083	12	AC034272	AC034272 Homo sapi
c1121	205.8	15.9	153422	12	AC023408	AC023408 Homo sapi	c1194	205.6	15.9	174304	5	AL450327	AL450327 Human DNA
c1122	205.8	15.9	155902	5	AP002852	AP002852 Homo sapi	c1195	205.6	15.9	174596	12	AC022812	AC022812 Homo sapi
c1123	205.8	15.9	157569	12	AC139428	AC139428 Homo sapi	c1196	205.6	15.9	174615	12	AC021249	AC021249 Homo sapi
c1124	205.8	15.9	158617	5	AC135972	AC135972 Homo sapi	1197	205.6	15.9	178199	12	AC018772	AC018772 Homo sapi
c1125	205.8	15.9	161015	12	AC024994	AC024994 Homo sapi	1198	205.6	15.9	178714	12	AC017008	AC017008 Homo sapi
c1126	205.8	15.9	165546	12	AC019056	AC019056 Homo sapi	c1199	205.6	15.9	179056	12	AC068936	AC068936 Homo sapi
c1127	205.8	15.9	165618	5	AC009334	AC009334 Homo sapi	1200	205.6	15.9	181626	5	AC116017	AC116017 Homo sapi
c1128	205.8	15.9	165652	12	AC068010	AC068010 Homo sapi	c1201	205.6	15.9	182997	5	AL355332	AL355332 Human DNA
c1129	205.8	15.9	165952	12	AC091674	AC091674 Homo sapi	1202	205.6	15.9	183625	5	AC053503	AC053503 Homo sapi
c1130	205.8	15.9	169616	5	AL355336	AL355336 Human DNA	c1203	205.6	15.9	184511	12	AC011721	AC011721 Homo sapi
c1131	205.8	15.9	170188	5	AP002090	AP002090 Homo sapi	c1204	205.6	15.9	185230	12	AC147410	AC147410 Homo sapi
c1132	205.8	15.9	170435	5	AC100767	AC100767 Homo sapi	1205	205.6	15.9	189806	5	AC021382	AC021382 Homo sapi
c1133	205.8	15.9	172203	5	AC005863	AC005863 Homo sapi	1206	205.6	15.9	191312	5	AC023772	AC023772 Homo sapi
c1134	205.8	15.9	173804	12	AC163754	Pan trogl	1207	205.6	15.9	191481	12	AC108123	AC108123 Homo sapi
c1135	205.8	15.9	179210	5	AC046202	AC046202 Homo sapi	1208	205.6	15.9	191946	5	CNS01DTK	AL132780 Human chr
c1136	205.8	15.9	181012	5	AC127070	AC127070 Homo sapi	c1209	205.6	15.9	200363	5	AC010895	AC010895 Homo sapi
c1137	205.8	15.9	181438	12	AC023047	AC023047 Homo sapi	c1210	205.6	15.9	201659	12	AC146419	AC146419 Pan trogl
c1138	205.8	15.9	181466	12	AC137089	AC137089 Homo sapi	1211	205.6	15.9	209421	5	AC090543	AC090543 Homo sapi
c1139	205.8	15.9	183509	12	AC068169	AC068169 Homo sapi	1212	205.6	15.9	215936	5	CNS05TCA	AL355076 Human chr
c1140	205.8	15.9	186455	5	AC123768	AC123768 Homo sapi	1213	205.6	15.9	222730	5	CNS01DUU	AL133246 BAC seque
c1141	205.8	15.9	188350	5	AL498605	AL498605 Human DNA	c1214	205.6	15.9	225432	2	AF027390	AF027390 Homo sapi
c1142	205.8	15.9	191549	5	AC010582	AC010582 Homo sapi	c1215	205.6	15.9	234999	2	AX647271	AX647271 Sequence
c1143	205.8	15.9	193569	5	AC100795	AC100795 Homo sapi	1216	205.4	15.9	5632	5	HSMB06360	BS337610 Homo sapi
c1144	205.8	15.9	195937	5	AC096762	AC096762 Homo sapi	1217	205.4	15.9	31839	5	AF000225	AF000225 Homo sapi
c1145	205.8	15.9	198070	12	AC044909	AC044909 Homo sapi	1218	205.4	15.9	32158	5	AF240626	AF240626 Homo sapi
c1146	205.8	15.9	199420	5	CNS01DVV	AL136040 Human chr	1219	205.4	15.9	33233	5	HSU51280	U51280 Human chrom
c1147	205.8	15.9	202037	5	AF168787	AF168787 Homo sapi	c1220	205.4	15.9	38381	5	AC000039	AC000039 Homo sapi
c1148	205.8	15.9	209216	5	AF190464	AF190464 Homo sapi	c1221	205.4	15.9	48385	5	AC118990	AC118990 Homo sapi
c1149	205.8	15.9	213729	12	AC150816	AC150816 Callithr	c1222	205.4	15.9	50612	5	AL513530	AL513530 Human DNA
c1150	205.8	15.9	216621	12	AC153309	AC153309 Gorilla g	c1223	205.4	15.9	67000	5	AP005018	AP005018 Homo sapi
c1151	205.8	15.9	218476	5	AC117503	AC117503 Homo sapi	c1224	205.4	15.9	78908	5	CR788300	CR788300 Human DNA
c1152	205.8	15.9	218980	12	AC064828	AC064828 Homo sapi	c1225	205.4	15.9	79305	5	AC005200	AC005200 Homo sapi
c1153	205.8	15.9	226696	5	AC138026	AC138026 Homo sapi	1226	205.4	15.9	79475	5	AC112250	AC112250 Homo sapi
c1154	205.6	15.9	747	7	BSV579950	BSV579950 G591P6171	c1227	205.4	15.9	83649	5	BSX927223	BSX927223 Human DNA
c1155	205.6	15.9	821	7	BSV490417	BSV490417 S221P6666	c1228	205.4	15.9	84657	5	AL136378	AL136378 Human DNA
c1156	205.6	15.9	4741	2	AR014241	AR014241 Sequence	c1229	205.4	15.9	95499	5	AC126339	AC126339 Homo sapi
c1157	205.6	15.9	4741	2	AR302267	AR302267 Sequence	1230	205.4	15.9	104380	12	AL355869	AL355869 Homo sapi
c1158	205.6	15.9	4742	2	I73182	I73182 Sequence 35	c1231	205.4	15.9	107661	5	AL162734	AL162734 Human DNA
c1159	205.6	15.9	29638	5	AC090011	AC090011 Homo sapi	1232	205.4	15.9	110000	5	AP438327_2	Continuation (3 of
c1160	205.6	15.9	34836	12	AC134663	AC134663 Homo sapi	1233	205.4	15.9	112392	5	AL357500	AL357500 Human DNA
c1161	205.6	15.9	48103	5	AL356282	AL356282 Human DNA	1234	205.4	15.9	113656	5	AC112253	AC112253 Homo sapi
c1162	205.6	15.9	65922	5	AL359881	AL359881 Human DNA	1235	205.4	15.9	119514	12	AC139536	AC139536 Homo sapi
c1163	205.6	15.9	97015	5	AP002085	AP002085 Homo sapi	1236	205.4	15.9	126454	5	AC008377	AC008377 Homo sapi
c1164	205.6	15.9	110000	12	AL831785_1	Continuation (2 of	c1237	205.4	15.9	127280	5	CR759766	CR759766 Human DNA
c1165	205.6	15.9	110000	12	BSX293534_0	BSX293534 Homo sapi	c1238	205.4	15.9	131694	5	AC012321	AC012321 Homo sapi
c1166	205.6	15.9	117847	5	AL137016	AL137016 Human DNA	c1239	205.4	15.9	133455	5	AC009451	AC009451 Homo sapi
c1167	205.6	15.9	118584	2	AX647884	AX647884 Sequence	1240	205.4	15.9	133587	5	AL445648	AL445648 Human DNA
c1168	205.6	15.9	119072	5	AL136531	AL136531 Human DNA	c1241	205.4	15.9	134403	5	HS436M11	HS436M11 Human DNA
c1169	205.6	15.9	120825	5	AC010469	AC010469 Homo sapi	1242	205.4	15.9	134995	5	AL160398	AL160398 Human DNA
c1170	205.6	15.9	121600	5	AP003555	AP003555 Homo sapi	1243	205.4	15.9	146853	5	AL136527	AL136527 Human DNA
c1171	205.6	15.9	122480	5	AC010339	AC010339 Homo sapi	1244	205.4	15.9	148698	5	AC011295	AC011295 Homo sapi
c1172	205.6	15.9	123436	5	AC009872	AC009872 Homo sapi	1245	205.4	15.9	148832	12	AC074285	AC074285 Homo sapi
c1173	205.6	15.9	124699	5	AL590617	AL590617 Human DNA	1246	205.4	15.9	152252	5	AP003039	AP003039 Homo sapi
c1174	205.6	15.9	139544	5	HS436M6	HS436M6 Human DNA	c1247	205.4	15.9	152358	12	AC018379	AC018379 Homo sapi
c1175	205.6	15.9	153292	5	AL513318	AL513318 Human DNA	c1248	205.4	15.9	153553	12	AL513012	AL513012 Homo sapi
c1176	205.6	15.9	156997	5	AC011465	AC011465 Homo sapi	1249	205.4	15.9	155122	12	AC141847	AC141847 Pan trogl
c1177	205.6	15.9	157588	5	AL356094	AL356094 Human DNA	1250	205.4	15.9	156064	5	AC083864	AC083864 Homo sapi
c1178	205.6	15.9	159693	12	AC009781	AC009781 Homo sapi	1251	205.4	15.9	157010	5	CNS01DX7	AL139099 Human chr
c1179	205.6	15.9	160915	12	AP001084	AP001084 Homo sapi	c1252	205.4	15.9	157200	5	AC010724	AC010724 Homo sapi
c1180	205.6	15.9	162696	12	AC148537	AC148537 Pan trogl	c1253	205.4	15.9	157246	5	AC135995	AC135995 Homo sapi
c1181	205.6	15.9	163300	12	AC060820	AC060820 Homo sapi	c1254	205.4	15.9	157533	5	AC092868	AC092868 Homo sapi
c1182	205.6	15.9	163375	12	AC027777	AC027777 Homo sapi	c1255	205.4	15.9	158626	12	AC149853	AC149853 Papio anu
c1183	205.6	15.9	164444	5	AL391867	AL391867 Human DNA	c1256	205.4	15.9	159734	5	AC016567	AC016567 Homo sapi
c1184	205.6	15.9	165203	5	AC093928	AC093928 Homo sapi	1257	205.4	15.9	160570	12	AC092317	AC092317 Homo sapi
c1185	205.6	15.9	165669	5	AC157216	AC157216 Pan trogl	c1258	205.4	15.9	160570	12	AC092317	AC092317 Homo sapi
c1186	205.6	15.9	165733	12	AC069072	AC069072 Homo sapi	c1259	205.4	15.9	161366	5	AC090939	AC090939 Homo sapi

1260	205.4	15.9	161990	12	AL357313	AL357313 Homo sapi	1333	205.2	15.8	131708	5	AL354710	Human DNA
1261	205.4	15.9	162172	12	AC027384	AC027384 Homo sapi	1334	205.2	15.8	132049	5	AL954207	Pan trogl
1262	205.4	15.9	163666	5	AC095038	AC095038 Homo sapi	1335	205.2	15.8	141534	5	CNS01050	Human chr
1263	205.4	15.9	166378	12	AC142745	AC142745 Macaca mu	1336	205.2	15.8	147114	5	BS000121	Pan trogl
1264	205.4	15.9	166905	12	AC025729	AC025729 Homo sapi	1337	205.2	15.8	149425	12	AC013320	Homo sapi
1265	205.4	15.9	170108	12	AC163741	AC163741 Pan trogl	1338	205.2	15.8	158107	12	AC025997	Homo sapi
1266	205.4	15.9	170399	5	HS036805	AL121992 Human DNA	1339	205.2	15.8	161449	5	AC005341	Homo sapi
1267	205.4	15.9	172035	12	AC027594	AC027594 Homo sapi	1340	205.2	15.8	162516	5	AC130464	Homo sapi
1268	205.4	15.9	173049	5	AC008653	AC008653 Homo sapi	1341	205.2	15.8	162792	12	AF001856	Homo sapi
1269	205.4	15.9	173049	5	AC022142	AC022142 Homo sapi	1342	205.2	15.8	163427	5	AC009053	Homo sapi
1270	205.4	15.9	173749	12	AC020567	AC020567 Homo sapi	1343	205.2	15.8	163499	12	AC021109	Homo sapi
1271	205.4	15.9	174818	5	AL390061	AL390061 Human DNA	1344	205.2	15.8	165221	5	AC170813	Rhesus Ma
1272	205.4	15.9	175707	12	AC022030	AC022030 Homo sapi	1345	205.2	15.8	167319	5	AC090541	Homo sapi
1273	205.4	15.9	175982	12	AC113210	AC113210 Homo sapi	1346	205.2	15.8	168602	12	AF271406	Homo sapi
1274	205.4	15.9	176694	5	AC018718	AC018718 Homo sapi	1347	205.2	15.8	169714	12	AC138876	Homo sapi
1275	205.4	15.9	176709	5	AC011737	AC011737 Homo sapi	1348	205.2	15.8	170815	5	AL591662	Human DNA
1276	205.4	15.9	177988	12	AC022760	AC022760 Homo sapi	1349	205.2	15.8	170815	12	AL591662	Human DNA
1277	205.4	15.9	178029	12	AC182396	AC182396 Pan trogl	1350	205.2	15.8	171905	12	AL591609	Homo sapi
1278	205.4	15.9	178208	12	AC136432	AC136432 Homo sapi	1351	205.2	15.8	172246	5	AC024941	Homo sapi
1279	205.4	15.9	179084	5	AC091059	AC091059 Homo sapi	1352	205.2	15.8	173029	5	AC002059	Homo sapi
1280	205.4	15.9	181047	12	AC016765	AC016765 Homo sapi	1353	205.2	15.8	173304	5	AC023818	Homo sapi
1281	205.4	15.9	181123	5	AP001120	AP001120 Homo sapi	1354	205.2	15.8	176282	12	AC068507	Homo sapi
1282	205.4	15.9	181571	5	BS000206	BS000206 Pan trogl	1355	205.2	15.8	176307	12	AC015714	Homo sapi
1283	205.4	15.9	181772	12	AC007689	AC007689 Homo sapi	1356	205.2	15.8	176438	12	AC126761	Homo sapi
1284	205.4	15.9	182092	5	AC013477	AC013477 Homo sapi	1357	205.2	15.8	176584	12	AC027812	Homo sapi
1285	205.4	15.9	184511	5	AC090932	AC090932 Homo sapi	1358	205.2	15.8	176584	12	AC062010	Homo sapi
1286	205.4	15.9	185173	12	AC009056	AC009056 Homo sapi	1359	205.2	15.8	177479	5	AC009153	Homo sapi
1287	205.4	15.9	186812	5	AC110291	AC110291 Homo sapi	1360	205.2	15.8	177962	5	AC008763	Homo sapi
1288	205.4	15.9	187497	5	AC078841	AC078841 Homo sapi	1361	205.2	15.8	178714	12	AC017008	Homo sapi
1289	205.4	15.9	191158	5	AC006112	AC006112 Homo sapi	1362	205.2	15.8	178887	12	AC068981	Homo sapi
1290	205.4	15.9	191481	12	AC108123	AC108123 Homo sapi	1363	205.2	15.8	178976	12	AL391095	Homo sapi
1291	205.4	15.9	199230	12	AC048360	AC048360 Homo sapi	1364	205.2	15.8	179155	5	AL353748	Human DNA
1292	205.4	15.9	200638	5	AL356253	AL356253 Human DNA	1365	205.2	15.8	181188	12	AC067983	Homo sapi
1293	205.4	15.9	212131	12	AC142554	AC142554 Pan trogl	1366	205.2	15.8	181688	12	AC169824	Macaca mu
1294	205.4	15.9	212426	5	AC104335	AC104335 Homo sapi	1367	205.2	15.8	182740	2	BS000163	Pan trogl
1295	205.4	15.9	214821	12	AC068785	AC068785 Homo sapi	1368	205.2	15.8	183046	2	CS086327	Sequence
1296	205.4	15.9	215580	12	AC140526	AC140526 Homo sapi	1369	205.2	15.8	184562	5	AP005718	Homo sapi
1297	205.4	15.9	222366	12	AC119799	AC119799 Pan trogl	1370	205.2	15.8	186104	5	AP005718	Homo sapi
1298	205.4	15.9	244254	12	HSAC001228	AC001228 244Kb Con	1371	205.2	15.8	188933	5	HS26885	Human DNA
1299	205.4	15.9	253389	12	AC008605	AC008605 Homo sapi	1372	205.2	15.8	188933	5	AC069257	Homo sapi
1300	205.2	15.8	444	7	AB137424	AB137424 Homo sapi	1373	205.2	15.8	189056	12	AC147331	Pan trogl
1301	205.2	15.8	653	7	BSA342703	BSA342703 Homo sapi	1374	205.2	15.8	189220	5	AC147331	Pan trogl
1302	205.2	15.8	686	7	BSV04316	BSV04316 prx09f11.	1375	205.2	15.8	191755	5	AC021016	Homo sapi
1303	205.2	15.8	712	7	BSV04433	BSV04433 qne78d09.	1376	205.2	15.8	192104	5	AC006994	Homo sapi
1304	205.2	15.8	798	7	BSV517267	BSV517267 r1m36a02.	1377	205.2	15.8	192805	5	AC146435	Pan trogl
1305	205.2	15.8	801	7	BSV546732	BSV546732 ste34g04.	1378	205.2	15.8	196934	5	AL355530	Human DNA
1306	205.2	15.8	835	7	BSV528766	BSV528766 G591P6102	1379	205.2	15.8	198295	5	AC105129	Homo sapi
1307	205.2	15.8	864	7	BSV323235	BSV323235 G591P6239	1380	205.2	15.8	203720	5	AC093861	Homo sapi
1308	205.2	15.8	885	7	BSV522170	BSV522170 G591P6254	1381	205.2	15.8	208417	5	AL954209	Pan trogl
1309	205.2	15.8	902	7	BSV569486	BSV569486 G591P6006	1382	205.2	15.8	209816	12	AC105911	Homo sapi
1310	205.2	15.8	7617	5	AL391693	AL391693 Human DNA	1383	205.2	15.8	214250	5	AC108050	Homo sapi
1311	205.2	15.8	24504	5	AC008059	AC008059 Homo sapi	1384	205.2	15.8	214722	5	AL954208	Pan trogl
1312	205.2	15.8	69474	5	BSX927180	BSX927180 Human DNA	1385	205.2	15.8	218723	5	AL732314	Human DNA
1313	205.2	15.8	71452	5	AP000269	AP000269 Homo sapi	1386	205.2	15.8	220581	12	AC015918	Homo sapi
1314	205.2	15.8	74029	5	AL356512	AL356512 Human DNA	1387	205.2	15.8	224292	12	AC026873	Homo sapi
1315	205.2	15.8	75620	5	CR812478	CR812478 Human DNA	1388	205.2	15.8	230956	5	AC090614	Homo sapi
1316	205.2	15.8	80063	5	BSX284686	BSX284686 Human DNA	1389	205.2	15.8	340000	5	AP001714	Homo sapi
1317	205.2	15.8	80141	5	HSXSWGAR	Y07848 Homo sapien	1390	205	15.8	1317	5	HSFGRCALU	
1318	205.2	15.8	87294	5	AL671511	AL671511 Human DNA	1391	205	15.8	6933	5	AF293463	Sequence
1319	205.2	15.8	90064	5	AL356376	AL356376 Homo sapi	1392	205	15.8	10283	2	AX468746	Sequence
1320	205.2	15.8	98593	5	AL356472	AL356472 Human DNA	1393	205	15.8	34250	5	AL356129	Human DNA
1321	205.2	15.8	100000	5	AP000032	AP000032 Homo sapi	1394	205	15.8	36532	5	AC118342	Homo sapi
1322	205.2	15.8	100000	5	AP000103	AP000103 Homo sapi	1395	205	15.8	45746	5	AC005619	Homo sapi
1323	205.2	15.8	100000	5	AP000179	AP000179 Homo sapi	1396	205	15.8	55001	5	AL133507	Human DNA
1324	205.2	15.8	110000	12	CR936382_2	Continuation (3 of	1397	205	15.8	60606	12	AC055734	Homo sapi
1325	205.2	15.8	110000	12	CR936382_2	Continuation (3 of	1398	205	15.8	63332	5	AC024938	Homo sapi
1326	205.2	15.8	112132	2	AR399481	AR399481 Sequence	1399	205	15.8	63412	5	AC093367	Homo sapi
1327	205.2	15.8	117482	5	AC105028	AC105028 Homo sapi	1400	205	15.8	64512	5	AP000255	Homo sapi
1328	205.2	15.8	119378	5	AL449323	AL449323 Human DNA	1401	205	15.8	67729	12	AP0073035	Homo sapi
1329	205.2	15.8	123520	5	HSJ447E21	AL050336 Human DNA	1402	205	15.8	69411	5	AC011322	Homo sapi
1330	205.2	15.8	125406	5	AC008614	AC008614 Homo sapi	1403	205	15.8	77192	12	AL713858_3	Continuation (4 of
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1332	205.2	15.8	127725	5	AC023813	AC023813 Homo sapi	1405	205	15.8	79544	12	AC016859	Homo sapi

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c1408	205	15.8	96153	5	AC092651	AC092651 Homo sapi	c1481	205	15.8	213466	12	AC019224	AC019224 Homo sapi
c1409	205	15.8	98828	5	HSJ388E23	AL049552 Human DNA	c1482	205	15.8	218371	5	AP001025	AP001025 Homo sapi
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c1411	205	15.8	100000	5	AP000213	AP000213 Homo sapi	c1484	205	15.8	226916	5	AC005066	AC005066 Homo sapi
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c1419	205	15.8	110000	12	AC146444_1	Continuation (2 of	c1492	204.8	15.8	922	7	BV569699	BV569699 G591P6199
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c1426	205	15.8	136653	5	AC090111	AC090111 Homo sapi	c1499	204.8	15.8	86101	5	AV436640	AV436640 Homo sapi
c1427	205	15.8	136653	5	AL353786	AL353786 Human DNA	c1500	204.8	15.8	92000	5	AC004596	AC004596 Homo sapi
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c1433	205	15.8	148271	5	AL392046	AL392046 Human DNA							
c1434	205	15.8	148463	12	AC012140	AC012140 Homo sapi							
c1435	205	15.8	148527	5	AF274857	AF274857 Homo sapi							
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c1461	205	15.8	176121	5	AC131011	AC131011 Homo sapi							
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c1474	205	15.8	191827	5	AC093904	AC093904 Homo sapi							
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c1477	205	15.8	197295	5	AC073585	AC073585 Homo sapi							
c1478	205	15.8	200277	12	AC024555	AC024555 Homo sapi							

ALIGNMENTS

RESULT 1	BD075420	1295 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD075420	Secretory and transmembrane polypeptide and nucleic acid encoding			
DEFINITION	Secretory and transmembrane polypeptide and nucleic acid encoding				
ACCESSION	BD075420				
VERSION	BD075420.1	GI:22621023			
KEYWORDS	JP 2001516580-A/53				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1295)				
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.				
TITLE	Secretory and transmembrane polypeptide and nucleic acid encoding				
JOURNAL	Patent: JP 2001516580-A 53 02-OCT-2001;				
COMMENT	GENENTECH INC				
	OS Homo sapiens (human)				
	PN JP 2001516580-A/53				
	PD 02-OCT-2001				
	PF 16-SEP-1998	JP 2000511867			
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24-NOV-1997 US	60/066770,24-NOV-1997 US	60/066511 PR
24-NOV-1997 US	60/066453,25-NOV-1997 US	60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI		
JIAN ZHENG,		
PI JEAN YUAN		
PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC		
C12N5/10,		
PC		
C12P21/02//C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:91), PC		
(C12P21/02,C12R1:645),C12N15/00,C12N5/00		
CC Secreted and transmembrane polypeptides and nucleic CC acids		
encoding the same		
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	/organism='Homo sapiens'	
	/mol_type='genomic DNA'	
	/db_xref='taxon:9606'	
ORIGIN		
Query Match	100.0%; Score 1295; DB 2; Length 1295;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 1	CCCAAGAGTTCAAGGGCCCGGGCTCTCGCTCCCTCGCGCGGGACCCCTCGACCTCCT	60
DB 1	CCCAAGAGTTCAAGGGCCCGGGCTCTCGCTCCCTCGCGCGGGACCCCTCGACCTCCT	60
QY 61	CAGACGACCGGGTCCCGCCCGGGAAGATGGCAGAGGAGCGCCACCGCTCCTCCT	120
DB 61	CAGACGACCGGGTCCCGCCCGGGAAGATGGCAGAGGAGCGCCACCGCTCCTCCT	120
QY 121	GCTGCTGCTGGCTACCTGGTGGTGGCTGGCTGGCTATCAAGGCTATGGGTTTCTGC	180
DB 121	GCTGCTGCTGGCTACCTGGTGGTGGCTGGCTATCAAGGCTATGGGTTTCTGC	180
QY 181	CCCAAAAGACCAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA	240
DB 181	CCCAAAAGACCAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA	240
QY 241	AACCCCAAGAAGACTGTTTCTCCAGATTAGAGTGGAAAGAACTGGGTGGAGTGCTC	300
DB 241	AACCCCAAGAAGACTGTTTCTCCAGATTAGAGTGGAAAGAACTGGGTGGAGTGCTC	300
QY 301	CTTTGCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGAGA	360
DB 301	CTTTGCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGAGA	360
QY 361	TTTCAATATCCGATCAAAATGTGACAAGAGTGATCGGGGAATATCTGTTGTGAAT	420
DB 361	TTTCAATATCCGATCAAAATGTGACAAGAGTGATCGGGGAATATCTGTTGTGAAT	420
QY 421	TAGTGCCCTCTCTGAGCAAGGCCAAAACCTGGAAAGAGATACAGTCACTCTGGAAGTATT	480
DB 421	TAGTGCCCTCTCTGAGCAAGGCCAAAACCTGGAAAGAGATACAGTCACTCTGGAAGTATT	480

QY 481	AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCTCTTCTGCTCTCTGAGTGGAACTGGT	540
DB 481	AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCTCTTCTGCTCTCTGAGTGGAACTGGT	540
QY 541	AGAGCTACGATGTCAAGACAAAGAGGGAATCCAGCTCTCTGAAATACACATGGTTTAAAGGA	600
DB 541	AGAGCTACGATGTCAAGACAAAGAGGGAATCCAGCTCTCTGAAATACACATGGTTTAAAGGA	600
QY 601	TGCGATCCGTTTCTGAGAAATCCAGACTTGGCTCCCAAGCACCACCAAGCTCATACAC	660
DB 601	TGCGATCCGTTTCTGAGAAATCCAGACTTGGCTCCCAAGCACCACCAAGCTCATACAC	660
QY 661	AATGAATACAAAACTCGAACTCTGCAATTTAATATCTGTTTCCAAACTGGACACTGGAGA	720
DB 661	AATGAATACAAAACTCGAACTCTGCAATTTAATATCTGTTTCCAAACTGGACACTGGAGA	720
QY 721	ATATCTGTGAAGCCCGCAATTTCTGTGTGATATCGCAGGTGCTCGGGAACCAATGCA	780
DB 721	ATATCTGTGAAGCCCGCAATTTCTGTGTGATATCGCAGGTGCTCGGGAACCAATGCA	780
QY 781	AGTAGATGATCTCAACATAGTGGCATCATAGCAGCGGTAGTGTGGCTTAGTGAT	840
DB 781	AGTAGATGATCTCAACATAGTGGCATCATAGCAGCGGTAGTGTGGCTTAGTGAT	840
QY 841	TTCCGTTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC	900
DB 841	TTCCGTTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC	900
QY 901	CTCCTTCCAGAGAGTAATTTCTCATCTAAAGCCACGACAAATGAGTGAATAATGTCAGTG	960
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QY 961	GCTCAGCCTGTAAATCCAGCACTTTTGGAGGCGCGGGGGGATCAGAGGTCAAGGA	1020
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DB 1021	GTTCTAGACCAAGTCTGGCCAAATATGTTGAAACCCCATCTCTACTAAATAACAAAAATTAG	1080
QY 1081	CTGGGATGTTGGCATGTGCTCAGTTCCAGTCTGGGAGACAGGAGAAATCACTTGA	1140
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DB 1141	ACCGGGAGCGGAGGTTGCAAGTGAAGTCAAGCTGAGTCAAGCTGAGCTCGGCTGGGTAA	1200
QY 1201	CAGAGCAAGATTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1260
DB 1201	CAGAGCAAGATTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1260
QY 1261	TGTAGAAATCTTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1295
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RESULT 3		
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LOCUS	Secreted and transmembrane polypeptides and nucleic acids encoding	
DEFINITION	the same.	
ACCESSION	BD172599	
VERSION	BD172599.1 GI:28413901	
KEYWORDS	JP 2002238586-A/53.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
REFERENCE	1 (bases 1 to 1295)	
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and	

Yuan,J.		Secreted and transmembrane polypeptides and nucleic acids encoding	
the same			
Patent: JP 2002238586-A 53 27-AUG-2002;			
GENENTECH INC			
OS Homo sapiens (human)			
PN JP 2002238586-A/53			
PD 27-AUG-2002			
PF 18-DEC-2001 JP 2001385205			
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI			
JIAN ZHENG,			
PI JEAN YUAN			
PC C12N15/09,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC			
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ACCESSION	BD172918		
VERSION	BD172918.1	GI:28414224	
KEYWORDS	JP 2002238587-A/53.		
SOURCE	Homo sapiens		
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		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
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REFERENCE	1	(bases 1 to 1295)	
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and		
	Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
JOURNAL	the same		
COMMENT	Patent: JP 2002238587-A 53 27-AUG-2002;		
	GENENTECH INC		
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DEFINITION	Sequence 8 from Patent EP1481990.		
ACCESSION	CQ957874		
VERSION	CQ957874.1 GI:56399637		
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SOURCE	Homo sapiens		
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REFERENCE	1		
AUTHORS	Ashkenazi, A., Fong, S., Goddard, A., Gurney, A.L., Napier, M.A., Tuma, D. and Wood, W.I.		
TITLE	A-33 related antigens and their pharmacological uses		
JOURNAL	Patent: EP 1481990-A 8 01-DEC-2004; Genentech, Inc. (US)		
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ACCESSION AR473033
VERSION AR473033.1 GI:42708408
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1295)
AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L., Mather,J.P., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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Db 1201 CAGAGCAAGATTCCATCTCAAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 1260
Qy 1261 TGTAGAATTCTTACAATAAATATAGCTTGTATATTC 1295
Db 1261 TGTAGAATTCTTACAATAAATATAGCTTGTATATTC 1295
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Search completed: May 17, 2006, 23:12:46
Job time : 7873 secs

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Run on: May 17, 2006, 19:38:15 ; Search time 914 Seconds
(without alignments)
9878.623 Million cell updates/sec

Title: US-10-785-221-8

Perfect score: 1295

Sequence: 1 ccagaagttcaaggcccc.....ataaatagcttgatattc 1295

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: Geneseqn2005s:*

15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAX37664	standard;	cdna;	1295	BP.	
DE	Human PRO245	cdna.				
PN	WO9914241-A2.					
PD	25-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 2;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 2						
ID	AAX52225	standard;	DNA;	1295	BP.	
DE	Protein PRO245	cdna clone	'DNA35638-1141.			
PN	WO9914328-A2.					
PD	25-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 2;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 3						
ID	AAC58586	standard;	cdna;	1295	BP.	
DE	Human PRO245	protein UNQ219	encoding cdna	SEQ ID NO:35.		
PN	WO20003758-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 3;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 4						
ID	AAZ52202	standard;	cdna;	1295	BP.	
DE	Human PRO245	protein encoding	cdna, UNQ219.			
PN	WO200015797-A2.					
PD	23-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 3;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 5						
ID	AAZ75562	standard;	cdna;	1295	BP.	
DE	Human PRO245	cdna sequence	SEQ ID NO:66.			
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 3;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				

RESULT 6

ID ADC78383 standard; cdna; 1295 BP.

DE Human PRO245 cdna.

PN WO200015796-A2.

PD 23-MAR-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 3; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 7

ID AAF72383 standard; cdna; 1295 BP.

DE Human PRO245 cdna.

PN WO200104311-A1.

PD 18-JAN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 4; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 8

ID AAS21411 standard; cdna; 1295 BP.

DE Human cdna sequence encoding for PRO245 polypeptide.

PN WO200140466-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 4; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 9

ID AAC97437 standard; cdna; 1295 BP.

DE Human angiogenesis-associated protein PRO245 cdna, SEQ ID NO:90.

PN WO200053753-A2.

PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 4; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 10

ID AAC91463 standard; cdna; 1295 BP.

DE Human PRO245 cdna.

PN WO200073452-A2.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 5; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 11

ID ACA60052 standard; cdna; 1295 BP.

DE Human cdna for secreted/transmembrane protein PRO245.

PN US2003003530-A1.

PD 02-JAN-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 8; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 12

ID ACD07452 standard; cdna; 1295 BP.

DE Novel human secreted and transmembrane protein PRO245 cdna.

PN US2002197671-A1.

PD 26-DEC-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 8; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 13

ID ACA03770 standard; cdna; 1295 BP.

DE cdna encoding human PRO polypeptide #168.

PN US2003036180-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 8; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 14

ID ABX71500 standard; cdna; 1295 BP.

DE Human cdna encoding secreted/transmembrane protein PRO245.

PN US2002132240-A1.

PD 19-SEP-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 8; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 15

ID AAX37664

ID ACH06832 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane polypeptide PRO245 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ABX89308 standard; cDNA; 1295 BP.
DE DNA encoding novel secreted and transmembrane protein PRO245.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ACD41962 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #168.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ABX9069 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ACA05390 standard; cDNA; 1295 BP.
DE cDNA encoding human secreted protein PRO245.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ACD20057 standard; cDNA; 1295 BP.
DE Human secreted / transmembrane polypeptide PRO245 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ABX93348 standard; cDNA; 1295 BP.
DE cDNA encoding human A-33 related antigen PRO245.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID ACA04191 standard; cDNA; 1295 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 335.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ACA54860 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ACD19695 standard; cDNA; 1295 BP.
DE Human secreted / transmembrane polypeptide PRO245 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ADA45854 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ADA76285 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ADB29268 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ADA18935 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ADA61558 standard; cDNA; 1295 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ADB19343 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ADB27884 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ADA86363 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ADB15927 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.

PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ADA47713 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ADA18124 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ACD66842 standard; cDNA; 1295 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO245.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ADA67508 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ADB30515 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ADA85811 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ADA97023 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ADA79327 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ADA87466 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087345-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ADB16668 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ACD83003 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ADA16099 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ADA91760 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ADB14823 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ADB18784 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ADA93999 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ADB19895 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ADB13207 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082710-A1.
PD 01-MAY-2003.


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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADB24142 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ADA96471 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ADA81043 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADA95919 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADB26228 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADB21713 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ADA77492 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ADB18232 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADA86915 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADA16523 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADA12952 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ADA41820 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ADA88018 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ADA46406 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ADA17167 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ADA42670 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ADB28436 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ADB28988 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ADB28988 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ADA76940 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ADA88570 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ADA97575 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ADB27332 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ADB22265 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ACD23543 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ADA66956 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ADB22817 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ADB23590 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ADA92312 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ADB15375 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ADB38627 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ADB38075 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 9; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ADB66547 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 10; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ADB89627 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 10; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ADB90359 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 10; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ADB77589 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 10; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ADB39460 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 10; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ADB74725 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003082542-A1.
PD 01-MAY-2003.
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PA (GETH ) GENENTECH INC.
Query Match
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RESULT 107
ID ADB47083 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 108
ID ADB86690 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 109
ID ADB77295 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 110
ID ADB34452 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 111
ID ADB35556 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 112
ID ADB33900 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 113
ID ADB35004 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 114
ID ADB36108 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 115
ID ADB46503 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 116
ID ADC28371 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 117
ID ADC39571 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 118
ID ADC40085 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 119
ID ADC18913 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 120
ID ADC34209 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 121
ID ADC29264 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 122
ID ADC28795 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 123
ID ADC40680 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
RESULT 124
ID ADC19337 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 10; Length 1295;
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ADC33785 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 126
ID ADC12855 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 127
ID ADC50376 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 128
ID ADC71923 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 129
ID ADC59902 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID ADC5909 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 131
ID ADC57263 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 132
ID ADC60454 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 133
ID ADC50929 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 134
ID ADC65456 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 135
ID ADC54554 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ADC53515 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ADC59038 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ADC55916 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ADC58486 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ADC12307 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID ADD03160 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ADC90152 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ADC50152 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ADC69571 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID ADC48460 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 145
ID ADD09989 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID ADD04564 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID ADC80520 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID ADD11027 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID ADC47908 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ADD04862 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID ADC79968 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID ADD09437 standard; cDNA; 1295 BP.

DE Human PRO polynucleotide #168.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID ADD03868 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID ADD03444 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID ADD41150 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ADD5289 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ADD53029 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ADD53581 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ADD51737 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ADD02536 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ADD01970 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.

PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ADD54152 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ADD92469 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ADD91365 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ADE03979 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ADE32276 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ADE22208 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ADD79432 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ADE41968 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ADE17785 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199023-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ADD91917 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ADE33390 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ADE33932 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ADD79984 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ADD93021 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ADE19441 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ADE34696 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ADE18889 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ADE43085 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199033-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID AD95874 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ADE22760 standard; cDNA; 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID AD78878 standard; cDNA; 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ADE32828 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ADE42520 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ADD80536 standard; cDNA; 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ADD89564 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ADE40848 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ADE04647 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ADE92776 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ADG21485 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ADG23126 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ADF97461 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ADG80525 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ADG79973 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ADH62535 standard; cDNA; 1295 BP.
DE Human DNA35638 cDNA encoding PRO245 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK//) ASHKENARI, FONG S.
PA (FONG//) GODDARD A.
PA (GODD//) GURNEY A L.
PA (GURN//) NAPIER M A.
PA (NAPI//) TUMAS D.
PA (TUMA//) WOOD W I.
PA (WOOD//) WOOD W I.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ADH59179 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197

ID ADH55265 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ADH55817 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ADI37958 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ADI64036 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ADI64985 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ADI63484 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ADH81898 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ADH81346 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ACA58948 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ACD24020 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ACA58345 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #11.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ACA67161 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ADJ26226 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 210
ID ADM82515 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ADNI5914 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ADNI6543 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ADNI5362 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
ID ADNI4810 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ADC81072 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.


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PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 216
ID ADE79141 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 217
ID ADD76520 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 218
ID ADD87884 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ADD86288 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 220
ID ADE79565 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ADE75736 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ADE73241 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ADE23312 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ADE23864 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092110-A1.

PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ADE24507 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ADD87332 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ADE89198 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ADE73776 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 229
ID ADE18337 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 230
ID ADE86646 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 231
ID ADE99330 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 232
ID ADE94666 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1295; DB 12; Length 1295;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 233
ID ADE91077 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199061-A1.
PD 23-OCT-2003.
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 234
ID ADE95218 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 235
ID ADE93328 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 236
ID ADF34909 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 237
ID ADE98449 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 238
ID ADE92224 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 239
ID ADE90525 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 240
ID ADE91672 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 241
ID ADE98876 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 242
ID ADG0346 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.

PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHUR J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 243
ID ADF73740 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 244
ID ADG02251 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 245
ID ADG22037 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 246
ID ADG20107 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 247
ID ADF98013 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 248
ID ADG24230 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 249
ID ADF98584 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 250
ID ADG03415 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 251
ID ADG03415 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;


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ID ADF99136 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207353-A1.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 252
ID ADG16721 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 253
ID ADG05180 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 254
ID ADF19447 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 255
ID ADF73316 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003168051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 256
ID ADG13284 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 257
ID ADG08341 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 258
ID ADG15511 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 259
ID ADF96909 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 260
ID ADG06094 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003207374-A1.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 261
ID ADG23678 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 262
ID ADG03967 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 263
ID ADG24868 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 264
ID ADG07165 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 265
ID ADG07717 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 266
ID ADG55212 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 267
ID ADG60876 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 268
ID ADG61980 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 269
ID ADG92159 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
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PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 270
ID ADG82181 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 271
ID ADG57420 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 272
ID ADG56868 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 273
ID ADG5764 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 274
ID ADG58524 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 275
ID ADG70890 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 276
ID ADG92586 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 277
ID ADG57972 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 278
ID ADG53556 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027415-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 279
ID ADG71442 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 280
ID ADG81629 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003027805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 281
ID ADH30591 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 282
ID ADH11958 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 283
ID ADG52380 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 284
ID ADG44108 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 285
ID ADG81077 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 286
ID ADG56316 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 287
ID ADH12582 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003027378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 288
ID ADG61428 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 289
ID ADH28515 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ADG54660 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ADG59700 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ADH20375 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ADH07230 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN) DESNOYERS L.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P. J.
PA (GURN) GURNEY A. L.
PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ADH59775 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ADH06803 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN) DESNOYERS L.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P. J.
PA (GURN) GURNEY A. L.

PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ADI81124 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ADI18545 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ADI65265 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ADI37528 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ADG09867 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ADH97332 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ADI15338 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ADG03215 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ADI65692 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003148371-A1.


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PD 07-AUG-2003
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ADI14670 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ADH60435 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ADI18265 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 308
ID ADJ99492 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ADL08685 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ADM25030 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ADJ63546 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ADM29776 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ADJ77441 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ADJ65563 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ADM27699 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ADM42423 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ADO06098 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #13.
PN US6586451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ADN35291 standard; DNA; 1295 BP.
DE Human PRO245 gene.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ADM28285 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ADRI0950 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ADRI7859 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
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PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
RESULT 322
ID ADI95767 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
RESULT 323
ID ADI96319 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
RESULT 324
ID HUT94236 standard; cDNA; 1295 BP.
DE Human secreted; cDNA; 1295 BP.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
RESULT 325
ID ADS74498 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane cDNA #13.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.

PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
RESULT 326
ID ADS32271 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
RESULT 327
ID ADT03255 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
RESULT 328
ID AUT03535 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
RESULT 329
ID ADZ03306 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane PRO245 cDNA.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 14; Length 1295;
RESULT 330
ID ABA37773 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 14; Length 1295;
RESULT 331
ID ABB14052 standard; cDNA; 1295 BP.
DE Cancer cell diagnosis method-related human cDNA sequence - SEQ ID 335.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 14; Length 1295;
RESULT 332
ID AED23807 standard; cDNA; 1295 BP.
DE Human secreted protein PRO 245 encoding gene, SEQ ID 63.
PN US2005214904-A1.

PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 14; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 333
ID AED86250 standard; cDNA; 1295 BP.
DE Human PRO cDNA, seq id 335.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 14; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 334
ID AEE68976 standard; cDNA; 1295 BP.
DE Tyrosine kinase homologous PRO245 encoding gene, SEQ ID 63.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 15; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 335
ID AAX81770 standard; cDNA; 1295 BP.
DE cDNA DNA35638 encoding A33 related antigen PRO245.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1293.4; DB 2; Length 1295;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 336
ID AAS00157 standard; cDNA; 1295 BP.
DE Human cDNA clone DNA35638-1141 encoding PRO245 (UNQ219).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1293.4; DB 4; Length 1295;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 337
ID ACN40835 standard; cDNA; 1721 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326887, SEQ ID NO:5879.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 73.6%; Score 953.2; DB 13; Length 1721;
Best Local Similarity 99.2%; Pred. No. 7.7e-239;
RESULT 338
ID AAS00512 standard; cDNA; 1131 BP.
DE Human junctional adhesion protein (JAM2) cDNA.
PN WO200114404-A1.
PD 01-MAR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 73.5%; Score 951.6; DB 4; Length 1131;
Best Local Similarity 99.1%; Pred. No. 1.7e-238;
RESULT 339
ID ACC72652 standard; cDNA; 1397 BP.
DE Human vascular endothelial junction-associated molecule cDNA.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EQSB-) EOS BIOTECHNOLOGY INC.
Query Match 73.5%; Score 951.6; DB 10; Length 1397;
Best Local Similarity 99.1%; Pred. No. 1.8e-238;
RESULT 340
ID AAV82780 standard; cDNA; 1076 BP.
DE Clone ct684.4 isolated from human adult brain cDNA library.
PN WO9842739-A2.
PD 01-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 73.5%; Score 951.2; DB 2; Length 1076;
Best Local Similarity 99.2%; Pred. No. 2.1e-238;
RESULT 341
ID ABQ92017 standard; cDNA; 1076 BP.
DE Human polynucleotide SEQ ID NO 14.
PN US2002065394-A1.
PD 30-MAY-2002.

PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 73.5%; Score 951.2; DB 6; Length 1076;
Best Local Similarity 99.2%; Pred. No. 2.1e-238;
RESULT 342
ID AAL60897 standard; cDNA; 1389 BP.
DE Human novel splice variant of VEJAM (NOJAM) cDNA.
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GEST) GENSET SA.
Query Match 72.2%; Score 935.2; DB 9; Length 1389;
Best Local Similarity 98.8%; Pred. No. 3.6e-234;
RESULT 343
ID AAH98352 standard; cDNA; 1416 BP.
DE Human EST-derived coding sequence SEQ ID NO: 209.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSB-) HYSEQ INC.
Query Match 71.7%; Score 928.2; DB 4; Length 1416;
Best Local Similarity 97.7%; Pred. No. 2.5e-232;
RESULT 344
ID ADP56686 standard; cDNA; 972 BP.
DE Human junction adhesion molecule 2 splice variant (huJAM2sv) cDNA.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (LELL) LILLY & CO ELI.
Query Match 71.5%; Score 926; DB 12; Length 972;
Best Local Similarity 100.0%; Pred. No. 7.9e-232;
RESULT 345
ID AAV34310 standard; DNA; 1022 BP.
DE Human secreted protein gene 25 clone HTEEB42.
PN WO9840483-A2.
PD 17-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 71.2%; Score 923.4; DB 2; Length 1022;
Best Local Similarity 98.9%; Pred. No. 7.1e-231;
RESULT 346
ID AAD44660 standard; cDNA; 1022 BP.
DE Human secreted protein-encoding Gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
PN US200207287-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
Query Match 71.2%; Score 922.4; DB 6; Length 1022;
Best Local Similarity 98.9%; Pred. No. 7.1e-231;
RESULT 347
ID AAD44878 standard; cDNA; 1022 BP.
DE Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
PN US2002076756-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 Query Match 71.2%; Score 922.4; DB 6; Length 1022;
 Best Local Similarity 98.9%; Pred. No. 7.1e-231;
 RESULT 348
 ID AC50637 standard; cDNA; 1022 BP.
 DE Human secreted protein coding sequence, SEQ ID 304.
 PN WO200295010-A2.
 PD 28-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 71.2%; Score 922.4; DB 8; Length 1022;
 Best Local Similarity 98.9%; Pred. No. 7.1e-231;
 RESULT 349
 ID AB271351 standard; cDNA; 1022 BP.
 DE Secreted protein-encoding gene 162 cDNA clone HTEEB42, SEQ ID NO:172.
 PN WO200276488-A1.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 71.2%; Score 922.4; DB 8; Length 1022;
 Best Local Similarity 98.9%; Pred. No. 7.1e-231;
 RESULT 350
 ID ABX96990 standard; cDNA; 1022 BP.
 DE Human secreted protein gene 25, cDNA.
 PN US2002172994-A1.
 PD 21-NOV-2002.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYI/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 Query Match 71.2%; Score 922.4; DB 8; Length 1022;
 Best Local Similarity 98.9%; Pred. No. 7.1e-231;
 RESULT 351
 ID AD891286 standard; cDNA; 1022 BP.
 DE Human secreted protein cDNA #SEQ ID 232.
 PN WO2003004622-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 71.2%; Score 922.4; DB 9; Length 1022;
 Best Local Similarity 98.9%; Pred. No. 7.1e-231;
 RESULT 352
 ID ADC73716 standard; DNA; 1022 BP.
 DE Human secreted protein-related DNA - SEQ ID 349.
 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 71.2%; Score 922.4; DB 10; Length 1022;
 Best Local Similarity 98.9%; Pred. No. 7.1e-231;
 RESULT 353
 ID ADG89762 standard; cDNA; 1022 BP.
 DE Human cDNA from secreted protein gene 25.
 PN US2003225009-A1.
 PD 04-DEC-2003.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (LIYI/) LI Y.
 PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (HAST/) HASTINGS G A.
 Query Match 71.2%; Score 922.4; DB 12; Length 1022;
 Best Local Similarity 98.9%; Pred. No. 7.1e-231;
 RESULT 354
 ID AED10199 standard; cDNA; 1022 BP.
 DE Human secreted protein encoding cDNA clone, SEQ ID 35.
 PN US2005208621-A1.
 PD 22-SEP-2005.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 71.2%; Score 922.4; DB 14; Length 1022;
 Best Local Similarity 98.9%; Pred. No. 7.1e-231;
 RESULT 355
 ID ADV43971 standard; cDNA; 897 BP.
 DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1599.
 PN WO2004108899-A2.
 PD 16-DEC-2004.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 66.8%; Score 865.2; DB 14; Length 897;
 Best Local Similarity 99.1%; Pred. No. 6.3e-216;
 RESULT 356
 ID AAL51599 standard; DNA; 897 BP.
 DE Human junctional adhesion molecule 2 (huJAM2) coding sequence.
 PN WO2003008541-A2.
 PD 30-JAN-2003.
 PA (ELIL) LILLY & CO ELI.
 Query Match 66.6%; Score 862; DB 8; Length 897;
 Best Local Similarity 98.9%; Pred. No. 4.3e-215;
 RESULT 357
 ID AAS86528 standard; cDNA; 1430 BP.
 DE DNA encoding novel human diagnostic protein #22332.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 60.6%; Score 784.4; DB 5; Length 1430;
 Best Local Similarity 91.9%; Pred. No. 1.1e-194;
 RESULT 358
 ID AAI61103 standard; cDNA; 930 BP.
 DE Human polynucleotide SEQ ID NO 5092.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 49.3%; Score 638.2; DB 4; Length 930;
 Best Local Similarity 98.8%; Pred. No. 1.7e-156;
 RESULT 359
 ID AAF74414 standard; DNA; 905 BP.
 DE Angiogenesis protein AAL nucleotide sequence (Fig 7).
 PN WO20011086-A2.
 PD 15-FEB-2001.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 47.7%; Score 617.2; DB 5; Length 905;
 Best Local Similarity 98.7%; Pred. No. 5.3e-151;
 RESULT 360
 ID AAA95305 standard; cDNA; 1626 BP.
 DE Murine Cram-2 coding sequence.
 PN WO200053749-A2.
 PD 14-SEP-2000.
 PA (RMFD-) RMF DICTAGENE SA.
 Query Match 45.9%; Score 594.2; DB 3; Length 1626;
 Best Local Similarity 78.9%; Pred. No. 7.3e-145;
 RESULT 361
 ID ADQ53429 standard; DNA; 647 BP.
 DE Novel canine microarray-related DNA sequence SeqID4731.
 PN WO2004063324-A2.


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PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ ) PFIZER PROD INC.
Query Match 38.3%; Score 496.6; DB 13; Length 647;
Best Local Similarity 88.3%; Pred. No. 1.7e-119;
RESULT 362
ID RAI59317 standard; cDNA; 561 BP.
DE Human polynucleotide SEQ ID NO 1520.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 34.5%; Score 446.2; DB 4; Length 561;
Best Local Similarity 98.3%; Pred. No. 2.5e-106;
RESULT 363
ID ACH37074 standard; cDNA; 450 BP.
DE Human endothelial cell cDNA #5207.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 30.0%; Score 389; DB 9; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.2e-91;
RESULT 364
ID AAX81783 standard; DNA; 413 BP.
DE Consensus sequence DNA30954 encoding an A33 related antigen.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH ) GENENTECH INC.
Query Match 29.6%; Score 383.2; DB 2; Length 413;
Best Local Similarity 99.0%; Pred. No. 6.9e-90;
RESULT 365
ID AAX37665 standard; cDNA; 413 BP.
DE Human PRO protein derived EST consensus sequence DNA30954.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match 29.6%; Score 383.2; DB 2; Length 413;
Best Local Similarity 99.0%; Pred. No. 6.9e-90;
RESULT 366
ID ABX93489 standard; cDNA; 413 BP.
DE Consensus sequence expressed sequence tag, EST, DNA30954.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 29.6%; Score 383.2; DB 8; Length 413;
Best Local Similarity 99.0%; Pred. No. 6.9e-90;
RESULT 367
ID ADH62554 standard; DNA; 413 BP.
DE Human DNA30954 consensus DNA.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 29.6%; Score 383.2; DB 10; Length 413;
Best Local Similarity 99.0%; Pred. No. 6.9e-90;
RESULT 368
ID ADN35306 standard; DNA; 413 BP.
DE Human PRO245 consensus DNA fragment DNA30954.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 29.6%; Score 383.2; DB 12; Length 413;
Best Local Similarity 99.0%; Pred. No. 6.9e-90;
RESULT 369
ID AAS86525 standard; cDNA; 493 BP.
DE DNA encoding novel human diagnostic protein #22329.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 26.6%; Score 344.2; DB 5; Length 493;
Best Local Similarity 91.7%; Pred. No. 1.2e-79;
RESULT 370
ID AAL35849 standard; DNA; 3762 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2214.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.5%; Score 343.6; DB 4; Length 3762;
Best Local Similarity 98.9%; Pred. No. 4.2e-79;
RESULT 371
ID AAL35848 standard; DNA; 3762 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2213.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.5%; Score 343.6; DB 4; Length 3762;
Best Local Similarity 98.9%; Pred. No. 4.2e-79;
RESULT 372
ID AAL35847 standard; DNA; 3762 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2212.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.5%; Score 343.6; DB 4; Length 3762;
Best Local Similarity 98.9%; Pred. No. 4.2e-79;
RESULT 373
ID ABX58836 standard; cDNA; 3762 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1180.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 26.5%; Score 343.6; DB 8; Length 3762;
Best Local Similarity 98.9%; Pred. No. 4.2e-79;
RESULT 374
ID ABX58837 standard; cDNA; 3762 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1181.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 26.5%; Score 343.6; DB 8; Length 3762;
Best Local Similarity 98.9%; Pred. No. 4.2e-79;
RESULT 375
ID ABX58835 standard; cDNA; 3762 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1179.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 26.5%; Score 343.6; DB 8; Length 3762;
Best Local Similarity 98.9%; Pred. No. 4.2e-79;
RESULT 376
ID ADJ29585 standard; DNA; 3762 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2212.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.5%; Score 343.6; DB 12; Length 3762;
Best Local Similarity 98.9%; Pred. No. 4.2e-79;
RESULT 377
ID ADJ29587 standard; DNA; 3762 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2214.
PN US2004009488-A1.
PD 15-JAN-2004.
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PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.5%; Score 343.6; DB 12; Length 3762;
Best Local Similarity 98.9%; Pred. No. 4.2e-79;
RESULT 378
ID ADU29586 standard; DNA; 3762 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2213.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.5%; Score 343.6; DB 12; Length 3762;
Best Local Similarity 98.9%; Pred. No. 4.2e-79;
RESULT 379
ID AAV89708 standard; cDNA; 343 BP.
DE EST clone CT864.
PN WO9845436-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 23.4%; Score 302.6; DB 2; Length 343;
Best Local Similarity 97.2%; Pred. No. 8e-69;
RESULT 380
ID AAX37668 standard; cDNA; 301 BP.
DE Human PRO protein derived EST DNA sequence T89217.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 22.3%; Score 289; DB 2; Length 301;
Best Local Similarity 99.7%; Pred. No. 2.8e-65;
RESULT 381
ID ACH29690 standard; cDNA; 433 BP.
DE Human testis cDNA #76.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 21.8%; Score 282.4; DB 9; Length 433;
Best Local Similarity 99.6%; Pred. No. 1.7e-63;
RESULT 382
ID ADP28230 standard; DNA; 270 BP.
DE Human secreted protein encoding sequence SEQ ID #228.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 20.0%; Score 259.2; DB 12; Length 270;
Best Local Similarity 98.9%; Pred. No. 1.7e-57;
RESULT 383
ID AAX37669 standard; cDNA; 253 BP.
DE Human PRO protein derived EST DNA sequence 1861250.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 253; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.8e-56;
RESULT 384
ID AAX37666 standard; cDNA; 228 BP.
DE Human PRO protein derived EST DNA sequence 2715631.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 228; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
RESULT 385
ID AAX37667 standard; cDNA; 241 BP.
DE Human PRO protein derived EST DNA sequence 1622388.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 17.1%; Score 221.2; DB 2; Length 241;
Best Local Similarity 97.8%; Pred. No. 1.4e-47;
RESULT 386
ID AEF07223 standard; DNA; 94950 BP.

DE GRIN3A locus of the human genome.
PN WO2005118834-A2.
PD 15-DEC-2005.
PA (SEQU-) SEQUENOM INC.
Query Match 16.9%; Score 219.4; DB 15; Length 94950;
Best Local Similarity 87.5%; Pred. No. 5.7e-46;
RESULT 387
ID AAS30108 standard; DNA; 9474 BP.
DE Human lung antigen genomic DNA #178.
PN WO200155303-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.7%; Score 216.8; DB 5; Length 9474;
Best Local Similarity 86.8%; Pred. No. 1e-45;
RESULT 388
ID ADB33445 standard; DNA; 9474 BP.
DE Human novel lung related polypeptide DNA SEQ ID NO 372.
PN US2003054368-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.7%; Score 216.8; DB 10; Length 9474;
Best Local Similarity 86.8%; Pred. No. 1e-45;
RESULT 389
ID AEB31547 standard; DNA; 23353 BP.
DE Glutamate-cysteine ligase modulating subunit (GCLM) DNA.
PN WO2005068649-A1.
PD 28-JUL-2005.
PA (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG.
Query Match 16.6%; Score 215.6; DB 14; Length 23353;
Best Local Similarity 78.4%; Pred. No. 3e-45;
RESULT 390
ID ADQ97804 standard; DNA; 50807 BP.
DE Human cancer associated sequence HD10-048, SEQ ID 781.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 16.6%; Score 215.6; DB 12; Length 50807;
Best Local Similarity 78.0%; Pred. No. 4.3e-45;
RESULT 391
ID ACF62732 standard; DNA; 177531 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:660.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 16.6%; Score 215.2; DB 8; Length 177531;
Best Local Similarity 81.0%; Pred. No. 9.4e-45;
RESULT 392
ID ADB20847 standard; DNA; 177531 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:660.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 16.6%; Score 215.2; DB 8; Length 177531;
Best Local Similarity 81.0%; Pred. No. 9.4e-45;
RESULT 393
ID ADB87936 standard; DNA; 177531 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:660.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 16.6%; Score 215.2; DB 10; Length 177531;
Best Local Similarity 81.0%; Pred. No. 9.4e-45;
RESULT 394
ID ADB96919 standard; DNA; 177531 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:660.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 16.6%; Score 215.2; DB 10; Length 177531;
Best Local Similarity 81.0%; Pred. No. 9.4e-45;
RESULT 395
ID ADB92110 standard; DNA; 177531 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:660.

PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 16.6%; Score 215.2; DB 10; Length 177531;
Best Local Similarity 81.0%; Pred. No. 9.4e-45;
RESULT 396
ID ADH74617 standard; DNA; 177531 BP.
DE Human BAC clone GSI-259H13 CYP3A5 genomic DNA.
PN US2003143537-A1.
PD 31-JUL-2003.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match 16.6%; Score 215.2; DB 10; Length 177531;
Best Local Similarity 81.0%; Pred. No. 9.4e-45;
RESULT 397
ID AAK89905 standard; DNA; 9973 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3481.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.6%; Score 214.4; DB 4; Length 9973;
Best Local Similarity 85.7%; Pred. No. 4.3e-45;
RESULT 398
ID AAL35986 standard; DNA; 9973 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2351.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.6%; Score 214.4; DB 4; Length 9973;
Best Local Similarity 85.7%; Pred. No. 4.3e-45;
RESULT 399
ID ABX58974 standard; cDNA; 9973 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1318.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 16.6%; Score 214.4; DB 8; Length 9973;
Best Local Similarity 85.7%; Pred. No. 4.3e-45;
RESULT 400
ID ADJ29724 standard; DNA; 9973 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2351.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.6%; Score 214.4; DB 12; Length 9973;
Best Local Similarity 85.7%; Pred. No. 4.3e-45;
RESULT 401
ID ACN44674 standard; DNA; 129042 BP.
DE Human genomic sequence hCG27276.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 16.6%; Score 214.4; DB 11; Length 129042;
Best Local Similarity 82.4%; Pred. No. 1.3e-44;
RESULT 402
ID ADK41243 standard; DNA; 37790 BP.
DE DNA region of human chromosome 19, SEQ ID No 1.
PN WO2004003229-A2.
PD 08-JAN-2004.
PA (UYAA-) UNIV AARHUS.
PA (ARBE-) ARBEJDSMILJO INST NAT INST OCCUPA.
Query Match 16.5%; Score 214.2; DB 12; Length 37790;
Best Local Similarity 82.7%; Pred. No. 8.8e-45;
RESULT 403
ID AEF93651 standard; DNA; 37790 BP.
DE Human chromosome 19q r region DNA.
PN WO2006018023-A2.
PD 23-FEB-2006.
PA (UYAA-) UNIV AARHUS.
PA (ARBE-) ARBEJDSMILJOINSTITTUTET.
Query Match 16.5%; Score 214.2; DB 15; Length 37790;
Best Local Similarity 82.7%; Pred. No. 8.8e-45;

RESULT 404
ID ADK41244 standard; DNA; 38166 BP.
DE DNA region of human chromosome 19, SEQ ID No 2.
PN WO2004003229-A2.
PD 08-JAN-2004.
PA (UYAA-) UNIV AARHUS.
PA (ARBE-) ARBEJDSMILJO INST NAT INST OCCUPA.
Query Match 16.5%; Score 214.2; DB 12; Length 38166;
Best Local Similarity 82.7%; Pred. No. 8.8e-45;
RESULT 405
ID ACN44850 standard; DNA; 142318 BP.
DE Human genomic sequence hCG33122.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 16.4%; Score 212.2; DB 11; Length 142318;
Best Local Similarity 73.8%; Pred. No. 5.2e-44;
RESULT 406
ID ADA02714 standard; DNA; 53413 BP.
DE Human VDACL carcinoma associated gene, SEQ ID NO:1232.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 16.4%; Score 212; DB 9; Length 53413;
Best Local Similarity 72.3%; Pred. No. 3.8e-44;
RESULT 407
ID ADB72452 standard; DNA; 53413 BP.
DE Human VDACL gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 16.4%; Score 212; DB 10; Length 53413;
Best Local Similarity 72.3%; Pred. No. 3.8e-44;
RESULT 408
ID ADE95962 standard; DNA; 53413 BP.
DE Human VDACL Gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 16.4%; Score 212; DB 10; Length 53413;
Best Local Similarity 72.3%; Pred. No. 3.8e-44;
RESULT 409
ID ADL13638 standard; DNA; 186528 BP.
DE Osteoarthritis-associated polymorphic nucleotide #170.
PN WO2003054186-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 16.4%; Score 212; DB 10; Length 186528;
Best Local Similarity 82.5%; Pred. No. 6.6e-44;
RESULT 410
ID ABD33276 standard; DNA; 256190 BP.
DE Human cancer-associated (CA) gene HD07-048.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 16.4%; Score 212; DB 13; Length 256190;
Best Local Similarity 77.1%; Pred. No. 7.6e-44;
RESULT 411
ID ACN45138 standard; DNA; 23694 BP.
DE Human genomic sequence hCG17175.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 16.4%; Score 211.8; DB 11; Length 23694;
Best Local Similarity 86.9%; Pred. No. 3e-44;
RESULT 412
ID AAK69400 standard; DNA; 11456 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24212.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.3%; Score 211.4; DB 4; Length 11456;
Best Local Similarity 85.8%; Pred. No. 2.8e-44;

RESULT 413
 ID AAS12439 standard; DNA; 37590 BP.
 DE DNA encoding 1-aminocyclopropane carboxylate synthase #10.
 PN WO200168879-A2.
 PD 20-SEP-2001.
 PA (FARB) BAYER AG.
 Query Match 16.3%; Score 211.4; DB 4; Length 37590;
 Best Local Similarity 85.8%; Pred. No. 4.7e-44;
 RESULT 414
 Query Match 16.3%; Score 211; DB 14; Length 110000;
 Best Local Similarity 79.2%; Pred. No. 9.6e-44;
 RESULT 415
 ID ADH28900 standard; DNA; 5191 BP.
 DE Human chronic myelogenous leukaemia (CML) gene marker #168.
 PN US2003104426-A1.
 PD 05-JUN-2003.
 PA (LINS)/ LINSLEY P S.
 PA (MAOM)/ MAO M.
 PA (DAIH)/ DAI H.
 PA (HEYI)/ HE Y.
 PA (RADI)/ RADICH J P.
 Query Match 16.3%; Score 210.8; DB 10; Length 5191;
 Best Local Similarity 79.8%; Pred. No. 2.8e-44;
 RESULT 416
 ID ADG39645 standard; cDNA; 5191 BP.
 DE Human cDNA #5 of gene differentially expressed in colorectal cancer.
 PN US2003186302-A1.
 PD 02-OCT-2003.
 PA (WANG)/ WANG Y.
 Query Match 16.3%; Score 210.8; DB 12; Length 5191;
 Best Local Similarity 79.8%; Pred. No. 2.8e-44;
 RESULT 417
 ID ADG39694 standard; cDNA; 5191 BP.
 DE Human cDNA #5 of gene differentially expressed in colorectal cancer.
 PN US2003186303-A1.
 PD 02-OCT-2003.
 PA (WANG)/ WANG Y.
 Query Match 16.3%; Score 210.8; DB 12; Length 5191;
 Best Local Similarity 79.8%; Pred. No. 2.8e-44;
 RESULT 418
 ID ABQ99289 standard; cDNA; 5490 BP.
 DE Human coding sequence SEQ ID 22.
 PN WO200259260-A2.
 PD 01-AUG-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 16.3%; Score 210.8; DB 6; Length 5490;
 Best Local Similarity 79.8%; Pred. No. 2.9e-44;
 RESULT 419
 ID AEF74614 standard; DNA; 5906 BP.
 DE Human polynucleotide #128.
 PN WO2006013561-A2.
 PD 09-FEB-2006.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 Query Match 16.3%; Score 210.8; DB 15; Length 5906;
 Best Local Similarity 79.8%; Pred. No. 3e-44;
 RESULT 420
 ID ACN45066 standard; DNA; 27189 BP.
 DE Human genomic sequence hCG30694.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 16.3%; Score 210.8; DB 11; Length 27189;
 Best Local Similarity 85.8%; Pred. No. 5.9e-44;
 RESULT 421
 ID ADN48757 standard; DNA; 34827 BP.
 DE Human Notch (Drosophila) homologue 4 DNA #2.
 PN US200407569-A1.
 PD 22-APR-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 16.2%; Score 210.2; DB 12; Length 34827;
 Best Local Similarity 85.2%; Pred. No. 9.4e-44;
 RESULT 422

ID ADO01157 standard; DNA; 34827 BP.
 DE Human Notch (Drosophila) homologue 4 DNA #2.
 PN US2004077568-A1.
 PD 22-APR-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 16.2%; Score 210.2; DB 13; Length 34827;
 Best Local Similarity 85.2%; Pred. No. 9.4e-44;
 RESULT 423
 ID ASK83459 standard; cDNA; 128978 BP.
 DE Human cDNA differentially expressed in granulocytic cells #30.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 16.2%; Score 210.2; DB 6; Length 128978;
 Best Local Similarity 87.9%; Pred. No. 1.7e-43;
 RESULT 424
 ID AAD54587 standard; DNA; 128978 BP.
 DE Human LIM kinase (LIMK) DNA #6.
 PN WO200299048-A2.
 PD 12-DEC-2002.
 PA (EXEL-) EXELIXIS INC.
 Query Match 16.2%; Score 210.2; DB 8; Length 128978;
 Best Local Similarity 87.9%; Pred. No. 1.7e-43;
 RESULT 425
 ID ADR52994 standard; DNA; 128978 BP.
 DE Drug therapy altered expressed gene #345.
 PN WO2004072265-A2.
 PD 26-AUG-2004.
 PA (AMHP) WIETH.
 PA (BURC)/ BURCZYNSKI M.
 PA (TWIN)/ TWINE N.
 PA (DORN)/ DORNER A J.
 PA (TREP)/ TREPICCHIO W L.
 Query Match 16.2%; Score 210.2; DB 13; Length 128978;
 Best Local Similarity 87.9%; Pred. No. 1.7e-43;
 RESULT 426
 ID ADX07226 standard; DNA; 128978 BP.
 DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1791.
 PN WO2005012875-A2.
 PD 10-FEB-2005.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 16.2%; Score 210.2; DB 14; Length 128978;
 Best Local Similarity 87.9%; Pred. No. 1.7e-43;
 RESULT 427
 ID ADZ10962 standard; DNA; 74424 BP.
 DE Human STAT3 DNA sequence - SEQ ID 153.
 PN US2005074879-A1.
 PD 07-APR-2005.
 PA (KARR)/ KARRAS J G.
 Query Match 16.2%; Score 210; DB 14; Length 74424;
 Best Local Similarity 82.1%; Pred. No. 1.5e-43;
 RESULT 428
 ID ADL13748 standard; DNA; 169144 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #280.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 16.2%; Score 209.4; DB 10; Length 169144;
 Best Local Similarity 81.1%; Pred. No. 3e-43;
 RESULT 429
 ID ACN43926 standard; DNA; 53242 BP.
 DE Human genomic sequence hCG1782215.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 16.2%; Score 209.2; DB 11; Length 53242;
 Best Local Similarity 79.7%; Pred. No. 2.1e-43;
 RESULT 430
 ID AED14491 standard; DNA; 682 BP.
 DE Human cumulus cell differentially expressed gene.
 PN WO2005094306-A2.
 PD 13-OCT-2005.
 PA (UNMS) UNIV MICHIGAN STATE.

Query Match 16.1%; Score 208.6; DB 14; Length 682;
Best Local Similarity 85.1%; Pred. No. 4.4e-44;
RESULT 431
ID ABK83574 standard; cDNA; 147419 BP.
DE Human cDNA differentially expressed in granulocytic cells #145.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 16.1%; Score 208.6; DB 6; Length 147419;
Best Local Similarity 77.9%; Pred. No. 4.7e-43;
RESULT 432
ID ABA96565 standard; cDNA; 952 BP.
DE Human tyrosinase 9-encoding cDNA.
PN WO200190164-A1.
PD 29-NOV-2001.
PA (SHAN-) SHANGHAI BLOWNDOW GENE DEV INC.
Query Match 16.1%; Score 208.2; DB 6; Length 952;
Best Local Similarity 85.1%; Pred. No. 6.5e-44;
RESULT 433
ID AAK65774 standard; DNA; 2635 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20586.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.1%; Score 208.2; DB 4; Length 2635;
Best Local Similarity 81.7%; Pred. No. 1e-43;
RESULT 434
ID ABD33104 standard; DNA; 130877 BP.
DE Human cancer-associated (CA) gene HD07-009.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 16.1%; Score 208.2; DB 13; Length 130877;
Best Local Similarity 86.4%; Pred. No. 5.6e-43;
RESULT 435
ID AAS86526 standard; cDNA; 208 BP.
DE DNA encoding novel human diagnostic protein #22330.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSE INC.
Query Match 16.1%; Score 208; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.8e-44;
RESULT 436
ID AOQ97497 standard; DNA; 21850 BP.
DE Human cancer associated sequence HD09-005, SEQ ID 474.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 16.1%; Score 208; DB 12; Length 21850;
Best Local Similarity 76.5%; Pred. No. 2.9e-43;
RESULT 437
ID ABK42295 standard; DNA; 10256 BP.
DE Genomic sequence #194 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.0%; Score 207.8; DB 4; Length 10256;
Best Local Similarity 82.6%; Pred. No. 2.3e-43;
RESULT 438
ID ADB60451 standard; DNA; 10256 BP.
DE Connective tissue related genomic DNA #194.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.0%; Score 207.8; DB 9; Length 10256;
Best Local Similarity 82.6%; Pred. No. 2.3e-43;
RESULT 439
ID AED89402 standard; DNA; 155515 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 42.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 16.0%; Score 207.8; DB 14; Length 155515;

Best Local Similarity 85.4%; Pred. No. 7.7e-43;
RESULT 440
ID AED89421 standard; DNA; 159497 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 61.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 16.0%; Score 207.8; DB 14; Length 159497;
Best Local Similarity 85.4%; Pred. No. 7.8e-43;
RESULT 441
ID AED89403 standard; DNA; 159660 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 43.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 16.0%; Score 207.8; DB 14; Length 159660;
Best Local Similarity 85.4%; Pred. No. 7.8e-43;
RESULT 442
ID AED89401 standard; DNA; 177623 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 41.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 16.0%; Score 207.8; DB 14; Length 177623;
Best Local Similarity 85.4%; Pred. No. 8.2e-43;
RESULT 443
ID AAS20588 standard; DNA; 84495 BP.
DE Human methionine aminopeptidase protease genomic DNA.
PN US6329188-B1.
PD 11-DEC-2001.
PA (PEKE) PE CORP NY.
Query Match 16.0%; Score 207.6; DB 6; Length 84495;
Best Local Similarity 80.2%; Pred. No. 6.7e-43;
RESULT 444
ID ABA18609 standard; DNA; 538 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10940.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.0%; Score 207.4; DB 5; Length 538;
Best Local Similarity 85.6%; Pred. No. 8.2e-44;
RESULT 445
ID AA26440 standard; cDNA; 1175 BP.
DE Human secreted protein gene 95 SEQ ID NO:105.
PN WO200006698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.0%; Score 207; DB 3; Length 1175;
Best Local Similarity 80.5%; Pred. No. 1.5e-43;
RESULT 446
ID ADL71501 standard; cDNA; 1175 BP.
DE Novel human secreted protein cDNA seqid 105.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSU G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAF/) LAFLEUR D W.
PA (WEIY/) WEI Y.
Query Match 16.0%; Score 207; DB 12; Length 1175;
Best Local Similarity 80.5%; Pred. No. 1.5e-43;
RESULT 447
ID ABX04164 standard; cDNA; 2669 BP.
DE Human mRNA differentially expressed in mesenchymal cells #11.
PN WO200271927-A2.
PD 19-SEP-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 16.0%; Score 207; DB 6; Length 2669;
Best Local Similarity 73.3%; Pred. No. 2.1e-43;
RESULT 448

ID ABK84715 standard; cDNA; 2669 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1286.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 16.0%; Score 207; DB 6; Length 2669;
 Best Local Similarity 73.3%; Pred. No. 2.1e-43;
 RESULT 449
 ID AEF75349 standard; DNA; 2669 BP.
 DE Human polynucleotide #863.
 PN WO2006013561-A2.
 PD 09-FEB-2006.
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
 Query Match 16.0%; Score 207; DB 15; Length 2669;
 Best Local Similarity 73.3%; Pred. No. 2.1e-43;
 RESULT 450
 ID AED17971 standard; DNA; 145616 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 222.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 16.0%; Score 206.8; DB 14; Length 145616;
 Best Local Similarity 85.3%; Pred. No. 1.4e-42;
 RESULT 451
 ID AEC82893 standard; cDNA; 156321 BP.
 DE Breast cancer associated cDNA SEQ ID NO 461.
 PN WO2005083429-A2.
 PD 09-SEP-2005.
 PA (VERI-) VERIDEX LLC.
 Query Match 16.0%; Score 206.6; DB 14; Length 156321;
 Best Local Similarity 84.8%; Pred. No. 1.6e-42;
 RESULT 452
 ID AD56129 standard; DNA; 27740 BP.
 DE Human NOTCH1 carcinoma associated (CA) gene.
 PN WO2003035837-A2.
 PD 01-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 15.9%; Score 206.4; DB 8; Length 27740;
 Best Local Similarity 79.9%; Pred. No. 8.4e-43;
 RESULT 453
 ID ADA02492 standard; DNA; 27740 BP.
 DE Human NOTCH1 carcinoma associated gene, SEQ ID NO:1010.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 15.9%; Score 206.4; DB 9; Length 27740;
 Best Local Similarity 79.9%; Pred. No. 8.4e-43;
 RESULT 454
 ID ADB72230 standard; DNA; 27740 BP.
 DE Human NOTCH1 gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 15.9%; Score 206.4; DB 10; Length 27740;
 Best Local Similarity 79.9%; Pred. No. 8.4e-43;
 RESULT 455
 ID ADZ12496 standard; DNA; 72337 BP.
 DE Human cancer-associated genomic DNA #3.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 15.9%; Score 206.4; DB 14; Length 72337;
 Best Local Similarity 79.9%; Pred. No. 1.3e-42;
 RESULT 456
 ID ACA64895 standard; DNA; 134292 BP.
 DE Human GABBR1 DNA corresponding to AL031983.
 PN DE10127572-A1.
 PD 05-DEC-2002.
 PA (PATH-) PATHOARRAY GMBH.
 Query Match 15.9%; Score 206.4; DB 8; Length 134292;
 Best Local Similarity 81.8%; Pred. No. 1.7e-42;
 RESULT 457

ID AED18093 standard; DNA; 134292 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 344.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 15.9%; Score 206.4; DB 14; Length 134292;
 Best Local Similarity 81.8%; Pred. No. 1.7e-42;
 RESULT 458
 ID ABK89372 standard; DNA; 6566 BP.
 DE Human monocarboxylate transporter related genomic DNA.
 PN WO200248364-A2.
 PD 20-JUN-2002.
 PA (PEKE) PE CORP NY.
 Query Match 15.9%; Score 206.2; DB 6; Length 6566;
 Best Local Similarity 82.3%; Pred. No. 5e-43;
 RESULT 459
 ID ADX08890 standard; DNA; 7639 BP.
 DE Human matrix metalloproteinase 9 gene.
 PN WO2005017113-A2.
 PD 24-FEB-2005.
 PA (LOVE-) LOVELACE RESPIRATORY RES INST.
 Query Match 15.9%; Score 206.2; DB 14; Length 7639;
 Best Local Similarity 84.6%; Pred. No. 5.4e-43;
 RESULT 460
 ID ADB85543 standard; DNA; 51256 BP.
 DE Human sentrin-specific family-related protease genomic DNA sequence.
 Query Match 15.9%; Score 206.2; DB 10; Length 51256;
 Best Local Similarity 74.9%; Pred. No. 1.2e-42;
 RESULT 461
 ID ADK66161 standard; DNA; 51256 BP.
 DE Human protease gene.
 Query Match 15.9%; Score 206.2; DB 10; Length 51256;
 Best Local Similarity 74.9%; Pred. No. 1.2e-42;
 RESULT 462
 ID ADQ97223 standard; DNA; 63751 BP.
 DE Human cancer associated sequence HD08-015, SEQ ID 199.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 15.9%; Score 206.2; DB 12; Length 63751;
 Best Local Similarity 82.4%; Pred. No. 1.4e-42;
 RESULT 463
 ID ADQ97313 standard; DNA; 121062 BP.
 DE Human cancer associated sequence HD08-030, SEQ ID 290.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 15.9%; Score 206.2; DB 12; Length 121062;
 Best Local Similarity 76.7%; Pred. No. 1.8e-42;
 RESULT 464
 ID ADP67269 standard; DNA; 152501 BP.
 DE Human chromosome 1 7500-160000bp.
 PN US2004110143-A1.
 PD 10-JUN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 15.9%; Score 206.2; DB 12; Length 152501;
 Best Local Similarity 81.5%; Pred. No. 2e-42;
 RESULT 465
 ID AED89410 standard; DNA; 170189 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 50.
 PN WO2005106044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 15.9%; Score 206.2; DB 14; Length 170189;
 Best Local Similarity 86.3%; Pred. No. 2.1e-42;
 RESULT 466
 ID ADQ20606 standard; DNA; 195917 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3426.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 15.9%; Score 206.2; DB 12; Length 195917;
 Best Local Similarity 82.9%; Pred. No. 2.2e-42;

RESULT 467
ID ADQ18927 standard; DNA; 210204 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1746.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 15.9%; Score 206.2; DB 12; Length 210204;
Best Local Similarity 82.4%; Pred. No. 2.3e-42;
RESULT 468
ID ADM01487 standard; cDNA; 2345 BP.
DE Human cDNA of the invention SEQ ID NO:172.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.9%; Score 206; DB 11; Length 2345;
Best Local Similarity 80.1%; Pred. No. 3.6e-43;
RESULT 469
ID AEC84417 standard; cDNA; 2345 BP.
DE Human cDNA clone BRACE20228480, SEQ ID 172.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.9%; Score 206; DB 14; Length 2345;
Best Local Similarity 80.1%; Pred. No. 3.6e-43;
RESULT 470
ID ADA02696 standard; DNA; 59554 BP.
DE Human TK2 carcinoma associated gene, SEQ ID NO:1214.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.9%; Score 206; DB 9; Length 59554;
Best Local Similarity 79.7%; Pred. No. 1.5e-42;
RESULT 471
ID ADB72434 standard; DNA; 59554 BP.
DE Human TK2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.9%; Score 206; DB 10; Length 59554;
Best Local Similarity 79.7%; Pred. No. 1.5e-42;
RESULT 472
ID ADE95944 standard; DNA; 59554 BP.
DE Human TK2 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.9%; Score 206; DB 10; Length 59554;
Best Local Similarity 79.7%; Pred. No. 1.5e-42;
RESULT 473
ID AAK83109 standard; DNA; 2816 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37921.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.9%; Score 205.6; DB 4; Length 2816;
Best Local Similarity 83.5%; Pred. No. 5e-43;
RESULT 474
ID ACD28669 standard; DNA; 4741 BP.
DE DNA encoding human acid sphingomyelinase, ASM.
PN US6541218-B1.
PD 01-APR-2003.
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
Query Match 15.9%; Score 205.6; DB 9; Length 4741;
Best Local Similarity 84.3%; Pred. No. 6.3e-43;
RESULT 475
ID AAQ33392 standard; DNA; 4742 BP.
DE ASM genomic DNA.
PN EP520843-A2.
PD 30-DEC-1992.
PA (MOUN) MOUNT SINAI MEDICAL CENT.
Query Match 15.9%; Score 205.6; DB 2; Length 4742;
Best Local Similarity 84.2%; Pred. No. 6.3e-43;
RESULT 476

ID AAT95070 standard; DNA; 4742 BP.
DE Human acid sphingomyelinase genomic DNA.
PN US5686240-A.
PD 11-NOV-1997.
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
Query Match 15.9%; Score 205.6; DB 2; Length 4742;
Best Local Similarity 84.2%; Pred. No. 6.3e-43;
RESULT 477
ID ABA19132 standard; DNA; 14617 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11463.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.9%; Score 205.6; DB 5; Length 14617;
Best Local Similarity 86.3%; Pred. No. 1e-42;
RESULT 478
ID ADC87623 standard; DNA; 118584 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2076.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.9%; Score 205.6; DB 10; Length 118584;
Best Local Similarity 84.8%; Pred. No. 2.6e-42;
RESULT 479
ID ADC87010 standard; DNA; 349999 BP.
DE Human GPCR gene SEQ ID NO:1463.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.9%; Score 205.6; DB 10; Length 349999;
Best Local Similarity 84.8%; Pred. No. 4.1e-42;
RESULT 480
ID ACN44490 standard; DNA; 32865 BP.
DE Human genomic sequence hCG25375.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.9%; Score 205.4; DB 11; Length 32865;
Best Local Similarity 80.9%; Pred. No. 1.7e-42;
RESULT 481
ID ABK90888 standard; DNA; 112132 BP.
DE Human ATP-dependent protease, genomic sequence.
PN US2002081704-A1.
PD 27-JUN-2002.
PA (GUEG/) GUEGLER K.
PA (WEBS/) WEBSTER M.
PA (YANC/) YAN C.
PA (SHAO/) SHAO W.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 15.8%; Score 205.2; DB 6; Length 112132;
Best Local Similarity 82.2%; Pred. No. 3.2e-42;
RESULT 482
ID ADM56267 standard; DNA; 112132 BP.
DE Human ATP-dependent protease DNA.
PN US6620607-B1.
PD 16-SEP-2003.
PA (APPL-) APPLERA CORP.
Query Match 15.8%; Score 205.2; DB 11; Length 112132;
Best Local Similarity 82.2%; Pred. No. 3.2e-42;
RESULT 483
ID ADV85874 standard; DNA; 112132 BP.
DE Human protease gene.
PN US2004253705-A1.
PD 16-DEC-2004.
PA (APPL-) APPLERA CORP.
Query Match 15.8%; Score 205.2; DB 14; Length 112132;
Best Local Similarity 82.2%; Pred. No. 3.2e-42;
RESULT 484
ID ABL56821 standard; DNA; 10283 BP.

RESULT 508
Query Match 15.8%; Score 204.4; DB 12; Length 110000;
Best Local Similarity 70.4%; Pred. No. 5.1e-42;
RESULT 509
Query Match 15.8%; Score 204.4; DB 14; Length 110000;
Best Local Similarity 70.4%; Pred. No. 5.1e-42;
RESULT 510
Query Match 15.8%; Score 204.4; DB 14; Length 110000;
Best Local Similarity 70.4%; Pred. No. 5.1e-42;
RESULT 511
ID AEB32385 standard; DNA; 207542 BP.
DE Human genomic DNA #26.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 15.8%; Score 204.4; DB 14; Length 207542;
Best Local Similarity 78.8%; Pred. No. 6.8e-42;
RESULT 512
ID AEB32371 standard; DNA; 207557 BP.
DE Human genomic DNA #12.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 15.8%; Score 204.4; DB 14; Length 207557;
Best Local Similarity 78.8%; Pred. No. 6.8e-42;
RESULT 513
ID AAK87099 standard; DNA; 16817 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41911.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.8%; Score 204.2; DB 4; Length 16817;
Best Local Similarity 84.9%; Pred. No. 2.5e-42;
RESULT 514
ID AAD56105 standard; DNA; 26874 BP.
DE Human CCND3 carcinoma associated (CA) gene.
PN WO2003035837-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.8%; Score 204.2; DB 8; Length 26874;
Best Local Similarity 81.9%; Pred. No. 3.1e-42;
RESULT 515
ID ADA02467 standard; DNA; 26874 BP.
DE Human CCND3 carcinoma associated gene, SEQ ID NO:986.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.8%; Score 204.2; DB 9; Length 26874;
Best Local Similarity 81.9%; Pred. No. 3.1e-42;
RESULT 516
ID ADB72206 standard; DNA; 26874 BP.
DE Human CCND3 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.8%; Score 204.2; DB 10; Length 26874;
Best Local Similarity 81.9%; Pred. No. 3.1e-42;
RESULT 517
ID ADY25730 standard; DNA; 86453 BP.
DE SULF related nucleic acid #5.
PN WO2005017118-A2.
PD 24-FEB-2005.
PA (EXEL-) EXELIXIS INC.
Query Match 15.8%; Score 204.2; DB 14; Length 86453;
Best Local Similarity 81.8%; Pred. No. 5.2e-42;
RESULT 518
ID ADN16203 standard; DNA; 264965 BP.
DE Human sulfatase SULF2 gene.
PN WO2004031365-A2.
PD 15-APR-2004.
PA (REGC) UNIV CALIFORNIA.
PA (THIO-) THIOS PHARM INC.
Query Match 15.8%; Score 204.2; DB 12; Length 264965;

Best Local Similarity 81.8%; Pred. No. 8.5e-42;
RESULT 519
ID ABS56563 standard; DNA; 268685 BP.
DE Human SULF2 genomic DNA sequence.
PN WO200259327-A2.
PD 01-AUG-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 15.8%; Score 204.2; DB 6; Length 268685;
Best Local Similarity 81.8%; Pred. No. 8.6e-42;
RESULT 520
ID ABA18607 standard; DNA; 2854 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10938.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.8%; Score 204; DB 5; Length 2854;
Best Local Similarity 85.7%; Pred. No. 1.3e-42;
RESULT 521
ID ABL70108 standard; DNA; 5588 BP.
DE Pancreas cancer related gene sequence SEQ ID NO:8445.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 15.8%; Score 204; DB 6; Length 5588;
Best Local Similarity 83.9%; Pred. No. 1.8e-42;
RESULT 522
ID ABK84092 standard; cDNA; 5588 BP.
DE Human cDNA differentially expressed in granulocytic cells #663.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 15.8%; Score 204; DB 6; Length 5588;
Best Local Similarity 83.9%; Pred. No. 1.8e-42;
RESULT 523
ID AAL05229 standard; DNA; 23748 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7917.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.8%; Score 204; DB 4; Length 23748;
Best Local Similarity 81.0%; Pred. No. 3.3e-42;
RESULT 524
ID ABL98112 standard; DNA; 23748 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2764.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.8%; Score 204; DB 4; Length 23748;
Best Local Similarity 81.0%; Pred. No. 3.3e-42;
RESULT 525
ID ABD33553 standard; DNA; 68495 BP.
DE Human cancer-associated (CA) gene HD07-110.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.8%; Score 204; DB 13; Length 68495;
Best Local Similarity 77.7%; Pred. No. 5.3e-42;
RESULT 526
ID ADS36495 standard; DNA; 77522 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1709.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 15.8%; Score 204; DB 13; Length 77522;
Best Local Similarity 81.0%; Pred. No. 5.6e-42;
RESULT 527
ID ACN44342 standard; DNA; 78268 BP.
DE Human genomic sequence HCG17932.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.8%; Score 204; DB 11; Length 78268;
Best Local Similarity 82.1%; Pred. No. 5.6e-42;

RESULT 528
ID ABD33280 standard; DNA; 105499 BP.
DE Human cancer-associated (CA) gene HD07-049.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.8%; Score 204; DB 13; Length 105499;
Best Local Similarity 81.7%; Pred. No. 6.4e-42;
RESULT 529
ID ABQ76673 standard; DNA; 160820 BP.
DE Androgen receptor signalling pathway-associated DNA AB043547.
PN WO200382081-A2.
PD 17-OCT-2002.
PA (UTRP) UNIV ROCHESTER.
Query Match 15.8%; Score 204; DB 8; Length 160820;
Best Local Similarity 84.4%; Pred. No. 7.7e-42;
RESULT 530
ID ACM44350 standard; DNA; 276276 BP.
DE Human genomic sequence hCG17121.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.8%; Score 204; DB 11; Length 276276;
Best Local Similarity 80.8%; Pred. No. 9.8e-42;
RESULT 531
ID AAK67404 standard; DNA; 5069 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22216.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.8; DB 4; Length 5069;
Best Local Similarity 78.6%; Pred. No. 1.9e-42;
RESULT 532
ID AAL07199 standard; DNA; 6637 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9887.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.8; DB 4; Length 6637;
Best Local Similarity 81.2%; Pred. No. 2.2e-42;
RESULT 533
ID AAD16780 standard; DNA; 8369 BP.
DE Human novel protein-encoding gene 11 genomic DNA, SEQ ID NO:67.
PN WO200155202-A1.
PD 02-AUG-2001.
Query Match 15.7%; Score 203.8; DB 4; Length 8369;
Best Local Similarity 79.1%; Pred. No. 2.4e-42;
RESULT 534
ID ADC22098 standard; DNA; 8369 BP.
DE Human DNA from secreted protein gene 11 #3.
PN US2003082681-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.8; DB 10; Length 8369;
Best Local Similarity 79.1%; Pred. No. 2.4e-42;
RESULT 535
ID AAL07198 standard; DNA; 11888 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9886.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.8; DB 4; Length 11888;
Best Local Similarity 81.2%; Pred. No. 2.8e-42;
RESULT 536
ID AAS33381 standard; DNA; 18402 BP.
DE DNA encoding human secreted protein, Seq ID No 664.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.8; DB 4; Length 18402;
Best Local Similarity 83.9%; Pred. No. 3.4e-42;
RESULT 537
ID AAS33382 standard; DNA; 18403 BP.
DE DNA encoding human secreted protein, Seq ID No 665.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.8; DB 4; Length 18403;
Best Local Similarity 83.9%; Pred. No. 3.4e-42;
RESULT 538
ID ADN75983 standard; DNA; 31868 BP.
DE Human signal transduction-associated DNA SEQ ID 808.
PN WO2004016735-A2.
PD 26-FEB-2004.
PA (CEPT-) CEPTYR INC.
Query Match 15.7%; Score 203.8; DB 12; Length 31868;
Best Local Similarity 81.6%; Pred. No. 4.3e-42;
RESULT 539
ID ADY37041 standard; DNA; 31868 BP.
DE Protein tyrosine phosphatase DNA sequence #21.
PN WO2005019446-A2.
PD 03-MAR-2005.
PA (TONK/) TONKS N K.
PA (BARF/) BARFORD D.
PA (NEEL/) NEEL B G.
PA (FLIN/) FLINT A J.
Query Match 15.7%; Score 203.8; DB 14; Length 31868;
Best Local Similarity 81.6%; Pred. No. 4.3e-42;
RESULT 540
ID AAZ35351 standard; DNA; 41599 BP.
DE Cosmid including sequence spanning human chromosome 9p21.
PN WO9967634-A1.
PD 29-DEC-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 15.7%; Score 203.8; DB 3; Length 41599;
Best Local Similarity 82.7%; Pred. No. 4.8e-42;
RESULT 541
ID ACN43874 standard; DNA; 58845 BP.
DE Human genomic sequence hCG25637.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 203.8; DB 11; Length 58845;
Best Local Similarity 79.1%; Pred. No. 5.6e-42;
RESULT 542
ID ADC85452 standard; DNA; 67782 BP.
DE Human Gic2 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 203.8; DB 10; Length 67782;
Best Local Similarity 75.7%; Pred. No. 6e-42;
RESULT 543
ID ADA02972 standard; DNA; 67783 BP.
DE Human GIT2 carcinoma associated gene, SEQ ID NO:1490.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 203.8; DB 9; Length 67783;
Best Local Similarity 75.7%; Pred. No. 6e-42;
RESULT 544
ID ADB72710 standard; DNA; 67783 BP.
DE Human GIT2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 203.8; DB 10; Length 67783;
Best Local Similarity 75.7%; Pred. No. 6e-42;
RESULT 545
ID ADM74567 standard; DNA; 67783 BP.
DE Human carcinoma associated (CA) nucleic acid #118.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.


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Query Match      15.7%; Score 203.8; DB 12; Length 67783;
Best Local Similarity 75.7%; Pred. No. 6e-42;
RESULT 546
ID AD213582 standard; DNA; 73702 BP.
DE Human cancer-associated genomic DNA #94.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR ) CHIRON CORP.
Query Match      15.7%; Score 203.8; DB 14; Length 73702;
Best Local Similarity 83.9%; Pred. No. 6.2e-42;
RESULT 547
ID ABD33145 standard; DNA; 73723 BP.
DE Human cancer-associated (CA) gene HD07-018.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match      15.7%; Score 203.8; DB 13; Length 73723;
Best Local Similarity 83.9%; Pred. No. 6.2e-42;
RESULT 548
ID ADT77142 standard; DNA; 93500 BP.
DE Type II diabetes gene SEQ ID NO 19.
PN WO2004084797-A2.
PD 07-OCT-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (DAIM/) DAIMON M.
PA (KATO/) KATO T.
Query Match      15.7%; Score 203.8; DB 13; Length 93500;
Best Local Similarity 83.9%; Pred. No. 6.9e-42;
RESULT 549
ID AEN96931 standard; DNA; 99014 BP.
DE Gene #3429 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match      15.7%; Score 203.8; DB 6; Length 99014;
Best Local Similarity 74.3%; Pred. No. 7.1e-42;
RESULT 550
ID AEF74705 standard; DNA; 152037 BP.
DE Human polynucleotide #219.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match      15.7%; Score 203.8; DB 15; Length 152037;
Best Local Similarity 81.6%; Pred. No. 8.5e-42;
RESULT 551
ID AED18452 standard; DNA; 180283 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 703.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL ) UNIV FLORIDA RES FOUND INC.
Query Match      15.7%; Score 203.8; DB 14; Length 180283;
Best Local Similarity 82.7%; Pred. No. 9.2e-42;
RESULT 552
ID ADL13931 standard; DNA; 180385 BP.
DE Osteoarthritis-associated polymorphic nucleotide #463.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match      15.7%; Score 203.8; DB 10; Length 180385;
Best Local Similarity 76.7%; Pred. No. 9.2e-42;
RESULT 553
ID AAL05708 standard; DNA; 27154 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8396.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      15.7%; Score 203.6; DB 4; Length 27154;
Best Local Similarity 82.3%; Pred. No. 4.5e-42;
RESULT 554
ID ADG88848 standard; DNA; 55001 BP.
DE Human Notchi DNA #1.
PN US2003224513-A1.
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PD 04-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match      15.7%; Score 203.6; DB 12; Length 55001;
Best Local Similarity 82.3%; Pred. No. 6.1e-42;
RESULT 555
ID ADH74825 standard; DNA; 55001 BP.
DE Human Notchi genomic sequence.
PN US2003225019-A1.
PD 04-DEC-2003.
PA (FREI/) FREIER S M.
PA (DOBI/) DOBIE K W.
PA (KOLL/) KOLLER E.
Query Match      15.7%; Score 203.6; DB 12; Length 55001;
Best Local Similarity 82.3%; Pred. No. 6.1e-42;
RESULT 556
ID ADZ84380 standard; DNA; 55001 BP.
DE Human Notchi genomic sequence, seq id 4.
PN US2005096292-A1.
PD 05-MAY-2005.
PA (FREI/) FREIER S M.
PA (DOBI/) DOBIE K W.
PA (KOLL/) KOLLER E.
Query Match      15.7%; Score 203.6; DB 14; Length 55001;
Best Local Similarity 82.3%; Pred. No. 6.1e-42;
RESULT 557
ID ABK84756 standard; cDNA; 81800 BP.
DE Human cDNA differentially expressed in granulocytic cells #1327.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match      15.7%; Score 203.6; DB 6; Length 81800;
Best Local Similarity 83.4%; Pred. No. 7.3e-42;
RESULT 558
ID ADQ59518 standard; DNA; 100762 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:154.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match      15.7%; Score 203.6; DB 12; Length 100762;
Best Local Similarity 81.0%; Pred. No. 8e-42;
RESULT 559
ID ADZ13899 standard; DNA; 100822 BP.
DE Human cancer-associated genomic DNA #122.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR ) CHIRON CORP.
Query Match      15.7%; Score 203.6; DB 14; Length 100822;
Best Local Similarity 81.0%; Pred. No. 8e-42;
RESULT 560
ID AEE04879 standard; DNA; 681142 BP.
DE Cancer-associated gene SEQ ID NO:197.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR ) CHIRON CORP.
Query Match      15.7%; Score 203.6; DB 14; Length 110000;
Best Local Similarity 81.5%; Pred. No. 8.3e-42;
RESULT 561
ID AEB32366 standard; DNA; 117231 BP.
DE Human genomic DNA #7.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match      15.7%; Score 203.6; DB 14; Length 117231;
Best Local Similarity 84.7%; Pred. No. 8.6e-42;
RESULT 562
ID AEB32396 standard; DNA; 119226 BP.
DE Human genomic DNA #37.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match      15.7%; Score 203.6; DB 14; Length 119226;
Best Local Similarity 84.7%; Pred. No. 8.6e-42;
RESULT 563
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ID AAA34791 standard; DNA; 138169 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2480.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 15.7%; Score 203.6; DB 3; Length 138169;
Best Local Similarity 86.0%; Pred. No. 9.2e-42;
RESULT 564
ID ABD20695 standard; DNA; 141586 BP.
DE Human pulmonary and inflammatory target DNA #306.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 15.7%; Score 203.6; DB 11; Length 141586;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 565
ID AAA35005 standard; DNA; 141589 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2694.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 15.7%; Score 203.6; DB 3; Length 141589;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 566
ID AAA35030 standard; DNA; 141589 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2719.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 15.7%; Score 203.6; DB 3; Length 141589;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 567
ID AAF21152 standard; DNA; 141589 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2719.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 15.7%; Score 203.6; DB 3; Length 141589;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 568
ID AAF20913 standard; DNA; 141589 BP.
DE Human ELAM-1 polynucleotide fragment #2480.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 15.7%; Score 203.6; DB 3; Length 141589;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 569
ID AAF21127 standard; DNA; 141589 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2694.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 15.7%; Score 203.6; DB 3; Length 141589;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 570
ID AAF21127 standard; DNA; 141589 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2694.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 15.7%; Score 203.6; DB 3; Length 141589;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 571
ID AAF21127 standard; DNA; 141589 BP.
DE Human ELAM-1 nucleic acid.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 15.7%; Score 203.6; DB 10; Length 141589;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 572
ID AAF21127 standard; DNA; 141589 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 15.7%; Score 203.6; DB 10; Length 141589;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 573
ID ABD20670 standard; DNA; 141589 BP.
DE Human pulmonary and inflammatory target DNA #281.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 15.7%; Score 203.6; DB 11; Length 141589;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 574
ID ABD19162 standard; DNA; 141601 BP.
DE Human ELAM-1 DNA fragment #2.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 15.7%; Score 203.6; DB 11; Length 141601;
Best Local Similarity 86.0%; Pred. No. 9.3e-42;
RESULT 575
ID AAF21442 standard; DNA; 146981 BP.
DE Human ELAM-1 polynucleotide fragment #3009.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 15.7%; Score 203.6; DB 3; Length 146981;
Best Local Similarity 86.0%; Pred. No. 9.5e-42;
RESULT 576
ID ABZ97136 standard; DNA; 146982 BP.
DE Human ELAM-1 antisense fragment no.1738.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 15.7%; Score 203.6; DB 10; Length 146982;
Best Local Similarity 86.0%; Pred. No. 9.5e-42;
RESULT 577
ID ABD19160 standard; DNA; 146984 BP.
DE Human ELAM-1 DNA fragment 1738.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 15.7%; Score 203.6; DB 11; Length 146984;
Best Local Similarity 86.0%; Pred. No. 9.5e-42;
RESULT 578
ID ACN43914 standard; DNA; 160482 BP.
DE Human genomic sequence hCG26773.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 203.6; DB 11; Length 160482;
Best Local Similarity 84.7%; Pred. No. 9.8e-42;
RESULT 579
ID ACN43946 standard; DNA; 174448 BP.
DE Human genomic sequence hCG21793.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 203.6; DB 11; Length 174448;
Best Local Similarity 80.1%; Pred. No. 1e-41;
RESULT 580
ID ASD18538 standard; DNA; 184666 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 789.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 15.7%; Score 203.6; DB 14; Length 184666;

Best Local Similarity 83.4%; Pred. No. 1e-41;
RESULT 581
ID AAF21437 standard; DNA; 209273 BP.
DE Human factor-related antisense polynucleotide #3004.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 15.7%; Score 203.6; DB 3; Length 209273;
Best Local Similarity 86.0%; Pred. No. 1.1e-41;
RESULT 582
ID ABZ97131 standard; DNA; 209274 BP.
DE Human enzyme-related antisense polynucleotide.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 15.7%; Score 203.6; DB 10; Length 209274;
Best Local Similarity 86.0%; Pred. No. 1.1e-41;
RESULT 583
ID ABD1970 standard; DNA; 209284 BP.
DE Human factor-related antisense polynucleotide.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 15.7%; Score 203.6; DB 11; Length 209284;
Best Local Similarity 86.0%; Pred. No. 1.1e-41;
RESULT 584
ID AAK67132 standard; DNA; 310 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21944.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 4; Length 310;
Best Local Similarity 84.2%; Pred. No. 7.2e-43;
RESULT 585
ID AAC79899 standard; cDNA; 1154 BP.
DE Human secreted protein encoding cDNA for gene 2.
PN WO200055200-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 3; Length 1154;
Best Local Similarity 81.8%; Pred. No. 1.3e-42;
RESULT 586
ID AAL05707 standard; DNA; 2563 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8395.
PN WO200153320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 4; Length 2563;
Best Local Similarity 78.6%; Pred. No. 1.8e-42;
RESULT 587
ID AAI59874 standard; cDNA; 5381 BP.
DE Human polynucleotide SEQ ID NO 3863.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.7%; Score 203.4; DB 4; Length 5381;
Best Local Similarity 76.9%; Pred. No. 2.5e-42;
RESULT 588
ID AAI59875 standard; cDNA; 5381 BP.
DE Human polynucleotide SEQ ID NO 3864.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.7%; Score 203.4; DB 4; Length 5381;
Best Local Similarity 76.9%; Pred. No. 2.5e-42;
RESULT 589
ID AAK83176 standard; DNA; 15201 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37988.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 4; Length 15201;
Best Local Similarity 80.7%; Pred. No. 5.7e-42;
Best Local Similarity 77.0%; Pred. No. 3.9e-42;
RESULT 590
ID ADR12626 standard; DNA; 27145 BP.
DE Human muscle glycogen synthase 1 gene.
PN WO200406771-A1.
PD 12-AUG-2004.
PA (HVID-) HVIDOVRE HOSPITAL.
Query Match 15.7%; Score 203.4; DB 13; Length 27145;
Best Local Similarity 84.2%; Pred. No. 5.1e-42;
RESULT 591
ID ADR50939 standard; DNA; 27145 BP.
DE Human glycogen synthase 1 (GYS1) gene sequence.
PN WO2004074428-A2.
PD 02-SEP-2004.
PA (HVID-) HVIDOVRE HOSPITAL.
Query Match 15.7%; Score 203.4; DB 13; Length 27145;
Best Local Similarity 84.2%; Pred. No. 5.1e-42;
RESULT 592
ID AAI99172 standard; DNA; 32134 BP.
DE Human excretory related polynucleotide SEQ ID NO 936.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 4; Length 32134;
Best Local Similarity 80.7%; Pred. No. 5.5e-42;
RESULT 593
ID AAI63522 standard; DNA; 32134 BP.
DE Human kidney related polynucleotide SEQ ID NO 837.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 5; Length 32134;
Best Local Similarity 80.7%; Pred. No. 5.5e-42;
RESULT 594
ID AAI99173 standard; DNA; 32192 BP.
DE Human excretory related polynucleotide SEQ ID NO 937.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 4; Length 32192;
Best Local Similarity 80.7%; Pred. No. 5.5e-42;
RESULT 595
ID AAI63523 standard; DNA; 32192 BP.
DE Human kidney related polynucleotide SEQ ID NO 838.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 5; Length 32192;
Best Local Similarity 80.7%; Pred. No. 5.5e-42;
RESULT 596
ID AAK69767 standard; DNA; 35100 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24579.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 4; Length 35100;
Best Local Similarity 80.7%; Pred. No. 5.7e-42;
RESULT 597
ID AAK65700 standard; DNA; 35100 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20512.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 4; Length 35100;
Best Local Similarity 80.7%; Pred. No. 5.7e-42;
RESULT 598
ID AAK69766 standard; DNA; 35115 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24578.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 4; Length 35115;
Best Local Similarity 80.7%; Pred. No. 5.7e-42;

RESULT 599
ID AAK56599 standard; DNA; 35115 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20511.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.4; DB 4; Length 35115;
Best Local Similarity 80.7%; Pred. No. 5.7e-42;
RESULT 600
ID AAH28355 standard; DNA; 52216 BP.
DE Nucleotide sequence of the human musashi promoter.
PN WO200146384-A2.
PD 28-JUN-2001.
PA (CORR) CORNELL RES FOUND INC.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 15.7%; Score 203.4; DB 4; Length 52216;
Best Local Similarity 81.6%; Pred. No. 6.8e-42;
RESULT 601
ID ABL50307 standard; DNA; 52216 BP.
DE Human musashi promoter DNA sequence SEQ ID NO:1.
PN JP2002034580-A.
PD 05-FEB-2002.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (CORR) CORNELL RES FOUND INC.
Query Match 15.7%; Score 203.4; DB 6; Length 52216;
Best Local Similarity 81.6%; Pred. No. 6.8e-42;
RESULT 602
ID ADY70791 standard; DNA; 104424 BP.
DE Human soluble adenylyl cyclase (SAC) gene SEQ ID NO:21.
PN CN1548557-A.
PD 24-NOV-2004.
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
Query Match 15.7%; Score 203.4; DB 14; Length 104424;
Best Local Similarity 83.0%; Pred. No. 9.2e-42;
RESULT 603
ID ADZ46659 standard; DNA; 104424 BP.
DE Type-II diabetes susceptibility gene SAC, SEQ ID 27.
PN CN1548553-A.
PD 24-NOV-2004.
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
Query Match 15.7%; Score 203.4; DB 14; Length 104424;
Best Local Similarity 83.0%; Pred. No. 9.2e-42;
RESULT 604
ID AAL38336 standard; DNA; 143899 BP.
DE Genomic sequence encoding a human Ngr2 protein.
PN WO200229059-A2.
PD 11-APR-2002.
PA (UYA) UNIV YALE.
PA (BIOJ) BIOGEN INC.
Query Match 15.7%; Score 203.4; DB 6; Length 143899;
Best Local Similarity 84.2%; Pred. No. 1.1e-41;
RESULT 605
ID AEA17302 standard; DNA; 197140 BP.
DE Human GNAL gene locus Seq 12.
PN WO2005047318-A1.
PD 26-MAY-2005.
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
Query Match 15.7%; Score 203.4; DB 14; Length 197140;
Best Local Similarity 72.8%; Pred. No. 1.2e-41;
RESULT 606
ID AEE04958 standard; DNA; 212235 BP.
DE Cancer-associated gene SEQ ID NO:276.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.7%; Score 203.4; DB 14; Length 212235;
Best Local Similarity 83.0%; Pred. No. 1.3e-41;
RESULT 607
ID ADP75187 standard; DNA; 302603 BP.
DE Human Endophilin 1 gene.
PN WO2003031594-A2.
PD 17-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.7%; Score 203.4; DB 11; Length 302603;
Best Local Similarity 79.7%; Pred. No. 1.5e-41;
RESULT 608
ID AAH18205 standard; cDNA; 3877 BP.
DE Human cDNA sequence SEQ ID NO:18124.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 15.7%; Score 203.2; DB 4; Length 3877;
Best Local Similarity 82.5%; Pred. No. 2.4e-42;
RESULT 609
ID ABA17155 standard; DNA; 32249 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9486.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203.2; DB 5; Length 32249;
Best Local Similarity 86.2%; Pred. No. 6.2e-42;
RESULT 610
Query Match 15.7%; Score 203.2; DB 11; Length 110000;
Best Local Similarity 84.9%; Pred. No. 1.1e-41;
RESULT 611
ID ADL13962 standard; DNA; 160198 BP.
DE Osteoarthritis-associated polymorphic nucleotide #494.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.7%; Score 203.2; DB 10; Length 160198;
Best Local Similarity 83.7%; Pred. No. 1.3e-41;
RESULT 612
ID AED89398 standard; DNA; 171162 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 38.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.7%; Score 203.2; DB 14; Length 171162;
Best Local Similarity 86.0%; Pred. No. 1.3e-41;
RESULT 613
ID ADE43315 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 15.7%; Score 203.2; DB 10; Length 202100;
Best Local Similarity 84.9%; Pred. No. 1.4e-41;
RESULT 614
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 15.7%; Score 203.2; DB 12; Length 202100;
Best Local Similarity 84.9%; Pred. No. 1.4e-41;
RESULT 615
ID ASN65466 standard; cDNA; 509 BP.
DE Human cancer related polynucleotide SEQ ID NO 5433.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 15.7%; Score 203; DB 6; Length 509;
Best Local Similarity 84.4%; Pred. No. 1.1e-42;
RESULT 616
ID ASN65693 standard; cDNA; 609 BP.
DE Human cancer related polynucleotide SEQ ID NO 5660.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 15.7%; Score 203; DB 6; Length 609;
Best Local Similarity 78.9%; Pred. No. 1.2e-42;

RESULT 617
ID ABA20581 standard; DNA; 1661 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12912.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 5; Length 1661;
Best Local Similarity 74.4%; Pred. No. 1.9e-42;
RESULT 618
ID ABA20582 standard; DNA; 1661 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12913.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 5; Length 1661;
Best Local Similarity 74.4%; Pred. No. 1.9e-42;
RESULT 619
ID AAK83192 standard; DNA; 3608 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38004.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 4; Length 3608;
Best Local Similarity 83.2%; Pred. No. 2.7e-42;
RESULT 620
ID AAK74891 standard; DNA; 3608 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29703.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 4; Length 3608;
Best Local Similarity 83.2%; Pred. No. 2.7e-42;
RESULT 621
ID AAK67271 standard; DNA; 3608 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22083.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 4; Length 3608;
Best Local Similarity 83.2%; Pred. No. 2.7e-42;
RESULT 622
ID AAK64788 standard; DNA; 10740 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19600.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 4; Length 10740;
Best Local Similarity 85.7%; Pred. No. 4.3e-42;
RESULT 623
ID AAK74867 standard; DNA; 21621 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29679.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 4; Length 21621;
Best Local Similarity 77.2%; Pred. No. 5.9e-42;
RESULT 624
ID AAK83153 standard; DNA; 31405 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37965.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 4; Length 31405;
Best Local Similarity 77.2%; Pred. No. 6.9e-42;
RESULT 625
ID AAK74865 standard; DNA; 31405 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29677.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 4; Length 31405;
Best Local Similarity 77.2%; Pred. No. 6.9e-42;
RESULT 626

ID AAK67293 standard; DNA; 31405 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22105.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.7%; Score 203; DB 4; Length 31405;
Best Local Similarity 77.2%; Pred. No. 6.9e-42;
RESULT 627
ID AAD47150 standard; DNA; 31814 BP.
DE Human Ras-like protein encoding gene.
PN WO200277190-A2.
PD 03-OCT-2002.
PA (PEXS) PE CORP NY.
Query Match 15.7%; Score 203; DB 10; Length 31814;
Best Local Similarity 84.4%; Pred. No. 6.9e-42;
RESULT 628
ID ADC86412 standard; DNA; 42863 BP.
DE Human GPCR gene SEQ ID NO:865.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAI INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.7%; Score 203; DB 10; Length 42863;
Best Local Similarity 85.7%; Pred. No. 7.9e-42;
RESULT 629
ID ADA02666 standard; DNA; 52242 BP.
DE Human MDM2 carcinoma associated gene, SEQ ID NO:1184.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 203; DB 9; Length 52242;
Best Local Similarity 82.0%; Pred. No. 8.6e-42;
RESULT 630
ID ADB72404 standard; DNA; 52242 BP.
DE Human MDM2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 203; DB 10; Length 52242;
Best Local Similarity 82.0%; Pred. No. 8.6e-42;
RESULT 631
ID ADE95914 standard; DNA; 52242 BP.
DE Human MDM2 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 203; DB 10; Length 52242;
Best Local Similarity 82.0%; Pred. No. 8.6e-42;
RESULT 632
ID AED89420 standard; DNA; 171427 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 60.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.7%; Score 203; DB 14; Length 171427;
Best Local Similarity 77.9%; Pred. No. 1.5e-41;
RESULT 633
ID AAA81720 standard; DNA; 683 BP.
DE N. meningitidis partial DNA sequence gnm_267 SEQ ID NO:267.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Query Match 15.7%; Score 202.8; DB 3; Length 683;
Best Local Similarity 75.4%; Pred. No. 1.5e-42;
RESULT 634
ID ABK52899 standard; DNA; 31208 BP.
DE Genomic DNA encoding human drug metabolising enzyme protein.
Query Match 15.7%; Score 202.8; DB 6; Length 31208;
Best Local Similarity 82.3%; Pred. No. 7.8e-42;
RESULT 635
ID AEB96546 standard; DNA; 32704 BP.
DE Human FGL1 gene, SEQ ID 30.
Query Match 15.7%; Score 202.8; DB 14; Length 32704;

Best Local Similarity 79.5%; Pred. No. 7.9e-42;
RESULT 636
ID ABD33190 standard; DNA; 33478 BP.
DE Human cancer-associated (CA) gene HD07-028.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.7%; Score 202.8; DB 13; Length 33478;
Best Local Similarity 75.7%; Pred. No. 8e-42;
RESULT 637
ID ABD33295 standard; DNA; 64125 BP.
DE Human cancer-associated (CA) gene HD07-052.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.7%; Score 202.8; DB 13; Length 64125;
Best Local Similarity 74.5%; Pred. No. 1.1e-41;
RESULT 638
ID ACN44766 standard; DNA; 77478 BP.
DE Human genomic sequence hCG32368.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.7%; Score 202.8; DB 11; Length 77478;
Best Local Similarity 79.5%; Pred. No. 1.2e-41;
RESULT 639
Query Match 15.7%; Score 202.8; DB 11; Length 110000;
Best Local Similarity 79.5%; Pred. No. 1.3e-41;
RESULT 640
Query Match 15.7%; Score 202.8; DB 14; Length 110000;
Best Local Similarity 85.1%; Pred. No. 1.3e-41;
RESULT 641
ID ADA42607 standard; DNA; 113604 BP.
DE Human LQTS genomic DNA #2.
PN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 15.7%; Score 202.8; DB 9; Length 113604;
Best Local Similarity 75.7%; Pred. No. 1.4e-41;
RESULT 642
ID ADA42606 standard; DNA; 113604 BP.
DE Human LQTS genomic DNA #1.
PN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 15.7%; Score 202.8; DB 9; Length 113604;
Best Local Similarity 75.7%; Pred. No. 1.4e-41;
RESULT 643
ID ADS19853 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:1.
PN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 15.7%; Score 202.8; DB 13; Length 113604;
Best Local Similarity 75.7%; Pred. No. 1.4e-41;
RESULT 644
ID ADS19854 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:2.
PN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 15.7%; Score 202.8; DB 13; Length 113604;
Best Local Similarity 75.7%; Pred. No. 1.4e-41;
RESULT 645
ID ADZ12550 standard; DNA; 117730 BP.
DE Human cancer-associated genomic DNA #8.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.

Query Match 15.7%; Score 202.8; DB 14; Length 117730;
Best Local Similarity 81.4%; Pred. No. 1.4e-41;
RESULT 646
ID AAD54480 standard; DNA; 117962 BP.
DE Human CIP DNA #1.
PN WO200299055-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 15.7%; Score 202.8; DB 8; Length 117962;
Best Local Similarity 78.2%; Pred. No. 1.4e-41;
RESULT 647
ID ADQ80254 standard; cDNA; 127145 BP.
DE Hermansky-Pudlak syndrome associated cDNA.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 15.7%; Score 202.8; DB 13; Length 127145;
Best Local Similarity 84.2%; Pred. No. 1.4e-41;
RESULT 648
ID ADX80726 standard; DNA; 213300 BP.
DE Human RALBP1 associated Eps domain containing 2 (REPS2) genomic DNA.
Query Match 15.7%; Score 202.8; DB 14; Length 213300;
Best Local Similarity 77.7%; Pred. No. 1.8e-41;
RESULT 649
ID ABE04926 standard; DNA; 312071 BP.
DE Cancer-associated gene SEQ ID NO:244.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.7%; Score 202.8; DB 14; Length 312071;
Best Local Similarity 83.6%; Pred. No. 2.1e-41;
RESULT 650
ID ADR83499 standard; DNA; 2428 BP.
DE Human VENT-like homeobox 2 DNA, target gene of miRNA.
PN WO2004076622-A2.
PD 10-SEP-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 15.6%; Score 202.6; DB 13; Length 2428;
Best Local Similarity 77.9%; Pred. No. 2.9e-42;
RESULT 651
ID AAH17745 standard; cDNA; 2451 BP.
DE Human cDNA sequence SEQ ID NO:17365.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 15.6%; Score 202.6; DB 4; Length 2451;
Best Local Similarity 77.0%; Pred. No. 2.9e-42;
RESULT 652
ID AAH16966 standard; cDNA; 2483 BP.
DE Human cDNA sequence SEQ ID NO:16252.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 15.6%; Score 202.6; DB 4; Length 2483;
Best Local Similarity 83.4%; Pred. No. 2.9e-42;
RESULT 653
ID AQO80838 standard; DNA; 14468 BP.
DE Human SPARC gene SEQ ID NO:7.
PN WO2004064785-A2.
PD 05-AUG-2004.
PA (DAND) DANA FARBER CANCER INST.
Query Match 15.6%; Score 202.6; DB 13; Length 14468;
Best Local Similarity 81.8%; Pred. No. 6.3e-42;
RESULT 654
ID AAK83283 standard; DNA; 21302 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38095.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.6; DB 4; Length 21302;
Best Local Similarity 84.6%; Pred. No. 7.4e-42;
RESULT 655
ID ABD33407 standard; DNA; 58922 BP.

DE Human cancer-associated (CA) gene HD07-076.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.6%; Score 202.6; DB 13; Length 58922;
Best Local Similarity 82.2%; Pred. No. 1.2e-41;
RESULT 656
ID ADR72312 standard; DNA; 63045 BP.
DE A truncated portion of DNA encoding human kinesin-like 1.
PN US2004180847-A1.
PD 16-SEP-2004.
PA (DOB/) DOBIE K W.
PA (KOLL/) KOLLER E.
Query Match 15.6%; Score 202.6; DB 13; Length 63045;
Best Local Similarity 81.3%; Pred. No. 1.2e-41;
RESULT 657
ID ADE43742 standard; DNA; 63824 BP.
DE Human KNSL1 genomic sequence, SEQ ID 347.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 15.6%; Score 202.6; DB 10; Length 63824;
Best Local Similarity 81.3%; Pred. No. 1.2e-41;
RESULT 658
ID ADE43743 standard; DNA; 63824 BP.
DE Polymorphic human KNSL1 genomic sequence, SEQ ID 348.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 15.6%; Score 202.6; DB 10; Length 63824;
Best Local Similarity 81.3%; Pred. No. 1.2e-41;
RESULT 659
ID ADH54220 standard; DNA; 63824 BP.
DE Human KNSL1 gene DNA sequence SeqID147.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 15.6%; Score 202.6; DB 12; Length 63824;
Best Local Similarity 81.3%; Pred. No. 1.2e-41;
RESULT 660
ID ADH54221 standard; DNA; 63824 BP.
DE Human KNSL1 gene variant DNA sequence SeqID348.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 15.6%; Score 202.6; DB 12; Length 63824;
Best Local Similarity 81.3%; Pred. No. 1.2e-41;
RESULT 661
ID AFB07225 standard; DNA; 96400 BP.
DE SERPINA5 locus of the human genome.
Query Match 15.6%; Score 202.6; DB 15; Length 96400;
Best Local Similarity 80.2%; Pred. No. 1.4e-41;
RESULT 662
ID ADL13471 standard; DNA; 214520 BP.
DE Osteoarthritis-associated polymorphic nucleotide #3.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.6%; Score 202.6; DB 10; Length 214520;
Best Local Similarity 80.2%; Pred. No. 2e-41;
RESULT 663
ID ADV16961 standard; DNA; 290040 BP.
DE Human protein associated with myc (PAM) genomic DNA.
PN EP1481685-A1.
PD 01-DEC-2004.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Query Match 15.6%; Score 202.6; DB 14; Length 290040;
Best Local Similarity 78.4%; Pred. No. 2.3e-41;
RESULT 664
ID ADU92049 standard; DNA; 290040 BP.
DE Human PAM (protein associated with myc) genomic DNA.
PN BP1481680-A1.
PD 01-DEC-2004.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Query Match 15.6%; Score 202.6; DB 14; Length 290040;
Best Local Similarity 78.4%; Pred. No. 2.3e-41;
RESULT 665
ID AAK78782 standard; DNA; 331 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33594.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 331;
Best Local Similarity 80.7%; Pred. No. 1.3e-42;
RESULT 666
ID ABA07424 standard; DNA; 614 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 743.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 614;
Best Local Similarity 84.1%; Pred. No. 1.8e-42;
RESULT 667
ID AAK91155 standard; DNA; 614 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4731.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 614;
Best Local Similarity 84.1%; Pred. No. 1.8e-42;
RESULT 668
ID AAS62224 standard; cDNA; 2157 BP.
DE cDNA sequence #11 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 15.6%; Score 202.4; DB 6; Length 2157;
Best Local Similarity 82.7%; Pred. No. 3.1e-42;
RESULT 669
ID ABK3114 standard; DNA; 7737 BP.
DE Genomic sequence #1013 encoding human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 7737;
Best Local Similarity 71.5%; Pred. No. 5.4e-42;
RESULT 670
ID AAK90942 standard; DNA; 7737 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4518.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 7737;
Best Local Similarity 71.5%; Pred. No. 5.4e-42;
RESULT 671
ID AAS31977 standard; DNA; 7737 BP.
DE Human liver associated genomic DNA #151.
PN WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 5; Length 7737;
Best Local Similarity 71.5%; Pred. No. 5.4e-42;
RESULT 672
ID ABN90332 standard; DNA; 7737 BP.
DE Human liver antigen HLDOS76 genomic sequence, SEQ ID NO:453.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.6%; Score 202.4; DB 6; Length 7737;
Best Local Similarity 71.5%; Pred. No. 5.4e-42;
RESULT 673
ID ADB61270 standard; DNA; 7737 BP.

DE Connective tissue related genomic DNA #1013.
PN US2003054375-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 9; Length 7737;
Best Local Similarity 71.5%; Pred. No. 5.4e-42;
RESULT 674
ID ADJ15245 standard; DNA; 7737 BP.
DE Human liver-related genomic DNA - SEQ ID 453.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 11; Length 7737;
Best Local Similarity 71.5%; Pred. No. 5.4e-42;
RESULT 675
ID AAL06055 standard; DNA; 10198 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8743.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 10198;
Best Local Similarity 84.1%; Pred. No. 6.1e-42;
RESULT 676
ID AAL06056 standard; DNA; 10198 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8744.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 10198;
Best Local Similarity 84.1%; Pred. No. 6.1e-42;
RESULT 677
ID ABL98621 standard; DNA; 10198 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3273.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 10198;
Best Local Similarity 84.1%; Pred. No. 6.1e-42;
RESULT 678
ID ABL98620 standard; DNA; 10198 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3272.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 10198;
Best Local Similarity 84.1%; Pred. No. 6.1e-42;
RESULT 679
ID AAK67371 standard; DNA; 13496 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22183.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 13496;
Best Local Similarity 79.6%; Pred. No. 6.8e-42;
RESULT 680
ID ADT77147 standard; DNA; 20001 BP.
DE Type II diabetes gene SEQ ID NO 24.
PN WO2004084797-A2.
PD 07-OCT-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (DAIM/) DAIMON M.
PA (KATO/) KATO T.
Query Match 15.6%; Score 202.4; DB 13; Length 20001;
Best Local Similarity 82.7%; Pred. No. 8.1e-42;
RESULT 681
ID AAK73847 standard; DNA; 22680 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28659.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 22680;
Best Local Similarity 81.8%; Pred. No. 8.6e-42;
RESULT 682

ID AAK73344 standard; DNA; 22680 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28156.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 22680;
Best Local Similarity 81.8%; Pred. No. 8.6e-42;
RESULT 683
ID AAK73934 standard; DNA; 22680 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28746.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 22680;
Best Local Similarity 81.8%; Pred. No. 8.6e-42;
RESULT 684
ID AAK73334 standard; DNA; 22680 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28146.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 22680;
Best Local Similarity 81.8%; Pred. No. 8.6e-42;
RESULT 685
ID AAK66308 standard; DNA; 22680 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21120.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 22680;
Best Local Similarity 81.8%; Pred. No. 8.6e-42;
RESULT 686
ID AAK78350 standard; DNA; 22680 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33162.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 22680;
Best Local Similarity 81.8%; Pred. No. 8.6e-42;
RESULT 687
ID AAK73625 standard; DNA; 22680 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28437.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 22680;
Best Local Similarity 81.8%; Pred. No. 8.6e-42;
RESULT 688
ID ACN44886 standard; DNA; 26332 BP.
DE Human genomic sequence hCG39434.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.6%; Score 202.4; DB 11; Length 26332;
Best Local Similarity 84.1%; Pred. No. 9.2e-42;
RESULT 689
ID AAL05461 standard; DNA; 31474 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8149.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 31474;
Best Local Similarity 78.5%; Pred. No. 9.9e-42;
RESULT 690
ID ABL98314 standard; DNA; 31474 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2966.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.4; DB 4; Length 31474;
Best Local Similarity 78.5%; Pred. No. 9.9e-42;
RESULT 691
ID ADJ53477 standard; DNA; 70000 BP.

DE Human PPP3CB genomic DNA #3.
PN US2004023382-A1.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.6%; Score 202.4; DB 12; Length 70000;
Best Local Similarity 81.8%; Pred. No. 1.4e-41;
RESULT 692
ID ABD32673 standard; DNA; 91359 BP.
DE Human cancer-associated genomic DNA HD13-075.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.6%; Score 202.4; DB 13; Length 91359;
Best Local Similarity 83.4%; Pred. No. 1.6e-41;
RESULT 693
Query Match 15.6%; Score 202.4; DB 10; Length 110000;
Best Local Similarity 79.3%; Pred. No. 1.7e-41;
ID AED89404 standard; DNA; 150437 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 44.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.6%; Score 202.4; DB 14; Length 150437;
Best Local Similarity 76.5%; Pred. No. 2e-41;
RESULT 695
ID AED89406 standard; DNA; 150491 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 46.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.8%; Score 202.4; DB 14; Length 150491;
Best Local Similarity 76.5%; Pred. No. 2e-41;
RESULT 696
ID AED89405 standard; DNA; 182314 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 45.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.6%; Score 202.4; DB 14; Length 182314;
Best Local Similarity 76.5%; Pred. No. 2.1e-41;
RESULT 697
ID ADJ12527 standard; DNA; 6257 BP.
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq381.
PN US2004010132-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (DUAN/) DUAN R D.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (GREE/) GREENE J M.
PA (YOUN/) YOUNG P E.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (FLOR/) FLORENCE C.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H.
Query Match 15.6%; Score 202.2; DB 12; Length 6257;
Best Local Similarity 83.8%; Pred. No. 5.5e-42;
RESULT 698
ID ABK50980 standard; DNA; 36568 BP.
DE Human solute carrier family 1 gene, SLC1A4.
PN WO200244198-A2.
PD 06-JUN-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 15.6%; Score 202.2; DB 6; Length 36568;
Best Local Similarity 82.4%; Pred. No. 1.2e-41;
RESULT 699
ID ABD32962 standard; DNA; 42016 BP.
DE Human cancer-associated genomic DNA HD20-018.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202.2; DB 4; Length 4611;
Best Local Similarity 79.8%; Pred. No. 5.4e-42;
RESULT 700
ID AAE04693 standard; DNA; 65071 BP.
DE Cancer-associated gene SEQ ID NO:11.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.6%; Score 202.2; DB 14; Length 65071;
Best Local Similarity 78.1%; Pred. No. 1.5e-41;
RESULT 701
ID ADQ97727 standard; DNA; 73063 BP.
DE Human cancer associated sequence HD10-034, SEQ ID 704.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.6%; Score 202.2; DB 12; Length 73063;
Best Local Similarity 84.8%; Pred. No. 1.6e-41;
RESULT 702
ID AAD46127 standard; DNA; 163350 BP.
DE Human tumour suppressor gene.
PN WO200268468-A2.
PD 06-SEP-2002.
PA (PEKE) PE CORP NY.
Query Match 15.6%; Score 202.2; DB 6; Length 163350;
Best Local Similarity 78.1%; Pred. No. 2.3e-41;
RESULT 703
ID ABT11173 standard; DNA; 168174 BP.
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 15.6%; Score 202.2; DB 6; Length 168174;
Best Local Similarity 83.6%; Pred. No. 2.3e-41;
RESULT 704
ID ABT11114 standard; DNA; 168273 BP.
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 15.6%; Score 202.2; DB 6; Length 168273;
Best Local Similarity 83.6%; Pred. No. 2.3e-41;
RESULT 705
ID AAK67294 standard; DNA; 699 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22106.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202; DB 4; Length 699;
Best Local Similarity 80.9%; Pred. No. 2.4e-42;
RESULT 706
ID AAK75871 standard; DNA; 4611 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30683.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202; DB 4; Length 4611;
Best Local Similarity 79.8%; Pred. No. 5.4e-42;
RESULT 707
ID AAK80697 standard; DNA; 4611 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35509.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202; DB 4; Length 4611;
Best Local Similarity 79.8%; Pred. No. 5.4e-42;
RESULT 708
ID AAS27823 standard; DNA; 16489 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1483.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 15.6%; Score 202; DB 4; Length 16489;
Best Local Similarity 76.8%; Pred. No. 9.5e-42;
RESULT 709
ID ADB94626 standard; DNA; 16489 BP.
DE Novel human protein DNA #235.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.6%; Score 202; DB 10; Length 16489;
Best Local Similarity 76.8%; Pred. No. 9.5e-42;
RESULT 710
ID ABA07345 standard; DNA; 30826 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 664.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202; DB 4; Length 30826;
Best Local Similarity 84.3%; Pred. No. 1.3e-41;
RESULT 711
ID AAS32772 standard; DNA; 30826 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 726.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202; DB 4; Length 30826;
Best Local Similarity 84.3%; Pred. No. 1.3e-41;
RESULT 712
ID AAL05410 standard; DNA; 31949 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8098.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202; DB 4; Length 31949;
Best Local Similarity 84.6%; Pred. No. 1.3e-41;
RESULT 713
ID ABL98269 standard; DNA; 31949 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2921.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202; DB 4; Length 31949;
Best Local Similarity 84.6%; Pred. No. 1.3e-41;
RESULT 714
ID AAL05411 standard; DNA; 32186 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8099.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202; DB 4; Length 32186;
Best Local Similarity 84.6%; Pred. No. 1.3e-41;
RESULT 715
ID ABL98270 standard; DNA; 32186 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2922.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 202; DB 4; Length 32186;
Best Local Similarity 84.6%; Pred. No. 1.3e-41;
RESULT 716
ID ACN44386 standard; DNA; 40136 BP.
DE Human genomic sequence hCG18551.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.6%; Score 202; DB 11; Length 40136;
Best Local Similarity 76.7%; Pred. No. 1.4e-41;
RESULT 717
ID ADZ13418 standard; DNA; 85920 BP.
DE Human cancer-associated genomic DNA #80.
PN WO2005031001-A2.
PD 07-APR-2005.

PA (CHIR) CHIRON CORP.
Query Match 15.6%; Score 202; DB 14; Length 85920;
Best Local Similarity 83.1%; Pred. No. 2e-41;
RESULT 718
ID ABQ76678 standard; DNA; 218336 BP.
DE Androgen receptor signalling pathway-associated DNA AF067844.
PN WO200282081-A2.
PD 17-OCT-2002.
PA (UVRP) UNIV ROCHESTER.
Query Match 15.6%; Score 202; DB 8; Length 218336;
Best Local Similarity 79.8%; Pred. No. 3e-41;
RESULT 719
ID ACN45146 standard; DNA; 226215 BP.
DE Human genomic sequence hCG1639824.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.6%; Score 202; DB 11; Length 226215;
Best Local Similarity 72.3%; Pred. No. 3e-41;
RESULT 720
ID ADQ59422 standard; DNA; 246940 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:58.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.6%; Score 202; DB 12; Length 246940;
Best Local Similarity 82.0%; Pred. No. 3.1e-41;
RESULT 721
ID ADC24763 standard; DNA; 334462 BP.
DE Human wild type HNL4X genomic sequence.
PN WO2003045998-A2.
PD 05-JUN-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP) INST PASTEUR.
PA (ASSI-) ASSIANCE PUBLIQUE HOPITAUX PARIS.
Query Match 15.6%; Score 202; DB 10; Length 334462;
Best Local Similarity 84.3%; Pred. No. 3.6e-41;
RESULT 722
ID AEB34391 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1971.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 15.6%; Score 201.8; DB 14; Length 601;
Best Local Similarity 78.0%; Pred. No. 2.5e-42;
RESULT 723
ID AEB32619 standard; DNA; 601 BP.
DE Human DNA polymorphic region #199.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 15.6%; Score 201.8; DB 14; Length 601;
Best Local Similarity 78.0%; Pred. No. 2.5e-42;
RESULT 724
ID AAL07263 standard; DNA; 1367 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9951.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 4; Length 1367;
Best Local Similarity 83.8%; Pred. No. 3.6e-42;
RESULT 725
ID ABL98809 standard; DNA; 1367 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3461.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 4; Length 1367;
Best Local Similarity 83.8%; Pred. No. 3.6e-42;
RESULT 726
ID AAF61133 standard; cDNA; 5700 BP.
DE Human BOLT cDNA.
PN DE19937846-A1.

PD 15-FEB-2001.
PA (BRUE/) BRUSSI M.
PA (BOEN/) BOENISCH H.
Query Match 15.6%; Score 201.8; DB 4; Length 5700;
Best Local Similarity 83.8%; Pred. No. 6.7e-42;
RESULT 727
ID ABA14861 standard; DNA; 6882 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7192.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 5; Length 6882;
Best Local Similarity 83.8%; Pred. No. 7.3e-42;
RESULT 728
ID ABA15569 standard; DNA; 6882 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7900.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 5; Length 6882;
Best Local Similarity 83.8%; Pred. No. 7.3e-42;
RESULT 729
ID AAL02817 standard; DNA; 16491 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5505.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 4; Length 16491;
Best Local Similarity 82.6%; Pred. No. 1.1e-41;
RESULT 730
ID AAK6943 standard; DNA; 19632 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21755.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 4; Length 19632;
Best Local Similarity 78.9%; Pred. No. 1.2e-41;
RESULT 731
ID AAK87657 standard; DNA; 21501 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42469.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 4; Length 21501;
Best Local Similarity 82.6%; Pred. No. 1.2e-41;
RESULT 732
ID ACC50933 standard; cDNA; 21501 BP.
DE Human secreted protein BAC clone SEQ ID NO 1113.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 8; Length 21501;
Best Local Similarity 82.6%; Pred. No. 1.2e-41;
RESULT 733
ID ABZ71531 standard; DNA; 21501 BP.
DE Secreted protein gene 139 genomic fragment HPRAL78, SEQ ID NO:641.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 8; Length 21501;
Best Local Similarity 82.8%; Pred. No. 1.2e-41;
RESULT 734
ID ADB91902 standard; DNA; 21501 BP.
DE Human secreted protein related DNA #SEQ ID 848.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 9; Length 21501;
Best Local Similarity 82.6%; Pred. No. 1.2e-41;
RESULT 735
ID ADC74690 standard; DNA; 21501 BP.
DE Human secreted protein-related DNA - SEQ ID 1323.
PN WO2003038063-A2.

PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.8; DB 10; Length 21501;
Best Local Similarity 82.6%; Pred. No. 1.2e-41;
RESULT 736
ID ADA02576 standard; DNA; 87878 BP.
DE Human PKBP5 carcinoma associated gene, SEQ ID NO:1094.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.6%; Score 201.8; DB 9; Length 87878;
Best Local Similarity 76.3%; Pred. No. 2.2e-41;
RESULT 737
ID ADB72314 standard; DNA; 87878 BP.
DE Human PKBP5 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.6%; Score 201.8; DB 10; Length 87878;
Best Local Similarity 76.3%; Pred. No. 2.2e-41;
RESULT 738
ID ADE95824 standard; DNA; 87878 BP.
DE Human PKBP5 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.6%; Score 201.8; DB 10; Length 87878;
Best Local Similarity 76.3%; Pred. No. 2.2e-41;
RESULT 739
ID ABD33432 standard; DNA; 106938 BP.
DE Human cancer-associated (CA) gene HD07-081.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.6%; Score 201.8; DB 13; Length 106938;
Best Local Similarity 76.8%; Pred. No. 2.4e-41;
RESULT 740
ID ADR67034 standard; DNA; 106938 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:80.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.6%; Score 201.8; DB 13; Length 106938;
Best Local Similarity 76.8%; Pred. No. 2.4e-41;
RESULT 741
ID ABN95044 standard; DNA; 110096 BP.
DE Gene #1542 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 15.6%; Score 201.8; DB 6; Length 110096;
Best Local Similarity 83.8%; Pred. No. 2.5e-41;
RESULT 742
ID AED18046 standard; DNA; 110096 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 297.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 15.6%; Score 201.8; DB 14; Length 110096;
Best Local Similarity 83.8%; Pred. No. 2.5e-41;
RESULT 743
ID AEF74649 standard; DNA; 110096 BP.
DE Human polynucleotide #163.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 15.6%; Score 201.8; DB 15; Length 110096;
Best Local Similarity 83.8%; Pred. No. 2.5e-41;
RESULT 744
ID AEF74540 standard; DNA; 110096 BP.
DE Human polynucleotide #54.
PN WO2006013561-A2.

PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 15.6%; Score 201.8; DB 15; Length 110096;
Best Local Similarity 83.8%; Pred. No. 2.5e-41;
RESULT 745
ID AEF74955 standard; DNA; 110096 BP.
DE Human polynucleotide #469.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 15.6%; Score 201.8; DB 15; Length 110096;
Best Local Similarity 83.8%; Pred. No. 2.5e-41;
RESULT 746
ID AEA61123 standard; DNA; 122673 BP.
DE Human PDB9A gene genomic sequence SEQ ID NO:33.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 15.6%; Score 201.8; DB 14; Length 122673;
Best Local Similarity 82.3%; Pred. No. 2.6e-41;
RESULT 747
ID AOS6277 standard; DNA; 200620 BP.
DE Human presynaptic cytomatrix protein, REPS2, genomic sequence.
PN WO2004044164-A2.
PD 27-MAY-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 15.6%; Score 201.8; DB 12; Length 200620;
Best Local Similarity 78.1%; Pred. No. 3.2e-41;
RESULT 748
ID ABD32868 standard; DNA; 238417 BP.
DE Human cancer-associated genomic DNA HD17-053.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.6%; Score 201.8; DB 13; Length 238417;
Best Local Similarity 81.3%; Pred. No. 3.5e-41;
RESULT 749
ID AAK68489 standard; DNA; 1958 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23301.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.6; DB 4; Length 1958;
Best Local Similarity 82.2%; Pred. No. 4.8e-42;
RESULT 750
ID ADU23043 standard; cDNA; 4470 BP.
DE LTRPC3 related DNA sequence, SEQ ID 106.
PN US2004229315-A1.
PD 18-NOV-2004.
PA (LEEN/) LEE N.
PA (CHEN/) CHEN J.
PA (FEDE/) FEDER J N.
PA (WUSS/) WU S.
PA (BLAN/) BLANAR M A.
PA (BOLD/) BOL D K.
PA (LEVE/) LEVESQUE P C.
PA (SUNL/) SUN L.
Query Match 15.6%; Score 201.6; DB 13; Length 4470;
Best Local Similarity 85.9%; Pred. No. 6.8e-42;
RESULT 751
ID AAL06913 standard; DNA; 13409 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9601.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.6; DB 4; Length 13409;
Best Local Similarity 84.6%; Pred. No. 1.1e-41;
RESULT 752
ID ABA08135 standard; DNA; 13409 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 930.
PN WO200155325-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.6; DB 4; Length 13409;
Best Local Similarity 84.6%; Pred. No. 1.1e-41;
RESULT 753
ID ABD33582 standard; DNA; 21823 BP.
DE Human cancer-associated (CA) gene HD07-117.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.6%; Score 201.6; DB 13; Length 21823;
Best Local Similarity 77.1%; Pred. No. 1.4e-41;
RESULT 754
ID AAL51353 standard; DNA; 39776 BP.
DE Human secreted protein genomic DNA sequence.
PN WO200299072-A2.
PD 12-DEC-2002.
PA (PEKE) PE CORP NY.
Query Match 15.6%; Score 201.6; DB 10; Length 39776;
Best Local Similarity 81.1%; Pred. No. 1.8e-41;
RESULT 755
ID ABX13974 standard; DNA; 46050 BP.
DE Human Ras-like protein gene.
PN US2002142382-A1.
PD 03-OCT-2002.
PA (MERK/) MERKULOV G V.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 15.6%; Score 201.6; DB 10; Length 46050;
Best Local Similarity 81.1%; Pred. No. 1.9e-41;
RESULT 756
ID AED01609 standard; DNA; 46050 BP.
DE Ras-like protein coding sequence, SEQ ID 3.
PN US2005208563-A1.
PD 22-SEP-2005.
PA (APPL-) APPLERA CORP.
Query Match 15.6%; Score 201.6; DB 14; Length 46050;
Best Local Similarity 81.1%; Pred. No. 1.9e-41;
RESULT 757
ID ABZ74178 standard; DNA; 47567 BP.
DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1325.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.6; DB 8; Length 47567;
Best Local Similarity 84.6%; Pred. No. 1.9e-41;
RESULT 758
ID ABZ74223 standard; DNA; 47567 BP.
DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1370.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.6; DB 8; Length 47567;
Best Local Similarity 84.6%; Pred. No. 1.9e-41;
RESULT 759
ID ADA98707 standard; DNA; 47567 BP.
DE Human secreted protein-related DNA sequence #300.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.6; DB 8; Length 47567;
Best Local Similarity 84.6%; Pred. No. 1.9e-41;
RESULT 760
ID ADA98752 standard; DNA; 47567 BP.
DE Human secreted protein-related DNA sequence #345.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.6; DB 8; Length 47567;
Best Local Similarity 84.6%; Pred. No. 1.9e-41;
RESULT 761
ID ABZ67744 standard; DNA; 47567 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1267.

PN WO20027186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.6; DB 10; Length 47567;
Best Local Similarity 84.6%; Pred. No. 1.9e-41;
RESULT 762
ID AB267789 standard; DNA; 47567 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1312.
PN WO20027186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.6; DB 10; Length 47567;
Best Local Similarity 84.6%; Pred. No. 1.9e-41;
RESULT 763
ID ADP65343 standard; DNA; 57038 BP.
DE Human sequence from clone RPS-1009E24 on chromosome 20 Contains DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 15.6%; Score 201.6; DB 11; Length 57038;
Best Local Similarity 74.6%; Pred. No. 2.1e-41;
RESULT 764
ID ADP65471 standard; DNA; 92794 BP.
DE Human sequence from clone RPS-1009E24 on chromosome 20 DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 15.6%; Score 201.6; DB 11; Length 92794;
Best Local Similarity 74.6%; Pred. No. 2.6e-41;
RESULT 765
ID AQ83210 standard; DNA; 397658 BP.
DE Human transporter protein genomic DNA SEQ ID NO:3.
Query Match 15.6%; Score 201.6; DB 8; Length 110000;
Best Local Similarity 79.8%; Pred. No. 2.8e-41;
RESULT 766
ID AEB32401 standard; DNA; 119313 BP.
DE Human genomic DNA #42.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NV.
Query Match 15.6%; Score 201.6; DB 14; Length 119313;
Best Local Similarity 84.6%; Pred. No. 2.9e-41;
RESULT 767
ID ADQ20606 standard; DNA; 195917 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3426.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 15.6%; Score 201.6; DB 12; Length 195917;
Best Local Similarity 84.6%; Pred. No. 3.6e-41;
RESULT 768
ID ABZ72040 standard; DNA; 207433 BP.
DE Gene 216 H194BAC1098L22 nucleotide sequence SEQ ID NO 5.
PN WO200178894-A2.
PD 23-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.6%; Score 201.6; DB 5; Length 207433;
Best Local Similarity 74.6%; Pred. No. 3.7e-41;
RESULT 769
ID AEBX74891 standard; DNA; 207433 BP.
DE BAC1098L22 DNA sequence.
PN WO200283077-A2.
PD 24-OCT-2002.
PA (SCHE-) SCHERING CORP.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.6%; Score 201.6; DB 8; Length 207433;
Best Local Similarity 74.6%; Pred. No. 3.7e-41;
RESULT 770
ID ADJ36614 standard; DNA; 207433 BP.
DE Bacterial artificial chromosome RPCI-11.
PN US2004002470-A1.
PD 01-JAN-2004.
PA (KEIT-) KEITH T.

PA (LITT/) LITTLE R D.
PA (VEER/) VAN ERDEWEGH P.
PA (DUPU/) DUPUIS J.
PA (DMAS/) DEL MASTRO R G.
PA (SIMO/) SIMON J.
PA (ALLE/) ALLEN K.
PA (PAND/) PANDIT S.
Query Match 15.6%; Score 201.6; DB 12; Length 207433;
Best Local Similarity 74.6%; Pred. No. 3.7e-41;
RESULT 771
ID ADL81193 standard; DNA; 207433 BP.
DE BAC1098L22 DNA sequence.
PN US2004023215-A1.
PD 05-FEB-2004.
PA (KEIT/) KEITH T.
PA (LITT/) LITTLE R D.
PA (VEER/) VAN ERDEWEGH P V.
PA (DUPU/) DUPUIS J.
PA (DMAS/) DEL MASTRO R G.
PA (SIMO/) SIMON J.
PA (ALLE/) ALLEN K.
PA (PAND/) PANDIT S.
Query Match 15.6%; Score 201.6; DB 12; Length 207433;
Best Local Similarity 74.6%; Pred. No. 3.7e-41;
RESULT 772
ID ACN44046 standard; DNA; 260027 BP.
DE Human genomic sequence HCG1735292.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.6%; Score 201.6; DB 11; Length 260027;
Best Local Similarity 81.1%; Pred. No. 4.1e-41;
RESULT 773
ID ABV50139 standard; cDNA; 587 BP.
DE Human prostate expression marker cDNA 50130.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.6%; Score 201.4; DB 5; Length 587;
Best Local Similarity 85.3%; Pred. No. 3.2e-42;
RESULT 774
ID ABV59189 standard; cDNA; 596 BP.
DE Human prostate expression marker cDNA 59180.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.6%; Score 201.4; DB 5; Length 596;
Best Local Similarity 85.3%; Pred. No. 3.2e-42;
RESULT 775
ID AAD57237 standard; cDNA; 1822 BP.
DE Human CGDD-17 cDNA.
PN WO2003050253-A2.
PD 19-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.6%; Score 201.4; DB 9; Length 1822;
Best Local Similarity 83.7%; Pred. No. 5.2e-42;
RESULT 776
ID AAK69721 standard; DNA; 16086 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24533.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.4; DB 4; Length 16086;
Best Local Similarity 82.8%; Pred. No. 1.4e-41;
RESULT 777
ID AAL36020 standard; DNA; 16086 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2385.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.6%; Score 201.4; DB 4; Length 16086;
Best Local Similarity 82.8%; Pred. No. 1.4e-41;
RESULT 778

ID ABX59008 standard; cDNA; 16086 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1352.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 8; Length 16086;
Best Local Similarity 82.8%; Pred. No. 1.4e-41;
RESULT 779
ID ADJ29758 standard; DNA; 16086 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2385.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 12; Length 16086;
Best Local Similarity 82.8%; Pred. No. 1.4e-41;
RESULT 780
ID ABA16118 standard; DNA; 32216 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8449.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 5; Length 32216;
Best Local Similarity 83.8%; Pred. No. 1.8e-41;
RESULT 781
ID ABL68024 standard; DNA; 38374 BP.
DE Kidney cancer related gene sequence SEQ ID NO:7161.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 6; Length 38374;
Best Local Similarity 82.8%; Pred. No. 2e-41;
RESULT 782
ID ABL68363 standard; DNA; 38374 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6700.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 6; Length 38374;
Best Local Similarity 82.8%; Pred. No. 2e-41;
RESULT 783
ID ABL68364 standard; DNA; 38374 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6701.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 6; Length 38374;
Best Local Similarity 82.8%; Pred. No. 2e-41;
RESULT 784
ID ABN96966 standard; DNA; 38374 BP.
DE Gene #3464 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 6; Length 38374;
Best Local Similarity 82.8%; Pred. No. 2e-41;
RESULT 785
ID AAK81745 standard; DNA; 46553 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36557.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 4; Length 46553;
Best Local Similarity 83.8%; Pred. No. 2.2e-41;
RESULT 786
ID AAK67926 standard; DNA; 46553 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22738.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 4; Length 46553;
Best Local Similarity 83.8%; Pred. No. 2.2e-41;

RESULT 787
ID ADZ12496 standard; DNA; 72337 BP.
DE Human cancer-associated genomic DNA #3.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 14; Length 72337;
Best Local Similarity 82.8%; Pred. No. 2.6e-41;
RESULT 788
ID AAV83940 standard; DNA; 80240 BP.
DE NC-contig derived from mardel(10) on chromosome 10q25.2.
PN WO9851790-A1.
PD 19-NOV-1998.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 2; Length 80240;
Best Local Similarity 77.7%; Pred. No. 2.7e-41;
RESULT 789
ID AAV83939 standard; DNA; 80595 BP.
DE HC-contig derived from normal human chromosome 10q25.2 region.
PN WO9851790-A1.
PD 19-NOV-1998.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 2; Length 80595;
Best Local Similarity 77.7%; Pred. No. 2.7e-41;
RESULT 790
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 14; Length 110000;
Best Local Similarity 77.7%; Pred. No. 3.1e-41;
RESULT 791
ID ABK83461 standard; cDNA; 128600 BP.
DE Human cDNA differentially expressed in granulocytic cells #32.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 6; Length 128600;
Best Local Similarity 81.3%; Pred. No. 3.4e-41;
RESULT 792
ID ACF62736 standard; DNA; 183610 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:664.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 8; Length 183610;
Best Local Similarity 78.6%; Pred. No. 3.9e-41;
RESULT 793
ID ADB20851 standard; DNA; 183610 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:664.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 8; Length 183610;
Best Local Similarity 78.6%; Pred. No. 3.9e-41;
RESULT 794
ID ADB87940 standard; DNA; 183610 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:664.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 10; Length 183610;
Best Local Similarity 78.6%; Pred. No. 3.9e-41;
RESULT 795
ID ADB96923 standard; DNA; 183610 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:664.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match
Best Local Similarity 15.6%; Score 201.4; DB 10; Length 183610;
Best Local Similarity 78.6%; Pred. No. 3.9e-41;
RESULT 796
ID ADB92114 standard; DNA; 183610 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:664.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.


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Query Match      15.6%; Score 201.4; DB 10; Length 183610;
Best Local Similarity 78.6%; Pred. No. 3.9e-41;
RESULT 797
ID ACF62750 standard; DNA; 186591 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:682.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 8; Length 186591;
Best Local Similarity 78.6%; Pred. No. 4e-41;
RESULT 798
ID ADB20869 standard; DNA; 186591 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:682.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 8; Length 186591;
Best Local Similarity 78.6%; Pred. No. 4e-41;
RESULT 799
ID ADB87958 standard; DNA; 186591 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:682.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 8; Length 186591;
Best Local Similarity 78.6%; Pred. No. 4e-41;
RESULT 800
ID ADB96941 standard; DNA; 186591 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:682.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 10; Length 186591;
Best Local Similarity 78.6%; Pred. No. 4e-41;
RESULT 801
ID ADB92132 standard; DNA; 186591 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:682.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 10; Length 186591;
Best Local Similarity 78.6%; Pred. No. 4e-41;
RESULT 802
ID ASD89383 standard; DNA; 188682 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 23.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match      15.6%; Score 201.4; DB 14; Length 188682;
Best Local Similarity 84.1%; Pred. No. 4e-41;
RESULT 803
ID ACF62735 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:663.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 8; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 804
ID ACF62740 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:668.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 8; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 805
ID ADB20850 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:663.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 8; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 806
ID ADB20855 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:668.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 8; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 807
ID ADB87944 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:668.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 10; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 808
ID ADB87939 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:663.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 10; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 809
ID ADB96922 standard; DNA; 208648 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:663.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 10; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 810
ID ADB96927 standard; DNA; 208648 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:668.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 10; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 811
ID ADB92113 standard; DNA; 208648 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:663.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 10; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 812
ID ADB92118 standard; DNA; 208648 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:668.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match      15.6%; Score 201.4; DB 10; Length 208648;
Best Local Similarity 78.6%; Pred. No. 4.2e-41;
RESULT 813
ID ABL42177 standard; cDNA; 1408 BP.
DE Nucleotide sequence of human big protein 9.13.
PN WO200220780-A1.
PD 14-MAR-2002.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match      15.5%; Score 201.2; DB 6; Length 1408;
Best Local Similarity 79.0%; Pred. No. 5.2e-42;
RESULT 814
ID AAV83945 standard; DNA; 1701 BP.
DE Bacterial artificial chromosome (BAC)-F2 contig 5.
PN WO9851790-A1.
PD 19-NOV-1998.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
Query Match      15.5%; Score 201.2; DB 2; Length 1701;
Best Local Similarity 84.8%; Pred. No. 5.7e-42;
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RESULT 815
ID ABV25545 standard; cDNA; 1866 BP.
DE Human prostate expression marker cDNA 25536.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.5%; Score 201.2; DB 5; Length 1866;
Best Local Similarity 80.0%; Pred. No. 5.9e-42;
RESULT 816
ID ABV29257 standard; cDNA; 1866 BP.
DE Human prostate expression marker cDNA 29248.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.5%; Score 201.2; DB 5; Length 1866;
Best Local Similarity 80.0%; Pred. No. 5.9e-42;
RESULT 817
ID AET13443 standard; DNA; 1888 BP.
DE Breast specific related polynucleotide SEQ ID NO 158.
PN WO20027732-A2.
PD 03-OCT-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 15.5%; Score 201.2; DB 8; Length 1888;
Best Local Similarity 80.0%; Pred. No. 6e-42;
RESULT 818
ID AAK76210 standard; DNA; 5434 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31022.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201.2; DB 4; Length 5434;
Best Local Similarity 79.2%; Pred. No. 9.5e-42;
RESULT 819
ID AQ59392 standard; DNA; 22173 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:28.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.5%; Score 201.2; DB 12; Length 22173;
Best Local Similarity 84.3%; Pred. No. 1.8e-41;
RESULT 820
ID ADZ13655 standard; DNA; 22173 BP.
DE Human cancer-associated genomic DNA #101.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Query Match 15.5%; Score 201.2; DB 14; Length 22173;
Best Local Similarity 84.3%; Pred. No. 1.8e-41;
RESULT 821
ID ADZ59535 standard; DNA; 22801 BP.
DE Secondary hyperparathyroidism detection human polymorphic gene, TGFBI.
PN JP2005102601-A.
PD 21-APR-2005.
PA (HYUB-) HYUBITTO GENOMICS KK.
PA (JIKE-) UNIV JIKEI.
Query Match 15.5%; Score 201.2; DB 14; Length 22801;
Best Local Similarity 80.6%; Pred. No. 1.8e-41;
RESULT 822
ID AEP96532 standard; DNA; 22801 BP.
DE Human TGFBI gene, SEQ ID 16.
PN JP2005204549-A.
PD 04-AUG-2005.
PA (HYUB-) HYUBITTO GENOMICS KK.
PA (KAWA-) KAWADA Y.
Query Match 15.5%; Score 201.2; DB 14; Length 22801;
Best Local Similarity 80.6%; Pred. No. 1.8e-41;
RESULT 823
ID ABK42170 standard; DNA; 32134 BP.
DE Genomic sequence #69 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201.2; DB 4; Length 32134;

Best Local Similarity 82.0%; Pred. No. 2.1e-41;
RESULT 824
ID AAL37170 standard; DNA; 32134 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3535.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201.2; DB 4; Length 32134;
Best Local Similarity 82.0%; Pred. No. 2.1e-41;
RESULT 825
ID AAL03669 standard; DNA; 32134 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6357.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201.2; DB 4; Length 32134;
Best Local Similarity 82.0%; Pred. No. 2.1e-41;
RESULT 826
ID ABA07858 standard; DNA; 32134 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 653.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201.2; DB 4; Length 32134;
Best Local Similarity 82.0%; Pred. No. 2.1e-41;
RESULT 827
ID ABX60158 standard; cDNA; 32134 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2502.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.5%; Score 201.2; DB 8; Length 32134;
Best Local Similarity 82.0%; Pred. No. 2.1e-41;
RESULT 828
ID ADB60326 standard; DNA; 32134 BP.
DE Connective tissue related genomic DNA #69.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201.2; DB 9; Length 32134;
Best Local Similarity 82.0%; Pred. No. 2.1e-41;
RESULT 829
ID ADJ30908 standard; DNA; 32134 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3535.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201.2; DB 12; Length 32134;
Best Local Similarity 82.0%; Pred. No. 2.1e-41;
RESULT 830
ID AAS32454 standard; DNA; 32150 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 408.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201.2; DB 4; Length 32150;
Best Local Similarity 80.8%; Pred. No. 2.1e-41;
RESULT 831
ID AAK71358 standard; DNA; 37314 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26170.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201.2; DB 4; Length 37314;
Best Local Similarity 83.6%; Pred. No. 2.2e-41;
RESULT 832
ID ABD33436 standard; DNA; 52710 BP.
DE Human cancer-associated (CA) gene HD07-082.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 15.5%; Score 201.2; DB 13; Length 52710;
 Best Local Similarity 78.4%; Pred. No. 2.6e-41;
 RESULT 833
 ID AAS13655 standard; DNA; 53552 BP.
 DE Genomic DNA sequence encoding human hepG15.
 PN WO200166752-A2.
 PD 13-SEP-2001.
 PA (WHEE) WHITEHEAD INST BIOMEDICAL RES.
 Query Match 15.5%; Score 201.2; DB 5; Length 53552;
 Best Local Similarity 83.6%; Pred. No. 2.6e-41;
 RESULT 834
 ID AAK65581 standard; DNA; 56632 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20393.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.5%; Score 201.2; DB 4; Length 56632;
 Best Local Similarity 82.0%; Pred. No. 2.6e-41;
 RESULT 835
 ID ACN37231 standard; DNA; 64796 BP.
 DE Human periodontal disease related gene COL17A1 SEQ ID NO:141.
 Query Match 15.5%; Score 201.2; DB 13; Length 64796;
 Best Local Similarity 80.9%; Pred. No. 2.8e-41;
 RESULT 836
 ID ABL62723 standard; DNA; 66109 BP.
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:1060.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 15.5%; Score 201.2; DB 6; Length 66109;
 Best Local Similarity 81.7%; Pred. No. 2.8e-41;
 RESULT 837
 ID ABN97273 standard; DNA; 66109 BP.
 DE Gene #3771 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 15.5%; Score 201.2; DB 6; Length 66109;
 Best Local Similarity 81.7%; Pred. No. 2.8e-41;
 RESULT 838
 ID ABK84756 standard; cDNA; 81800 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1327.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 15.5%; Score 201.2; DB 6; Length 81800;
 Best Local Similarity 84.3%; Pred. No. 3.1e-41;
 RESULT 839
 ID ADH69807 standard; DNA; 684973 BP.
 DE Human Vbeta gene.
 PN US2002150891-A1.
 PD 17-OCT-2002.
 PA (HOOD/) HOOD L E.
 PA (ROWE/) ROWEN L.
 Query Match 15.5%; Score 201.2; DB 12; Length 110000;
 Best Local Similarity 83.1%; Pred. No. 3.5e-41;
 RESULT 840
 Query Match 15.5%; Score 201.2; DB 12; Length 110000;
 Best Local Similarity 83.1%; Pred. No. 3.5e-41;
 RESULT 841
 ID ABE18531 standard; DNA; 135019 BP.
 DE Human Pmilio 1 genomic DNA.
 PN US2005261217-A1.
 PD 24-NOV-2005.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 15.5%; Score 201.2; DB 14; Length 135019;
 Best Local Similarity 81.2%; Pred. No. 3.9e-41;
 RESULT 842
 ID ABK84797 standard; cDNA; 149671 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1368.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.

Query Match 15.5%; Score 201.2; DB 6; Length 149671;
 Best Local Similarity 79.0%; Pred. No. 4.1e-41;
 RESULT 843
 ID ADB70361 standard; cDNA; 149671 BP.
 DE Moesin cDNA SEQ ID NO:53.
 PN WO2003021229-A2.
 PD 13-MAR-2003.
 PA (BIGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 15.5%; Score 201.2; DB 9; Length 149671;
 Best Local Similarity 79.0%; Pred. No. 4.1e-41;
 RESULT 844
 ID ADJ37140 standard; cDNA; 149671 BP.
 DE Human malignant pleural mesothelioma (MPM) cDNA #23.
 PN US2003219750-A1.
 PD 27-NOV-2003.
 PA (BIGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 15.5%; Score 201.2; DB 12; Length 149671;
 Best Local Similarity 79.0%; Pred. No. 4.1e-41;
 RESULT 845
 ID ABQ88207 standard; cDNA; 172570 BP.
 DE Human osteoblast differentiation related cDNA SEQ ID NO 114.
 PN WO200250301-A2.
 PD 27-JUN-2002.
 PA (PROC) PROCTER & GAMBLE CO.
 Query Match 15.5%; Score 201.2; DB 6; Length 172570;
 Best Local Similarity 83.6%; Pred. No. 4.3e-41;
 RESULT 846
 ID ADK43203 standard; DNA; 176001 BP.
 DE Human protein tyrosine phosphatase, receptor type alpha (PTPRA) gDNA 2.
 PN WO2004011623-A2.
 PD 05-FEB-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 15.5%; Score 201.2; DB 12; Length 176001;
 Best Local Similarity 84.8%; Pred. No. 4.4e-41;
 RESULT 847
 ID AED18538 standard; DNA; 184666 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 789.
 PN WO2005098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 15.5%; Score 201.2; DB 14; Length 184666;
 Best Local Similarity 84.3%; Pred. No. 4.4e-41;
 RESULT 848
 ID ADK43195 standard; DNA; 186739 BP.
 DE Human protein tyrosine phosphatase, receptor type alpha (PTPRA) gDNA.
 PN WO2004011623-A2.
 PD 05-FEB-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 15.5%; Score 201.2; DB 12; Length 186739;
 Best Local Similarity 84.8%; Pred. No. 4.5e-41;
 RESULT 849
 ID ABK84699 standard; cDNA; 198285 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1370.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 15.5%; Score 201.2; DB 6; Length 198285;
 Best Local Similarity 81.7%; Pred. No. 4.6e-41;
 RESULT 850
 ID ABN97319 standard; DNA; 198285 BP.
 DE Gene #3817 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 15.5%; Score 201.2; DB 6; Length 198285;
 Best Local Similarity 81.7%; Pred. No. 4.6e-41;
 RESULT 851
 ID ADR52987 standard; DNA; 198285 BP.
 DE Drug therapy altered expressed gene #338.
 PN WO2004072265-A2.
 PD 26-AUG-2004.
 PA (AMHP) WYETH.

PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 15.5%; Score 201.2; DB 13; Length 198285;
Best Local Similarity 81.7%; Pred. No. 4.6e-41;
RESULT 852
ID AD056277 standard; DNA; 200620 BP.
DE Human presynaptic cytomatrix protein, REPS2, genomic sequence.
PN WO2004044164-A2.
PD 27-MAY-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 15.5%; Score 201.2; DB 12; Length 200620;
Best Local Similarity 83.3%; Pred. No. 4.6e-41;
RESULT 853
ID AB168560 standard; DNA; 267156 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6897.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 15.5%; Score 201.2; DB 6; Length 267156;
Best Local Similarity 83.1%; Pred. No. 5.2e-41;
RESULT 854
ID AA543104 standard; DNA; 325791 BP.
DE Human Oestrogen receptor beta gene.
PN WO200162793-A2.
PD 30-AUG-2001.
PA (PEKE) PE CORP NY.
Query Match 15.5%; Score 201.2; DB 4; Length 325791;
Best Local Similarity 82.4%; Pred. No. 5.7e-41;
RESULT 855
ID ABV72713 standard; cDNA; 1874 BP.
DE Human trypsin inhibitor 10.12 CDNA.
PN CN1342685-A.
PD 03-APR-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 15.5%; Score 201; DB 6; Length 1874;
Best Local Similarity 84.1%; Pred. No. 6.7e-42;
RESULT 856
ID ADB63560 standard; cDNA; 2412 BP.
DE Human cDNA encoding clone THYMU20007750.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.5%; Score 201; DB 10; Length 2412;
Best Local Similarity 81.5%; Pred. No. 7.5e-42;
RESULT 857
ID ADM02168 standard; cDNA; 2567 BP.
DE Human cDNA of the invention SEQ ID NO:853.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.5%; Score 201; DB 11; Length 2567;
Best Local Similarity 81.5%; Pred. No. 7.7e-42;
RESULT 858
ID ASC85098 standard; cDNA; 2567 BP.
DE Human cDNA clone FEBR20017050, SEQ ID 853.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.5%; Score 201; DB 14; Length 2567;
Best Local Similarity 81.5%; Pred. No. 7.7e-42;
RESULT 859
ID ABA18201 standard; DNA; 3503 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10532.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201; DB 5; Length 3503;
Best Local Similarity 81.5%; Pred. No. 8.8e-42;
RESULT 860
ID ACN44346 standard; DNA; 31397 BP.

DE Human genomic sequence hCG33404.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 201; DB 11; Length 31397;
Best Local Similarity 84.1%; Pred. No. 2.3e-41;
RESULT 861
ID AAS26795 standard; DNA; 32248 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1769.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201; DB 4; Length 32248;
Best Local Similarity 83.6%; Pred. No. 2.3e-41;
RESULT 862
ID AAL37122 standard; DNA; 32248 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3487.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201; DB 4; Length 32248;
Best Local Similarity 83.6%; Pred. No. 2.3e-41;
RESULT 863
ID ABA20412 standard; DNA; 32248 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12743.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201; DB 5; Length 32248;
Best Local Similarity 83.6%; Pred. No. 2.3e-41;
RESULT 864
ID ABX74144 standard; DNA; 32248 BP.
DE Human novel polynucleotide #972.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.5%; Score 201; DB 8; Length 32248;
Best Local Similarity 83.6%; Pred. No. 2.3e-41;
RESULT 865
ID ABX60110 standard; cDNA; 32248 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2454.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.5%; Score 201; DB 8; Length 32248;
Best Local Similarity 83.6%; Pred. No. 2.3e-41;
RESULT 866
ID ADJ30860 standard; DNA; 32248 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3487.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 201; DB 12; Length 32248;
Best Local Similarity 83.6%; Pred. No. 2.3e-41;
RESULT 867
ID AAF54723 standard; DNA; 35465 BP.
DE Nucleotide sequence of a human polynucleotide sequence.
PN WO200105422-A2.
PD 25-JAN-2001.
PA (INMR) BIOMERIEUX STELHYS.
Query Match 15.5%; Score 201; DB 4; Length 35465;
Best Local Similarity 83.1%; Pred. No. 2.4e-41;
RESULT 868
ID ABT17380 standard; DNA; 35465 BP.
DE Human IG gene related nucleic acid SEQ ID No 6.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 15.5%; Score 201; DB 8; Length 35465;

Best Local Similarity 83.1%; Pred. No. 2.4e-41;
RESULT 869
ID APT17382 standard; DNA; 36991 BP.
DE Human IG gene related nucleic acid SEQ ID NO 8.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 15.5%; Score 201; DB 8; Length 36991;
Best Local Similarity 83.1%; Pred. No. 2.5e-41;
RESULT 870
ID AED18110 standard; DNA; 36991 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 361.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 15.5%; Score 201; DB 14; Length 36991;
Best Local Similarity 83.1%; Pred. No. 2.5e-41;
RESULT 871
ID AEF75130 standard; DNA; 36991 BP.
DE Human polynucleotide #644.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 15.5%; Score 201; DB 15; Length 36991;
Best Local Similarity 83.1%; Pred. No. 2.5e-41;
RESULT 872
ID AAF58067 standard; DNA; 39198 BP.
DE Human polyamine-modulated factor-1 PMF-1 gene.
PN WO200107610-A1.
PD 01-FEB-2001.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 15.5%; Score 201; DB 5; Length 39198;
Best Local Similarity 84.1%; Pred. No. 2.5e-41;
RESULT 873
ID AAX23517 standard; DNA; 50000 BP.
DE Human kidney aminopeptidase P genomic DNA fragment 1.
PN WO9911799-A2.
PD 11-MAR-1999.
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.
Query Match 15.5%; Score 201; DB 2; Length 50000;
Best Local Similarity 79.8%; Pred. No. 2.8e-41;
RESULT 874
ID ACN45018 standard; DNA; 81099 BP.
DE Human genomic sequence hCG17395.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 201; DB 11; Length 81099;
Best Local Similarity 81.5%; Pred. No. 3.5e-41;
RESULT 875
ID ABZ22285 standard; DNA; 86592 BP.
DE Human D-amino acid oxidase (DAO) genomic DNA sequence SEQ ID NO:1.
PN WO200266672-A2.
PD 29-AUG-2002.
PA (GEST) GENSET.
Query Match 15.5%; Score 201; DB 8; Length 86592;
Best Local Similarity 84.3%; Pred. No. 3.6e-41;
RESULT 876
ID AAL57236 standard; DNA; 86592 BP.
DE Human D-amino acid oxidase genomic DNA.
PN WO2003050303-A2.
PD 19-JUN-2003.
PA (GEST) GENSET SA.
Query Match 15.5%; Score 201; DB 9; Length 86592;
Best Local Similarity 84.3%; Pred. No. 3.6e-41;
RESULT 877
ID AAL60240 standard; DNA; 86592 BP.
DE Human D-amino acid oxidase (DAO) genomic DNA.
PN WO2003047558-A2.
Query Match 15.5%; Score 201; DB 9; Length 86592;
Best Local Similarity 84.3%; Pred. No. 3.6e-41;
RESULT 878

ID ADR52892 standard; DNA; 151152 BP.
DE Drug therapy altered expressed gene #243.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A.J.
PA (TREP/) TREPICCHIO W.L.
Query Match 15.5%; Score 201; DB 13; Length 151152;
Best Local Similarity 79.8%; Pred. No. 4.6e-41;
RESULT 879
ID ADL13570 standard; DNA; 193672 BP.
DE Osteoarthritis-associated polymorphic nucleotide #102.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.5%; Score 201; DB 10; Length 193672;
Best Local Similarity 81.9%; Pred. No. 5.1e-41;
RESULT 880
ID ADF69744 standard; DNA; 312477 BP.
DE Human ROCK 1 DNA #2.
PN US2004115641-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.5%; Score 201; DB 12; Length 312477;
Best Local Similarity 80.6%; Pred. No. 6.3e-41;
RESULT 881
ID ABV61726 standard; cDNA; 471 BP.
DE Human prostate expression marker cDNA 61717.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.5%; Score 200.8; DB 5; Length 471;
Best Local Similarity 84.3%; Pred. No. 4.1e-42;
RESULT 882
ID AAI96166 standard; cDNA; 804 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2241.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 15.5%; Score 200.8; DB 4; Length 804;
Best Local Similarity 63.2%; Pred. No. 5.2e-42;
RESULT 883
ID ADA52945 standard; cDNA; 1697 BP.
DE Human coding sequence, SEQ ID 513.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.5%; Score 200.8; DB 10; Length 1697;
Best Local Similarity 75.7%; Pred. No. 7.2e-42;
RESULT 884
ID AAK83072 standard; DNA; 10102 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37884.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.8; DB 4; Length 10102;
Best Local Similarity 82.3%; Pred. No. 1.6e-41;
RESULT 885
ID AAD32327 standard; DNA; 15765 BP.
DE Human NFKB1B gene, alternative version.
PN WO200212497-A2.
PD 14-FEB-2002.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 15.5%; Score 200.8; DB 6; Length 15765;
Best Local Similarity 82.6%; Pred. No. 1.9e-41;
RESULT 886
ID AAD32179 standard; DNA; 15765 BP.
DE Human NFKB1B gene.
PN WO200212497-A2.

PD 14-FEB-2002.
 PA (GENA-) GENAISSANCE PHARM INC.
 Query Match 15.5%; Score 200.8; DB 6; Length 15765;
 Best Local Similarity 82.6%; Pred. No. 1.9e-41;
 RESULT 887
 ID AB273865 standard; DNA; 18902 BP.
 DE Secreted protein gene 71 genomic fragment HCRBF72, SEQ ID NO:1012.
 PN WO200277013-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.5%; Score 200.8; DB 8; Length 18902;
 Best Local Similarity 78.4%; Pred. No. 2.1e-41;
 RESULT 888
 ID AB267444 standard; DNA; 18902 BP.
 DE Human secreted protein encoding genomic DNA SEQ ID NO 967.
 PN WO200277186-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.5%; Score 200.8; DB 10; Length 18902;
 Best Local Similarity 78.4%; Pred. No. 2.1e-41;
 RESULT 889
 ID AQ97189 standard; DNA; 23360 BP.
 DE Human cancer associated sequence HD08-012, SEQ ID 165.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 15.5%; Score 200.8; DB 12; Length 29360;
 Best Local Similarity 83.4%; Pred. No. 2.5e-41;
 RESULT 890
 ID ACN44778 standard; DNA; 56577 BP.
 DE Human genomic sequence hCG27352.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 15.5%; Score 200.8; DB 11; Length 56577;
 Best Local Similarity 83.8%; Pred. No. 3.4e-41;
 RESULT 891
 ID ADZ13149 standard; DNA; 57105 BP.
 DE Human cancer-associated genomic DNA #56.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 15.5%; Score 200.8; DB 14; Length 57105;
 Best Local Similarity 83.8%; Pred. No. 3.4e-41;
 RESULT 892
 ID ACN44686 standard; DNA; 57564 BP.
 DE Human genomic sequence hCG33029.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 15.5%; Score 200.8; DB 11; Length 57564;
 Best Local Similarity 75.5%; Pred. No. 3.4e-41;
 RESULT 893
 ID ADL27146 standard; DNA; 96593 BP.
 DE Human genomic sequence for PpP3CC.
 PN US2003216558-A1.
 PD 20-NOV-2003.
 PA (MORR/) MORRIS D W.
 PA (ENGEL/) ENGELHARD E K.
 Query Match 15.5%; Score 200.8; DB 11; Length 96593;
 Best Local Similarity 82.6%; Pred. No. 4.3e-41;
 RESULT 894
 ID ADA03068 standard; DNA; 96595 BP.
 DE Human PpP3CC carcinoma associated gene, SEQ ID NO:1586.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 15.5%; Score 200.8; DB 9; Length 96595;
 Best Local Similarity 82.6%; Pred. No. 4.3e-41;
 RESULT 895
 ID ADB72806 standard; DNA; 96595 BP.
 DE Human PpP3CC Gene.
 PN WO2003008583-A2.

PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 15.5%; Score 200.8; DB 10; Length 96595;
 Best Local Similarity 82.6%; Pred. No. 4.3e-41;
 RESULT 896
 ID ADA66352 standard; DNA; 96596 BP.
 DE Human PpP3CC gene genomic DNA sequence.
 PN WO2003053224-A2.
 PD 03-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 15.5%; Score 200.8; DB 9; Length 96596;
 Best Local Similarity 82.6%; Pred. No. 4.3e-41;
 RESULT 897
 Query Match 15.5%; Score 200.8; DB 14; Length 110000;
 Best Local Similarity 83.8%; Pred. No. 4.5e-41;
 RESULT 898
 ID AED89390 standard; DNA; 143389 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 30.
 PN WO2005105044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 15.5%; Score 200.8; DB 14; Length 143389;
 Best Local Similarity 82.6%; Pred. No. 5.1e-41;
 RESULT 899
 ID AED89384 standard; DNA; 150314 BP.
 DE Human breast cancer genetic marker BAC DNA SEQ ID NO 24.
 PN WO2005105044-A1.
 PD 10-NOV-2005.
 PA (EXAG-) EXAGEN DIAGNOSTICS INC.
 Query Match 15.5%; Score 200.8; DB 14; Length 150314;
 Best Local Similarity 82.6%; Pred. No. 5.2e-41;
 RESULT 900
 ID ACN44262 standard; DNA; 168821 BP.
 DE Human genomic sequence hCG18035.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 15.5%; Score 200.8; DB 11; Length 168821;
 Best Local Similarity 81.2%; Pred. No. 5.4e-41;
 RESULT 901
 ID ADL13512 standard; DNA; 178870 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #44.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 15.5%; Score 200.8; DB 10; Length 178870;
 Best Local Similarity 82.4%; Pred. No. 5.6e-41;
 RESULT 902
 ID AAD62832 standard; DNA; 180216 BP.
 DE Human BAC #1 containing formin (Fmn)-2 genomic DNA.
 PN US2003170683-A1.
 PD 11-SEP-2003.
 PA (LEDE/) LEADER P.
 PA (LEAD/) LEADER B.
 Query Match 15.5%; Score 200.8; DB 10; Length 180216;
 Best Local Similarity 79.3%; Pred. No. 5.6e-41;
 RESULT 903
 ID ADX80726 standard; DNA; 213300 BP.
 DE Human RALBP1 associated Eps domain containing 2 (REPS2) genomic DNA.
 Query Match 15.5%; Score 200.8; DB 14; Length 213300;
 Best Local Similarity 83.0%; Pred. No. 6e-41;
 RESULT 904
 ID AEF51726 standard; DNA; 304486 BP.
 DE Human p21-activated kinase 5 (PAK5) encoding DNA.
 PN EP1619504-A1.
 PD 25-JAN-2006.
 PA (FRAU-) FRAUNHOFER INST TOXIKOLOGIE & EXPERIMENT.
 Query Match 15.5%; Score 200.8; DB 15; Length 304486;
 Best Local Similarity 82.6%; Pred. No. 7e-41;
 RESULT 905
 ID ABD32843 standard; DNA; 326002 BP.
 DE Human cancer-associated genomic DNA HD17-014.
 PN WO2004074320-A2.

PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.5%; Score 200.8; DB 13; Length 326002;
Best Local Similarity 83.3%; Pred. No. 7.3e-41;
RESULT 906
ID AAL35996 standard; DNA; 1655 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2361.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 1655;
Best Local Similarity 85.8%; Pred. No. 8.1e-42;
RESULT 907
ID ABX58984 standard; cDNA; 1655 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1328.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.5%; Score 200.6; DB 8; Length 1655;
Best Local Similarity 85.8%; Pred. No. 8.1e-42;
RESULT 908
ID ADJ29734 standard; DNA; 1655 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2361.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 12; Length 1655;
Best Local Similarity 85.8%; Pred. No. 8.1e-42;
RESULT 909
ID ADY18705 standard; DNA; 3233 BP.
DE DNA encoding a PRO polypeptide, SEQ ID NO 4511.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 15.5%; Score 200.6; DB 14; Length 3233;
Best Local Similarity 78.8%; Pred. No. 1.1e-41;
RESULT 910
ID ADR06648 standard; cDNA; 3920 BP.
DE Full length human cDNA useful for treating neurological disease Seq 154.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.5%; Score 200.6; DB 13; Length 3920;
Best Local Similarity 83.8%; Pred. No. 1.2e-41;
RESULT 911
ID AAL36019 standard; DNA; 5930 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2384.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 5930;
Best Local Similarity 83.3%; Pred. No. 1.4e-41;
RESULT 912
ID ABX59007 standard; cDNA; 5930 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1351.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.5%; Score 200.6; DB 8; Length 5930;
Best Local Similarity 83.3%; Pred. No. 1.4e-41;
RESULT 913
ID ADJ29757 standard; DNA; 5930 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2384.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 12; Length 5930;
Best Local Similarity 83.3%; Pred. No. 1.4e-41;
RESULT 914

ID AAL04059 standard; DNA; 10339 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6747.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 10339;
Best Local Similarity 82.1%; Pred. No. 1.8e-41;
RESULT 915
ID AAS40445 standard; DNA; 10339 BP.
DE DNA encoding human prostate cancer antigen, Seq ID No 597.
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 5; Length 10339;
Best Local Similarity 82.1%; Pred. No. 1.8e-41;
RESULT 916
ID ADJ09651 standard; DNA; 10339 BP.
DE Human prostate cancer associated gene-related DNA SeqID597.
PN US2003054373-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 11; Length 10339;
Best Local Similarity 82.1%; Pred. No. 1.8e-41;
RESULT 917
ID AAK65854 standard; DNA; 11475 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20666.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 11475;
Best Local Similarity 77.5%; Pred. No. 1.9e-41;
RESULT 918
ID ADZ59524 standard; DNA; 20001 BP.
DE Secondary hyperparathyroidism detection human polymorphic gene, SLC2 A3.
PN JP2005102601-A.
PD 21-APR-2005.
PA (HYUB-) HYUBITTO GENOMICS KK.
PA (JIKE-) UNIV JIKEI.
Query Match 15.5%; Score 200.6; DB 14; Length 20001;
Best Local Similarity 82.1%; Pred. No. 2.4e-41;
RESULT 919
ID AAK81676 standard; DNA; 21461 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36488.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 21461;
Best Local Similarity 77.5%; Pred. No. 2.5e-41;
RESULT 920
ID AAK65853 standard; DNA; 21461 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20665.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 21461;
Best Local Similarity 77.5%; Pred. No. 2.5e-41;
RESULT 921
ID AAK78454 standard; DNA; 21461 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33266.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 21461;
Best Local Similarity 77.5%; Pred. No. 2.5e-41;
RESULT 922
ID AEB32367 standard; DNA; 30146 BP.
DE Human genomic DNA #8.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 15.5%; Score 200.6; DB 14; Length 30146;
Best Local Similarity 78.0%; Pred. No. 2.9e-41;
RESULT 923

ID AEB32420 standard; DNA; 30146 BP.
DE Human genomic DNA #61.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 15.5%; Score 200.6; DB 14; Length 30146;
Best Local Similarity 78.0%; Pred. No. 2.9e-41;
RESULT 924
ID ACN44386 standard; DNA; 40136 BP.
DE Human genomic sequence hCG18551.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.6; DB 11; Length 40136;
Best Local Similarity 76.5%; Pred. No. 3.3e-41;
RESULT 925
ID AAK85974 standard; DNA; 44211 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40786.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 44211;
Best Local Similarity 83.4%; Pred. No. 3.4e-41;
RESULT 926
ID AAK86025 standard; DNA; 54863 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40837.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 54863;
Best Local Similarity 73.8%; Pred. No. 3.7e-41;
RESULT 927
ID AAK86026 standard; DNA; 54877 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40838.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 4; Length 54877;
Best Local Similarity 73.8%; Pred. No. 3.7e-41;
RESULT 928
ID ABZ74225 standard; DNA; 54877 BP.
DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1372.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 8; Length 54877;
Best Local Similarity 73.8%; Pred. No. 3.7e-41;
RESULT 929
ID ADA98754 standard; DNA; 54877 BP.
DE Human secreted protein-related DNA sequence #347.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 8; Length 54877;
Best Local Similarity 73.8%; Pred. No. 3.7e-41;
RESULT 930
ID ABZ67791 standard; DNA; 54877 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1314.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.6; DB 10; Length 54877;
Best Local Similarity 73.8%; Pred. No. 3.7e-41;
RESULT 931
ID ACN43886 standard; DNA; 61103 BP.
DE Human genomic sequence hCG1784975.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.6; DB 11; Length 61103;
Best Local Similarity 82.3%; Pred. No. 3.9e-41;
RESULT 932
ID ACF42745 standard; DNA; 354391 BP.

DE Human ALMS1 genomic DNA sequence.
PN WO2003034072-A2.
PD 24-APR-2003.
PA (UYSO-) UNIV SOUTHAMPTON.
Query Match 15.5%; Score 200.6; DB 10; Length 110000;
Best Local Similarity 82.3%; Pred. No. 5.1e-41;
RESULT 933
ID AED20699 standard; DNA; 354396 BP.
DE Human ALMS1 gene region, SEQ ID 1.
PN US2005214757-A1.
PD 29-SEP-2005.
PA (WILS/) WILSON D I.
PA (HEAR/) HEARN T.
PA (WALK/) WALKER M.
Query Match 15.5%; Score 200.6; DB 14; Length 110000;
Best Local Similarity 82.3%; Pred. No. 5.1e-41;
RESULT 934
ID AED89419 standard; DNA; 168656 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 59.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.5%; Score 200.6; DB 14; Length 168656;
Best Local Similarity 78.8%; Pred. No. 6.1e-41;
RESULT 935
ID AED89418 standard; DNA; 170285 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 58.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.5%; Score 200.6; DB 14; Length 170285;
Best Local Similarity 78.8%; Pred. No. 6.2e-41;
RESULT 936
ID ACN44626 standard; DNA; 175077 BP.
DE Human genomic sequence hCG19724.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.6; DB 11; Length 175077;
Best Local Similarity 85.8%; Pred. No. 6.2e-41;
RESULT 937
ID ADL13719 standard; DNA; 199878 BP.
DE Osteoarthritis-associated polymorphic nucleotide #251.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.5%; Score 200.6; DB 10; Length 199878;
Best Local Similarity 78.9%; Pred. No. 6.6e-41;
RESULT 938
ID ABA15301 standard; DNA; 2317 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7632.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 5; Length 2317;
Best Local Similarity 83.7%; Pred. No. 1.1e-41;
RESULT 939
ID ADR06510 standard; cDNA; 2723 BP.
DE Full length human cDNA useful for treating neurological disease Seq 16.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.5%; Score 200.4; DB 13; Length 2723;
Best Local Similarity 76.5%; Pred. No. 1.1e-41;
RESULT 940
ID AAF97860 standard; DNA; 9799 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:74.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREPECTURE.
Query Match 15.5%; Score 200.4; DB 5; Length 9799;
Best Local Similarity 83.7%; Pred. No. 2e-41;


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RESULT 941
ID AAK83820 standard; DNA; 11840 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38632.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 11840;
Best Local Similarity 77.4%; Pred. No. 2.2e-41;
RESULT 942
ID AAK72738 standard; DNA; 12774 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27550.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 12774;
Best Local Similarity 83.7%; Pred. No. 2.2e-41;
RESULT 943
ID ABA15302 standard; DNA; 12774 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7633.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 5; Length 12774;
Best Local Similarity 83.7%; Pred. No. 2.2e-41;
RESULT 944
ID AAL37485 standard; DNA; 17146 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3850.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 17146;
Best Local Similarity 85.3%; Pred. No. 2.5e-41;
RESULT 945
ID ABX60473 standard; cDNA; 17146 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2817.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.5%; Score 200.4; DB 8; Length 17146;
Best Local Similarity 85.3%; Pred. No. 2.5e-41;
RESULT 946
ID ADJ31223 standard; DNA; 17146 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3850.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 12; Length 17146;
Best Local Similarity 85.3%; Pred. No. 2.5e-41;
RESULT 947
ID AAL05706 standard; DNA; 19371 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8394.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 19371;
Best Local Similarity 77.3%; Pred. No. 2.7e-41;
RESULT 948
ID AAS26724 standard; DNA; 19472 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1698.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 19472;
Best Local Similarity 77.7%; Pred. No. 2.7e-41;
RESULT 949
ID ABX74073 standard; DNA; 19472 BP.
DE Human novel polynucleotide #901.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
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PA (BARA/) BARASH S C.
Query Match 15.5%; Score 200.4; DB 8; Length 19472;
Best Local Similarity 77.7%; Pred. No. 2.7e-41;
RESULT 950
ID AAK83177 standard; DNA; 21332 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37989.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 21332;
Best Local Similarity 76.2%; Pred. No. 2.8e-41;
RESULT 951
ID AAK74878 standard; DNA; 21332 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29690.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 21332;
Best Local Similarity 76.2%; Pred. No. 2.8e-41;
RESULT 952
ID ACN44250 standard; DNA; 23909 BP.
DE Human genomic sequence hCG25929.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.4; DB 11; Length 23909;
Best Local Similarity 83.6%; Pred. No. 2.9e-41;
RESULT 953
ID AAL05708 standard; DNA; 27154 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8396.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 27154;
Best Local Similarity 77.3%; Pred. No. 3.1e-41;
RESULT 954
ID AAL37486 standard; DNA; 30568 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3851.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 30568;
Best Local Similarity 85.3%; Pred. No. 3.3e-41;
RESULT 955
ID ABX60474 standard; cDNA; 30568 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2818.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.5%; Score 200.4; DB 8; Length 30568;
Best Local Similarity 85.3%; Pred. No. 3.3e-41;
RESULT 956
ID ADJ31224 standard; DNA; 30568 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3851.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 12; Length 30568;
Best Local Similarity 85.3%; Pred. No. 3.3e-41;
RESULT 957
ID AAK67282 standard; DNA; 33147 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 33147;
Best Local Similarity 80.6%; Pred. No. 3.4e-41;
RESULT 958
ID AAK78275 standard; DNA; 35959 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33087.
PN WO200157182-A2.
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PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.4; DB 4; Length 35959;
Best Local Similarity 78.2%; Pred. No. 3.5e-41;
RESULT 959
Query Match 15.5%; Score 200.4; DB 10; Length 54391;
Best Local Similarity 84.0%; Pred. No. 4.2e-41;
RESULT 960
Query Match 15.5%; Score 200.4; DB 14; Length 54396;
Best Local Similarity 84.0%; Pred. No. 4.2e-41;
RESULT 961
ID ABU61395 standard; DNA; 89328 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:332.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 15.5%; Score 200.4; DB 6; Length 89328;
Best Local Similarity 85.0%; Pred. No. 5.2e-41;
RESULT 962
ID AED55991 standard; DNA; 98100 BP.
DE Human BVES DNA.
Query Match 15.5%; Score 200.4; DB 14; Length 98100;
Best Local Similarity 77.1%; Pred. No. 5.5e-41;
RESULT 963
Query Match 15.5%; Score 200.4; DB 10; Length 110000;
Best Local Similarity 77.7%; Pred. No. 5.7e-41;
RESULT 964
Query Match 15.5%; Score 200.4; DB 10; Length 110000;
Best Local Similarity 77.7%; Pred. No. 5.7e-41;
RESULT 965
ID ACN45054 standard; DNA; 133632 BP.
DE Human genomic sequence hCG28560.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.4; DB 11; Length 133632;
Best Local Similarity 77.6%; Pred. No. 6.2e-41;
RESULT 966
ID AD213285 standard; DNA; 133642 BP.
DE Human cancer-associated genomic DNA #66.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.5%; Score 200.4; DB 14; Length 133642;
Best Local Similarity 77.6%; Pred. No. 6.2e-41;
RESULT 967
ID ADS36461 standard; DNA; 158417 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1675.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 15.5%; Score 200.4; DB 13; Length 158417;
Best Local Similarity 85.3%; Pred. No. 6.7e-41;
RESULT 968
ID ADL08127 standard; DNA; 166043 BP.
DE Human gene associated with low HDL-C PPARγ.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 15.5%; Score 200.4; DB 12; Length 166043;
Best Local Similarity 85.3%; Pred. No. 6.9e-41;
RESULT 969
ID ACN44598 standard; DNA; 212231 BP.
DE Human genomic sequence hCG401221.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.4; DB 11; Length 212231;
Best Local Similarity 82.4%; Pred. No. 7.6e-41;
RESULT 970
ID AD213715 standard; DNA; 234882 BP.
DE Human cancer-associated genomic DNA #106.
PN WO2005031001-A2.

PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.5%; Score 200.4; DB 14; Length 234882;
Best Local Similarity 81.6%; Pred. No. 8e-41;
RESULT 971
ID ABD33362 standard; DNA; 301477 BP.
DE Human cancer-associated (CA) gene HD07-066.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.5%; Score 200.4; DB 13; Length 301477;
Best Local Similarity 82.4%; Pred. No. 8.9e-41;
RESULT 972
ID ADP69744 standard; DNA; 312477 BP.
DE Human ROCK 1 DNA #2.
PN US2004115641-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.5%; Score 200.4; DB 12; Length 312477;
Best Local Similarity 77.6%; Pred. No. 9.1e-41;
RESULT 973
ID A8N94666 standard; DNA; 412 BP.
DE Gene #1164 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 15.5%; Score 200.2; DB 6; Length 412;
Best Local Similarity 78.1%; Pred. No. 5.6e-42;
RESULT 974
ID AAI86022 standard; cDNA; 2118 BP.
DE Human polynucleotide SEQ ID NO 6082.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.5%; Score 200.2; DB 4; Length 2118;
Best Local Similarity 78.3%; Pred. No. 1.1e-41;
RESULT 975
ID AAI58089 standard; cDNA; 5387 BP.
DE Human polynucleotide SEQ ID NO 292.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.5%; Score 200.2; DB 4; Length 5387;
Best Local Similarity 76.3%; Pred. No. 1.7e-41;
RESULT 976
ID AAI58088 standard; cDNA; 5414 BP.
DE Human polynucleotide SEQ ID NO 291.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.5%; Score 200.2; DB 4; Length 5414;
Best Local Similarity 76.3%; Pred. No. 1.7e-41;
RESULT 977
ID AAK82834 standard; DNA; 8789 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37646.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 8789;
Best Local Similarity 76.2%; Pred. No. 2.1e-41;
RESULT 978
ID AAK83152 standard; DNA; 15364 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37964.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 15364;
Best Local Similarity 76.5%; Pred. No. 2.7e-41;
RESULT 979
ID AAK90339 standard; DNA; 17431 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3915.
PN WO200155314-A2.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 17431;
Best Local Similarity 79.2%; Pred. No. 2.9e-41;
RESULT 980
ID AAI57710 standard; DNA; 17431 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 247.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 17431;
Best Local Similarity 79.2%; Pred. No. 2.9e-41;
RESULT 981
ID ABS99887 standard; DNA; 17431 BP.
DE Genomic DNA #91 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.5%; Score 200.2; DB 6; Length 17431;
Best Local Similarity 79.2%; Pred. No. 2.9e-41;
RESULT 982
ID ADB93040 standard; DNA; 17431 BP.
DE Human colorectal cancer related polypeptide DNA #91.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 10; Length 17431;
Best Local Similarity 79.2%; Pred. No. 2.9e-41;
RESULT 983
ID AAS42161 standard; DNA; 21387 BP.
DE Genomic sequence #477 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 21387;
Best Local Similarity 82.3%; Pred. No. 3.2e-41;
RESULT 984
ID ABA08132 standard; DNA; 32152 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 927.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 32152;
Best Local Similarity 78.1%; Pred. No. 3.8e-41;
RESULT 985
ID ABA13666 standard; DNA; 32207 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11997.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 5; Length 32207;
Best Local Similarity 74.1%; Pred. No. 3.8e-41;
RESULT 986
ID ACN44494 standard; DNA; 60381 BP.
DE Human genomic sequence hCG27935.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.2; DB 11; Length 60381;
Best Local Similarity 83.2%; Pred. No. 5e-41;
RESULT 987
ID ACN45002 standard; DNA; 60430 BP.
DE Human genomic sequence hCG33210.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.2; DB 11; Length 60430;
Best Local Similarity 85.8%; Pred. No. 5e-41;
RESULT 988
ID ADA03080 standard; DNA; 63720 BP.
DE Human PRDM11 carcinoma associated gene, SEQ ID NO:1598.
PN WO2003057146-A2.

PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.2; DB 9; Length 63720;
Best Local Similarity 79.9%; Pred. No. 5.1e-41;
RESULT 989
ID ADA66364 standard; DNA; 63720 BP.
DE Human PRDM11 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.2; DB 9; Length 63720;
Best Local Similarity 79.9%; Pred. No. 5.1e-41;
RESULT 990
ID ADB72818 standard; DNA; 63720 BP.
DE Human PRDM11 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.5%; Score 200.2; DB 10; Length 63720;
Best Local Similarity 79.9%; Pred. No. 5.1e-41;
RESULT 991
ID ADL27158 standard; DNA; 63908 BP.
DE Human genomic sequence for PRDM11.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 15.5%; Score 200.2; DB 11; Length 63908;
Best Local Similarity 79.9%; Pred. No. 5.1e-41;
RESULT 992
ID AAK96282 standard; DNA; 65854 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41094.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 65854;
Best Local Similarity 74.1%; Pred. No. 5.2e-41;
RESULT 993
ID AAK83212 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38024.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 68356;
Best Local Similarity 76.5%; Pred. No. 5.3e-41;
RESULT 994
ID AAK83212 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38024.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 68356;
Best Local Similarity 75.5%; Pred. No. 5.3e-41;
RESULT 995
ID AAK67283 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22095.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 68356;
Best Local Similarity 75.5%; Pred. No. 5.3e-41;
RESULT 996
ID AAK67283 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22095.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 4; Length 68356;
Best Local Similarity 76.5%; Pred. No. 5.3e-41;
RESULT 997
ID AAK67283 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22095.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.5%; Score 200.2; DB 12; Length 87411;
Best Local Similarity 79.4%; Pred. No. 5.8e-41;
RESULT 998
ID ADA03080 standard; DNA; 63720 BP.
DE Human PRDM11 carcinoma associated gene, SEQ ID NO:1598.
PN WO2003057146-A2.

ID ADX06943 standard; DNA; 103738 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1508.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 15.5%; Score 200.2; DB 14; Length 103738;
Best Local Similarity 83.5%; Pred. No. 6.3e-41;
RESULT 999
ID ADQ97138 standard; DNA; 440684 BP.
DE Human cancer associated sequence HD08-006, SEQ ID 114.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.5%; Score 200.2; DB 12; Length 110000;
Best Local Similarity 75.9%; Pred. No. 6.5e-41;
RESULT 1000
Query Match 15.5%; Score 200.2; DB 14; Length 110000;
Best Local Similarity 84.7%; Pred. No. 6.5e-41;
RESULT 1001
ID ADL13752 standard; DNA; 190000 BP.
DE Osteoarthritis-associated polymorphic nucleotide #284.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.5%; Score 200.2; DB 10; Length 190000;
Best Local Similarity 83.5%; Pred. No. 8.2e-41;
RESULT 1002
ID AED76155 standard; DNA; 261108 BP.
DE Human CA genomic DNA sequence-ID hd25-006.
PN WO2005104810-A2.
PD 10-NOV-2005.
PA (SAGR-) SAGRES DISCOVERY INC.
PA (LAIJA/) LAI A.
PA (FATY/) FATYAEY A.
Query Match 15.5%; Score 200.2; DB 14; Length 261108;
Best Local Similarity 81.2%; Pred. No. 9.5e-41;
RESULT 1003
ID ADP43517 standard; DNA; 347001 BP.
DE Human MADI-like 1 DNA #7.
PN US2004115650-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.5%; Score 200.2; DB 12; Length 347001;
Best Local Similarity 82.5%; Pred. No. 1.1e-40;
RESULT 1004
ID ASL84631 standard; CDNA; 417 BP.
DE Human ovarian cancer related CDNA clone SEQ ID NO:7609.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 15.4%; Score 200; DB 6; Length 417;
Best Local Similarity 85.5%; Pred. No. 6.3e-42;
RESULT 1005
ID AAL02649 standard; CDNA; 499 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 2650.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 200; DB 4; Length 499;
Best Local Similarity 79.7%; Pred. No. 6.8e-42;
RESULT 1006
ID ABA07691 standard; CDNA; 499 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 248.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 200; DB 4; Length 499;
Best Local Similarity 79.7%; Pred. No. 6.8e-42;
RESULT 1007
ID AAL05754 standard; DNA; 6647 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8442.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 200; DB 4; Length 6647;
Best Local Similarity 79.7%; Pred. No. 2.1e-41;
RESULT 1008
ID ABA20362 standard; DNA; 6647 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12693.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 200; DB 5; Length 6647;
Best Local Similarity 79.7%; Pred. No. 2.1e-41;
RESULT 1009
ID AAC66550 standard; CDNA; 10682 BP.
DE Human kinesin-like protein HKLP coding sequence SEQ ID NO: 3.
PN WO200063375-A1.
PD 26-OCT-2000.
PA (GEST-) GENSET.
Query Match 15.4%; Score 200; DB 3; Length 10682;
Best Local Similarity 82.7%; Pred. No. 2.6e-41;
RESULT 1010
ID AAL07146 standard; DNA; 14403 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9834.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 200; DB 4; Length 14403;
Best Local Similarity 84.2%; Pred. No. 3e-41;
RESULT 1011
ID AAL05755 standard; DNA; 16579 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8443.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 200; DB 4; Length 16579;
Best Local Similarity 79.7%; Pred. No. 3.2e-41;
RESULT 1012
ID ABA20363 standard; DNA; 16579 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12694.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 200; DB 5; Length 16579;
Best Local Similarity 79.7%; Pred. No. 3.2e-41;
RESULT 1013
ID ASK86595 standard; DNA; 24964 BP.
DE Human SA (rat hypertension-associated) homologue gene.
PN WO200244201-A2.
PD 06-JUN-2002.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 15.4%; Score 200; DB 6; Length 24964;
Best Local Similarity 82.8%; Pred. No. 3.8e-41;
RESULT 1014
ID AAD56159 standard; DNA; 38045 BP.
DE Human salvador genomic DNA.
PN WO2003035845-A2.
PD 01-MAY-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 15.4%; Score 200; DB 9; Length 38045;
Best Local Similarity 80.7%; Pred. No. 4.6e-41;
RESULT 1015
ID AAA27475 standard; DNA; 49136 BP.
DE NTDMM1 region including CAPN10 and GPR35 genes.
PN WO200023603-A2.
PD 27-APR-2000.
PA (ARCH-) ARCH DEV CORP.
PA (TEXA) UNIV OF TEXAS SYSTEM.
Query Match 15.4%; Score 200; DB 3; Length 49136;
Best Local Similarity 85.3%; Pred. No. 5.1e-41;
RESULT 1016
ID ADQ97215 standard; DNA; 56018 BP.
DE Human cancer associated sequence HD08-014, SEQ ID 191.
PN WO2004060304-A2.
PD 22-JUL-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 200; DB 12; Length 56018;
Best Local Similarity 84.0%; Pred. No. 5.4e-41;
RESULT 1017
ID ADO79402 standard; DNA; 76600 BP.
DE DIG1 region, SEQ ID 1.
PN WO2004047514-A2.
PD 10-JUN-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 15.4%; Score 200; DB 12; Length 76600;
Best Local Similarity 82.8%; Pred. No. 6.2e-41;
RESULT 1018
ID ADO97028 standard; DNA; 84476 BP.
DE Human cancer associated sequence HD10-002, SEQ ID 4.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 200; DB 12; Length 84476;
Best Local Similarity 83.8%; Pred. No. 6.5e-41;
RESULT 1019
ID ADH10008 standard; DNA; 85873 BP.
DE Human chromosome 3p25 DNA fragment.
PN WO2003093310-A1.
PD 13-NOV-2003.
PA (UYBR-) UNIV BREMEN.
Query Match 15.4%; Score 200; DB 10; Length 85873;
Best Local Similarity 84.2%; Pred. No. 6.5e-41;
RESULT 1020
Query Match 15.4%; Score 200; DB 12; Length 110000;
Best Local Similarity 77.6%; Pred. No. 7.3e-41;
RESULT 1021
ID AEO4781 standard; DNA; 112679 BP.
DE Cancer-associated gene SEQ ID NO:99.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.4%; Score 200; DB 14; Length 112679;
Best Local Similarity 84.2%; Pred. No. 7.4e-41;
RESULT 1022
ID AED89402 standard; DNA; 155515 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 42.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.4%; Score 200; DB 14; Length 155515;
Best Local Similarity 82.7%; Pred. No. 8.5e-41;
RESULT 1023
ID AED89403 standard; DNA; 159660 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 43.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.4%; Score 200; DB 14; Length 159660;
Best Local Similarity 82.7%; Pred. No. 8.6e-41;
RESULT 1024
ID AED89401 standard; DNA; 177623 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 41.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.4%; Score 200; DB 14; Length 177623;
Best Local Similarity 82.7%; Pred. No. 9e-41;
RESULT 1025
ID AED18631 standard; DNA; 213541 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 882.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 15.4%; Score 200; DB 14; Length 213541;
Best Local Similarity 82.8%; Pred. No. 9.8e-41;
RESULT 1026
ID ASF74635 standard; DNA; 213541 BP.
DE Human polynucleotide #149.

PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 15.4%; Score 200; DB 15; Length 213541;
Best Local Similarity 82.8%; Pred. No. 9.8e-41;
RESULT 1027
ID ABL68560 standard; DNA; 267156 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6897.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 15.4%; Score 200; DB 6; Length 267156;
Best Local Similarity 77.6%; Pred. No. 1.1e-40;
RESULT 1028
ID ACN44042 standard; DNA; 338702 BP.
DE Human genomic sequence hCG32359.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 200; DB 11; Length 338702;
Best Local Similarity 77.6%; Pred. No. 1.2e-40;
RESULT 1029
ID ADM03474 standard; cDNA; 1756 BP.
DE Human cDNA of the invention SEQ ID NO:2159.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.4%; Score 199.8; DB 11; Length 1756;
Best Local Similarity 84.6%; Pred. No. 1.3e-41;
RESULT 1030
ID AEC86404 standard; cDNA; 1756 BP.
DE Human cDNA clone TESTI20433130, SEQ ID 2159.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.4%; Score 199.8; DB 14; Length 1756;
Best Local Similarity 84.6%; Pred. No. 1.3e-41;
RESULT 1031
ID AAL04727 standard; DNA; 11360 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7415.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.8; DB 4; Length 11360;
Best Local Similarity 83.7%; Pred. No. 3e-41;
RESULT 1032
ID AAL03820 standard; DNA; 11360 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6508.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.8; DB 4; Length 11360;
Best Local Similarity 83.7%; Pred. No. 3e-41;
RESULT 1033
ID ADC87690 standard; DNA; 15118 BP.
DE Human mammalian target of rapamycin genomic fragment #35.
PN WO2003048360-A1.
PD 12-JUN-2003.
PA (NEWI-) NEW IND RES ORG.
Query Match 15.4%; Score 199.8; DB 10; Length 15118;
Best Local Similarity 83.7%; Pred. No. 3.4e-41;
RESULT 1034
ID AAK83220 standard; DNA; 15772 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38032.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.8; DB 4; Length 15772;
Best Local Similarity 81.6%; Pred. No. 3.5e-41;
RESULT 1035
ID AAL04782 standard; DNA; 22927 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7470.

PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.8; DB 4; Length 22927;
Best Local Similarity 82.5%; Pred. No. 4.1e-41;
RESULT 1036
ID ABL97677 standard; DNA; 22927 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2329.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.8; DB 4; Length 22927;
Best Local Similarity 82.5%; Pred. No. 4.1e-41;
RESULT 1037
ID ADP88153 standard; DNA; 29750 BP.
DE Human ASAP gene, SEQ ID 16.
PN FR2849039-A1.
PD 25-JUN-2004.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 15.4%; Score 199.8; DB 12; Length 29750;
Best Local Similarity 83.7%; Pred. No. 4.6e-41;
RESULT 1038
ID AAL04676 standard; DNA; 32249 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7364.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.8; DB 4; Length 32249;
Best Local Similarity 76.5%; Pred. No. 4.8e-41;
RESULT 1039
ID ABL97583 standard; DNA; 32249 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2235.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.8; DB 4; Length 32249;
Best Local Similarity 76.5%; Pred. No. 4.8e-41;
RESULT 1040
ID ADC86832 standard; DNA; 39729 BP.
DE Human GPCR gene SEQ ID NO:1285.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.4%; Score 199.8; DB 10; Length 39729;
Best Local Similarity 77.4%; Pred. No. 5.3e-41;
RESULT 1041
ID ABK22784 standard; cDNA; 57273 BP.
DE Human high bone mass (HBM) polynucleotide clone #7.
PN WO200192891-A2.
PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 15.4%; Score 199.8; DB 6; Length 57273;
Best Local Similarity 77.4%; Pred. No. 6.2e-41;
RESULT 1042
ID ABR82625 standard; DNA; 66933 BP.
DE Human HBM gene region b200e21-h_contig4.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.4%; Score 199.8; DB 5; Length 66933;
Best Local Similarity 77.4%; Pred. No. 6.6e-41;
RESULT 1043
ID ACC45366 standard; DNA; 66933 BP.
DE Human HBM gene fragment #7.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 15.4%; Score 199.8; DB 8; Length 66933;
Best Local Similarity 77.4%; Pred. No. 6.6e-41;
RESULT 1044

ID ADB98066 standard; DNA; 66933 BP.
DE HBM-related clone contig b200e21-h contig4.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 15.4%; Score 199.8; DB 10; Length 66933;
Best Local Similarity 77.4%; Pred. No. 6.6e-41;
RESULT 1045
ID ADE82435 standard; DNA; 66933 BP.
DE Human DNA sequence related to the invention #7.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 15.4%; Score 199.8; DB 10; Length 66933;
Best Local Similarity 77.4%; Pred. No. 6.6e-41;
RESULT 1046
ID ADR16929 standard; DNA; 66933 BP.
DE BAC clone containing segments of the human Zmax1 gene #7.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.4%; Score 199.8; DB 13; Length 66933;
Best Local Similarity 77.4%; Pred. No. 6.6e-41;
RESULT 1047
ID ADR47580 standard; DNA; 66933 BP.
DE BAC clone containing segments of the human Zmax1 gene #7.
PN US2004178582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 15.4%; Score 199.8; DB 13; Length 66933;
Best Local Similarity 77.4%; Pred. No. 6.6e-41;
RESULT 1048
ID AEB69309 standard; DNA; 66933 BP.
DE Human High Bone Mass gene related contig b200e21-h_contig4, SEQ ID 11.
PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 15.4%; Score 199.8; DB 14; Length 66933;
Best Local Similarity 77.4%; Pred. No. 6.6e-41;
RESULT 1049
ID ASA82623 standard; DNA; 72049 BP.
DE Human HBM gene region b527d12-h_contig309G.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.4%; Score 199.8; DB 5; Length 72049;
Best Local Similarity 77.4%; Pred. No. 6.8e-41;
RESULT 1050
ID ACC45364 standard; DNA; 72049 BP.
DE Human HBM gene fragment #5.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 15.4%; Score 199.8; DB 8; Length 72049;
Best Local Similarity 77.4%; Pred. No. 6.8e-41;
RESULT 1051
ID ADB98064 standard; DNA; 72049 BP.
DE HBM-related clone contig b527d12-h contig309G.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 15.4%; Score 199.8; DB 10; Length 72049;
Best Local Similarity 77.4%; Pred. No. 6.8e-41;
RESULT 1052
ID ADE82433 standard; DNA; 72049 BP.
DE Human DNA sequence related to the invention #5.
PN WO200292015-A2.


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PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP ) WYETH.
Query Match 15.4%; Score 199.8; DB 10; Length 72049;
Best Local Similarity 77.4%; Pred. No. 6.8e-41;
RESULT 1053
ID ADR16927 standard; DNA; 72049 BP.
DE BAC clone containing segments of the human Zmax1 gene #5.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.4%; Score 199.8; DB 13; Length 72049;
Best Local Similarity 77.4%; Pred. No. 6.8e-41;
RESULT 1054
ID ADR47578 standard; DNA; 72049 BP.
DE BAC clone containing segments of the human Zmax1 gene #5.
PN US20041176582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON.
Query Match 15.4%; Score 199.8; DB 13; Length 72049;
Best Local Similarity 77.4%; Pred. No. 6.8e-41;
RESULT 1055
ID A2B69307 standard; DNA; 72049 BP.
DE Human High Bone Mass gene related contig b527d12-h_contig309G, SEQ ID 9.
PN US2005142617-A1.
PD 30-JUN-2005.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 15.4%; Score 199.8; DB 14; Length 72049;
Best Local Similarity 77.4%; Pred. No. 6.8e-41;
RESULT 1056
ID AAL57571 standard; cDNA; 83120 BP.
DE Human CGI-51 protein cDNA.
PN WO2003059148-A2.
PD 24-JUL-2003.
PA (GENE-) GENE LOGIC INC.
PA (LGBI-) LG BIOMEDICAL INST.
Query Match 15.4%; Score 199.8; DB 9; Length 83120;
Best Local Similarity 86.3%; Pred. No. 7.3e-41;
RESULT 1057
ID ADP08387 standard; DNA; 94400 BP.
DE Human glycoprotein VI (platelet) (GP6;GP1V;GPVI) genomic DNA.
Query Match 15.4%; Score 199.8; DB 12; Length 94400;
Best Local Similarity 78.0%; Pred. No. 7.7e-41;
RESULT 1058
ID A8N96931 standard; DNA; 99014 BP.
DE Gene #3429 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 15.4%; Score 199.8; DB 6; Length 99014;
Best Local Similarity 85.0%; Pred. No. 7.9e-41;
RESULT 1059
ID AEF07226 standard; DNA; 100100 BP.
DE LOC115209 locus of the human genome.
Query Match 15.4%; Score 199.8; DB 15; Length 100100;
Best Local Similarity 78.1%; Pred. No. 7.9e-41;
RESULT 1060
ID AAD54480 standard; DNA; 117962 BP.
DE Human CIP DNA #1.
PN WO200299055-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 15.4%; Score 199.8; DB 8; Length 117962;
Best Local Similarity 83.7%; Pred. No. 8.5e-41;
RESULT 1061
ID ADX06911 standard; DNA; 131078 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1476.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 15.4%; Score 199.8; DB 14; Length 131078;
Best Local Similarity 82.3%; Pred. No. 8.9e-41;
RESULT 1062
ID ABD32936 standard; DNA; 137046 BP.
DE Human cancer-associated genomic DNA HD20-001.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 199.8; DB 13; Length 137046;
Best Local Similarity 77.4%; Pred. No. 9.1e-41;
RESULT 1063
ID ADQ17784 standard; DNA; 154394 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 601.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 15.4%; Score 199.8; DB 12; Length 154394;
Best Local Similarity 85.0%; Pred. No. 9.6e-41;
RESULT 1064
ID ADX06954 standard; DNA; 154394 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1519.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 15.4%; Score 199.8; DB 14; Length 154394;
Best Local Similarity 85.0%; Pred. No. 9.6e-41;
RESULT 1065
ID ADZ80338 standard; DNA; 154394 BP.
DE Human nuclear transcription factor Y alpha, gene.
PN WO2005039573-A2.
PD 06-MAY-2005.
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS PHARMA GMBH.
Query Match 15.4%; Score 199.8; DB 14; Length 154394;
Best Local Similarity 85.0%; Pred. No. 9.6e-41;
RESULT 1066
ID AEF74999 standard; DNA; 154394 BP.
DE Human polynucleotide #513.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 15.4%; Score 199.8; DB 15; Length 154394;
Best Local Similarity 85.0%; Pred. No. 9.6e-41;
RESULT 1067
ID ACN44786 standard; DNA; 156843 BP.
DE Human genomic sequence hCG27192.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.8; DB 11; Length 156843;
Best Local Similarity 77.4%; Pred. No. 9.6e-41;
RESULT 1068
ID ADL13501 standard; DNA; 167932 BP.
DE Osteoarthritis-associated polymorphic nucleotide #33.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.4%; Score 199.8; DB 10; Length 167932;
Best Local Similarity 83.5%; Pred. No. 9.9e-41;
RESULT 1069
ID ADL13501 standard; DNA; 167932 BP.
DE Osteoarthritis-associated polymorphic nucleotide #33.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.4%; Score 199.8; DB 10; Length 167932;
Best Local Similarity 83.3%; Pred. No. 9.9e-41;
RESULT 1070
ID AEF85801 standard; DNA; 207740 BP.
DE Human chromosome 20 partial genomic sequence SEQ ID NO:1.
PN JP2006042735-A.
PD 16-FEB-2006.
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
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PA (MABU/) MABUCHI A.
 Query Match 15.4%; Score 199.8; DB 15; Length 207740;
 Best Local Similarity 81.6%; Pred. No. 1.1e-40;
 RESULT 1071
 ID ABO80552 standard; DNA; 237961 BP.
 DE Human Canlon gene fragment #2.
 PN WO200246404-A2.
 PD 13-JUN-2002.
 PA (G8ST-) GENSET.
 Query Match 15.4%; Score 199.8; DB 6; Length 237961;
 Best Local Similarity 78.9%; Pred. No. 1.2e-40;
 RESULT 1072
 ID ABA07249 standard; DNA; 310 BP.
 DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 568.
 PN WO200155206-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 199.6; DB 4; Length 310;
 Best Local Similarity 84.5%; Pred. No. 7.1e-42;
 RESULT 1073
 ID AAK89890 standard; DNA; 310 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3466.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 199.6; DB 4; Length 310;
 Best Local Similarity 84.5%; Pred. No. 7.1e-42;
 RESULT 1074
 ID AAO4982 standard; cDNA; 899 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:1817.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 15.4%; Score 199.6; DB 4; Length 899;
 Best Local Similarity 77.7%; Pred. No. 1.1e-41;
 RESULT 1075
 ID AAI17563 standard; cDNA; 2053 BP.
 DE Human cDNA sequence SEQ ID NO:17047.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 15.4%; Score 199.6; DB 4; Length 2053;
 Best Local Similarity 77.7%; Pred. No. 1.6e-41;
 RESULT 1076
 ID ADM01579 standard; cDNA; 2501 BP.
 DE Human cDNA of the invention SEQ ID NO:264.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.4%; Score 199.6; DB 11; Length 2501;
 Best Local Similarity 84.5%; Pred. No. 1.8e-41;
 RESULT 1077
 ID ASC84509 standard; cDNA; 2501 BP.
 DE Human cDNA clone BRAMY20195090, SEQ ID 264.
 PN EP1580263-A1.
 PD 28-SEP-2005.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.4%; Score 199.6; DB 14; Length 2501;
 Best Local Similarity 84.5%; Pred. No. 1.8e-41;
 RESULT 1078
 ID AAH18467 standard; cDNA; 3417 BP.
 DE Human cDNA sequence SEQ ID NO:18570.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 15.4%; Score 199.6; DB 4; Length 3417;
 Best Local Similarity 83.3%; Pred. No. 2e-41;
 RESULT 1079
 ID AAS32785 standard; DNA; 11853 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID No 739.
 PN WO200155319-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 15.4%; Score 199.6; DB 4; Length 11853;
 Best Local Similarity 73.7%; Pred. No. 3.5e-41;
 RESULT 1080
 ID AAS12088 standard; DNA; 18636 BP.
 DE Human tumour necrosis factor receptor-like genomic polynucleotide #1.
 PN WO200155440-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 199.6; DB 5; Length 18636;
 Best Local Similarity 77.7%; Pred. No. 4.3e-41;
 RESULT 1081
 ID AAO79004 standard; DNA; 18636 BP.
 DE Human tumour necrosis factor gene from clone HEOQR40 #1.
 PN US2002086820-A1.
 PD 04-JUL-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 15.4%; Score 199.6; DB 6; Length 18636;
 Best Local Similarity 77.7%; Pred. No. 4.3e-41;
 RESULT 1082
 ID ADC35307 standard; DNA; 18636 BP.
 DE Human TNFR-like gene 2 genomic sequence #1.
 PN US2003077703-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 199.6; DB 10; Length 18636;
 Best Local Similarity 77.7%; Pred. No. 4.3e-41;
 RESULT 1083
 ID ADA41524 standard; DNA; 26166 BP.
 DE Human secreted protein related DNA.
 PN WO2002102993-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 199.6; DB 8; Length 26166;
 Best Local Similarity 77.9%; Pred. No. 4.9e-41;
 RESULT 1084
 ID AGC50869 standard; cDNA; 26166 BP.
 DE Human secreted protein BAC clone SEQ ID NO 1049.
 PN WO200295010-A2.
 PD 28-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 199.6; DB 8; Length 26166;
 Best Local Similarity 77.9%; Pred. No. 4.9e-41;
 RESULT 1085
 ID ASZ71491 standard; DNA; 26166 BP.
 DE Secreted protein gene 21 genomic fragment HCEPB80, SEQ ID NO:601.
 PN WO200276488-A1.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 199.6; DB 8; Length 26166;
 Best Local Similarity 77.9%; Pred. No. 4.9e-41;
 RESULT 1086
 ID ADB91847 standard; DNA; 26166 BP.
 DE Human secreted protein related DNA #SEQ ID 793.
 PN WO2003004622-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 199.6; DB 9; Length 26166;
 Best Local Similarity 77.9%; Pred. No. 4.9e-41;
 RESULT 1087
 ID ADC74629 standard; DNA; 26166 BP.
 DE Human secreted protein-related DNA - SEQ ID 1262.
 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 199.6; DB 10; Length 26166;
 Best Local Similarity 77.9%; Pred. No. 4.9e-41;
 RESULT 1088
 ID ADA57652 standard; DNA; 26166 BP.
 DE BAC fragment containing human secreted protein gene #80.
 PN WO2002102994-A2.
 PD 27-DEC-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.6; DB 10; Length 26166;
Best Local Similarity 77.9%; Pred. No. 4.9e-41;
RESULT 1089
ID AAK89986 standard; DNA; 32224 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3562.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.6; DB 4; Length 32224;
Best Local Similarity 83.0%; Pred. No. 5.4e-41;
RESULT 1090
ID ADQ07738 standard; DNA; 32460 BP.
DE Nucleotide sequence of human DC1-1 genomic DNA.
PN WO2004053138-A1.
PD 24-JUN-2004.
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
Query Match 15.4%; Score 199.6; DB 12; Length 32460;
Best Local Similarity 84.2%; Pred. No. 5.4e-41;
RESULT 1091
ID AAD31198 standard; DNA; 34634 BP.
DE Human WKL-1 genomic DNA.
PN EP1209229-A1.
PD 29-MAY-2002.
PA (LESC/) LESCH K.
PA (MEYE/) MEYER J.
Query Match 15.4%; Score 199.6; DB 6; Length 34634;
Best Local Similarity 77.9%; Pred. No. 5.6e-41;
RESULT 1092
ID AEA61175 standard; DNA; 53779 BP.
DE Human ENTPD5 gene genomic sequence SEQ ID NO:85.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 15.4%; Score 199.6; DB 14; Length 53779;
Best Local Similarity 81.8%; Pred. No. 6.8e-41;
RESULT 1093
ID ACN44410 standard; DNA; 91760 BP.
DE Human genomic sequence hCG41365.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.6; DB 11; Length 91760;
Best Local Similarity 81.8%; Pred. No. 8.6e-41;
RESULT 1094
ID ADC85367 standard; DNA; 96593 BP.
DE Mouse B1m coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.6; DB 10; Length 96593;
Best Local Similarity 78.2%; Pred. No. 8.8e-41;
RESULT 1095
ID ADA02888 standard; DNA; 96594 BP.
DE Human BLM carcinoma associated gene, SEQ ID NO:1406.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.6; DB 9; Length 96594;
Best Local Similarity 78.2%; Pred. No. 8.8e-41;
RESULT 1096
ID ADB7626 standard; DNA; 96594 BP.
DE Human BLM gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.6; DB 10; Length 96594;
Best Local Similarity 78.2%; Pred. No. 8.8e-41;
RESULT 1097
ID ADM74483 standard; DNA; 96594 BP.
DE Human carcinoma associated (CA) nucleic acid #76.
PN US2004072154-A1.
PD 15-APR-2004.

PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 15.4%; Score 199.6; DB 12; Length 96594;
Best Local Similarity 78.2%; Pred. No. 8.8e-41;
RESULT 1098
ID AAD41740 standard; DNA; 99500 BP.
DE Human RECQL2 DNA #1.
PN US6399378-B1.
PD 04-JUN-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.4%; Score 199.6; DB 6; Length 99500;
Best Local Similarity 78.2%; Pred. No. 8.9e-41;
RESULT 1099
ID ADQ17814 standard; DNA; 101270 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 631.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 15.4%; Score 199.6; DB 12; Length 101270;
Best Local Similarity 77.9%; Pred. No. 9e-41;
RESULT 1100
Query Match 15.4%; Score 199.6; DB 8; Length 110000;
Best Local Similarity 79.1%; Pred. No. 9.3e-41;
RESULT 1101
ID ABK49450 standard; DNA; 147309 BP.
DE Human transporter genomic DNA sequence.
Query Match 15.4%; Score 199.6; DB 6; Length 147309;
Best Local Similarity 75.0%; Pred. No. 1.1e-40;
RESULT 1102
ID ADL13962 standard; DNA; 160198 BP.
DE Osteoarthritis-associated polymorphic nucleotide #494.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.4%; Score 199.6; DB 10; Length 160198;
Best Local Similarity 84.5%; Pred. No. 1.1e-40;
RESULT 1103
ID ABD33366 standard; DNA; 243390 BP.
DE Human cancer-associated (CA) gene HD07-067.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 199.6; DB 13; Length 243390;
Best Local Similarity 81.8%; Pred. No. 1.3e-40;
RESULT 1104
ID ADZ13446 standard; DNA; 243934 BP.
DE Human cancer-associated genomic DNA #82.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.4%; Score 199.6; DB 14; Length 243934;
Best Local Similarity 81.8%; Pred. No. 1.3e-40;
RESULT 1105
ID AAL05226 standard; DNA; 334 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7914.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 334;
Best Local Similarity 80.3%; Pred. No. 8.2e-42;
RESULT 1106
ID ABL98109 standard; DNA; 334 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2761.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 334;
Best Local Similarity 80.3%; Pred. No. 8.2e-42;
RESULT 1107
ID AAK67291 standard; DNA; 681 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22103.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 681;
Best Local Similarity 82.7%; Pred. No. 1.1e-41;
RESULT 1108
ID AAK81392 standard; DNA; 773 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36204.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 773;
Best Local Similarity 83.9%; Pred. No. 1.2e-41;
RESULT 1109
ID AED73229 standard; cDNA; 1398 BP.
DE Human placental protein encoding cDNA SEQ ID NO:57.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 15.4%; Score 199.4; DB 14; Length 1398;
Best Local Similarity 83.9%; Pred. No. 1.5e-41;
RESULT 1110
ID ADB62146 standard; cDNA; 2091 BP.
DE Human cDNA encoding clone BRHIP20005060.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.4%; Score 199.4; DB 10; Length 2091;
Best Local Similarity 81.2%; Pred. No. 1.8e-41;
RESULT 1111
ID AAK84424 standard; DNA; 10311 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39236.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 10311;
Best Local Similarity 84.2%; Pred. No. 3.7e-41;
RESULT 1112
ID AAK84423 standard; DNA; 10312 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39235.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 10312;
Best Local Similarity 84.2%; Pred. No. 3.7e-41;
RESULT 1113
ID AAK80686 standard; DNA; 10483 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35498.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 10483;
Best Local Similarity 87.9%; Pred. No. 3.7e-41;
RESULT 1114
ID ADA02810 standard; DNA; 27827 BP.
DE Human Fish homologue carcinoma associated gene, SEQ ID NO:1328.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.4; DB 9; Length 27827;
Best Local Similarity 79.3%; Pred. No. 5.7e-41;
RESULT 1115
ID ADB72548 standard; DNA; 27827 BP.
DE Human CA gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.4; DB 10; Length 27827;
Best Local Similarity 79.3%; Pred. No. 5.7e-41;
RESULT 1116
ID ADM74405 standard; DNA; 27827 BP.
DE Human carcinoma associated (CA) nucleic acid #37.
PN US2004072154-A1.
PD 15-APR-2004.

PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 15.4%; Score 199.4; DB 12; Length 27827;
Best Local Similarity 79.3%; Pred. No. 5.7e-41;
RESULT 1117
ID ADC85290 standard; DNA; 27828 BP.
DE Human genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.4; DB 10; Length 27828;
Best Local Similarity 79.3%; Pred. No. 5.7e-41;
RESULT 1118
ID ADL82795 standard; DNA; 36534 BP.
DE Human semaphorin3B, SEMA3B, DNA.
PN US2003166557-A1.
PD 04-SEP-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 15.4%; Score 199.4; DB 11; Length 36534;
Best Local Similarity 80.7%; Pred. No. 6.5e-41;
RESULT 1119
ID ABD33466 standard; DNA; 42360 BP.
DE Human cancer-associated (CA) gene HD07-089.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 199.4; DB 13; Length 42360;
Best Local Similarity 80.5%; Pred. No. 6.9e-41;
RESULT 1120
ID AAK78813 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33625.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 51469;
Best Local Similarity 85.2%; Pred. No. 7.5e-41;
RESULT 1121
ID AAK70270 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25082.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 51469;
Best Local Similarity 85.2%; Pred. No. 7.5e-41;
RESULT 1122
ID AAK69322 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24134.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 51469;
Best Local Similarity 85.2%; Pred. No. 7.5e-41;
RESULT 1123
ID AAK67426 standard; DNA; 55235 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22238.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.4; DB 4; Length 55235;
Best Local Similarity 78.8%; Pred. No. 7.7e-41;
RESULT 1124
ID AEA61156 standard; DNA; 67883 BP.
DE Human ABCG2 gene genomic sequence SEQ ID NO:66.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 15.4%; Score 199.4; DB 14; Length 67883;
Best Local Similarity 78.3%; Pred. No. 8.5e-41;
RESULT 1125
ID ACA60905 standard; DNA; 82615 BP.
DE Human transporter protein gene.
PN US2003017545-A1.
PD 23-JAN-2003.

PA (APPL-) APPLERA CORP.
Query Match 15.4%; Score 199.4; DB 9; Length 82615;
Best Local Similarity 79.3%; Pred. No. 9.2e-41;
RESULT 1126
ID AEA04986 standard; DNA; 82615 BP.
DE Human transporter coding sequence, SEQ ID 3.
PN US2005123982-A1.
PD 09-JUN-2005.
PA (APPL-) APPLERA CORP.
Query Match 15.4%; Score 199.4; DB 14; Length 82615;
Best Local Similarity 79.3%; Pred. No. 9.2e-41;
RESULT 1127
ID ADQ19964 standard; DNA; 83709 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2784.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 15.4%; Score 199.4; DB 12; Length 83709;
Best Local Similarity 79.5%; Pred. No. 9.3e-41;
RESULT 1128
ID ABD32761 standard; DNA; 103375 BP.
DE Human cancer-associated genomic DNA HD16-030.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 199.4; DB 13; Length 103375;
Best Local Similarity 83.9%; Pred. No. 1e-40;
RESULT 1129
ID ACN44422 standard; DNA; 114931 BP.
DE Human genomic sequence hCG27894.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.4; DB 11; Length 114931;
Best Local Similarity 80.1%; Pred. No. 1.1e-40;
RESULT 1130
ID AAZ93815 standard; DNA; 144460 BP.
DE Olfactory receptor operon.
PN WO200021985-A2.
PD 20-APR-2000.
PA (GEST) GENSET.
Query Match 15.4%; Score 199.4; DB 3; Length 144460;
Best Local Similarity 81.6%; Pred. No. 1.2e-40;
RESULT 1131
ID ADS36467 standard; DNA; 154799 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1681.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 15.4%; Score 199.4; DB 13; Length 154799;
Best Local Similarity 86.0%; Pred. No. 1.2e-40;
RESULT 1132
ID AED18452 standard; DNA; 180283 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 703.
PN WO2005038041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 15.4%; Score 199.4; DB 14; Length 180283;
Best Local Similarity 81.6%; Pred. No. 1.3e-40;
RESULT 1133
ID AEF19127 standard; DNA; 188056 BP.
DE Human NIPBL genomic sequence.
PN US2006003354-A1.
PD 05-JAN-2006.
PA (KRAN/) KRANTZ I D.
PA (JACK/) JACKSON L G.
Query Match 15.4%; Score 199.4; DB 15; Length 188056;
Best Local Similarity 79.5%; Pred. No. 1.3e-40;
RESULT 1134
ID AaK84798 standard; cDNA; 220895 BP.
DE Human cDNA differentially expressed in granulocytic cells #1369.
PN WO200228999-A2.
PD 11-APR-2002.

PA (GENE-) GENE LOGIC INC.
Query Match 15.4%; Score 199.4; DB 6; Length 220895;
Best Local Similarity 80.9%; Pred. No. 1.4e-40;
RESULT 1135
ID ADR52737 standard; DNA; 220895 BP.
DE Drug therapy altered expressed gene #88.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TRSP/) TREPICCHIO W L.
Query Match 15.4%; Score 199.4; DB 13; Length 220895;
Best Local Similarity 80.9%; Pred. No. 1.4e-40;
RESULT 1136
ID ACN45190 standard; DNA; 248436 BP.
DE Human genomic sequence hCG16330.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199.4; DB 11; Length 248436;
Best Local Similarity 84.2%; Pred. No. 1.5e-40;
RESULT 1137
ID AEE06394 standard; DNA; 267966 BP.
DE Glycogen synthase kinase-3beta (GSK-3beta) gene.
PN WO2005108582-A1.
PD 17-NOV-2005.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 15.4%; Score 199.4; DB 14; Length 267966;
Best Local Similarity 81.6%; Pred. No. 1.5e-40;
RESULT 1138
ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 15.4%; Score 199.4; DB 11; Length 304905;
Best Local Similarity 81.6%; Pred. No. 1.6e-40;
RESULT 1139
ID AAL03704 standard; DNA; 345 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6392.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 345;
Best Local Similarity 81.8%; Pred. No. 9.4e-42;
RESULT 1140
ID ABA07887 standard; DNA; 345 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 682.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 345;
Best Local Similarity 81.8%; Pred. No. 9.4e-42;
RESULT 1141
ID ABV25008 standard; cDNA; 1286 BP.
DE Human prostate expression marker cDNA 24999.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.4%; Score 199.2; DB 5; Length 1286;
Best Local Similarity 83.4%; Pred. No. 1.7e-41;
RESULT 1142
ID ADH70101 standard; DNA; 1400 BP.
DE Human Vbeta gene family genomic sequence #63.
PN US2002150891-A1.
PD 17-OCT-2002.
PA (HOOD/) HOOD L E.
PA (ROWE/) ROWEN L.
Query Match 15.4%; Score 199.2; DB 12; Length 1400;
Best Local Similarity 83.2%; Pred. No. 1.7e-41;
RESULT 1143

ID ADR07022 standard; cDNA; 1924 BP.
DE Full length human cDNA useful for treating neurological disease Seq 528.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.4%; Score 199.2; DB 13; Length 1924;
Best Local Similarity 78.1%; Pred. No. 2e-41;
RESULT 1144
ID AAK70074 standard; DNA; 3454 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24886.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 3454;
Best Local Similarity 78.9%; Pred. No. 2.6e-41;
RESULT 1145
ID AAK76608 standard; DNA; 5632 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31420.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 5632;
Best Local Similarity 79.9%; Pred. No. 3.2e-41;
RESULT 1146
ID AAK90086 standard; DNA; 16892 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3662.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 16892;
Best Local Similarity 79.0%; Pred. No. 5.2e-41;
RESULT 1147
ID AAK89201 standard; DNA; 16892 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2777.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 16892;
Best Local Similarity 79.0%; Pred. No. 5.2e-41;
RESULT 1148
ID AAK80873 standard; DNA; 16892 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35685.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 16892;
Best Local Similarity 79.0%; Pred. No. 5.2e-41;
RESULT 1149
ID AAS39745 standard; DNA; 16892 BP.
DE Genomic sequence #164 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 5; Length 16892;
Best Local Similarity 79.0%; Pred. No. 5.2e-41;
RESULT 1150
ID ADB32705 standard; DNA; 16892 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 642.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.4%; Score 199.2; DB 9; Length 16892;
Best Local Similarity 79.0%; Pred. No. 5.2e-41;
RESULT 1151
ID AAK83177 standard; DNA; 21332 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37989.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 21332;
Best Local Similarity 78.2%; Pred. No. 5.8e-41;

RESULT 1152
ID AAK74878 standard; DNA; 21332 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29690.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 21332;
Best Local Similarity 78.2%; Pred. No. 5.8e-41;
RESULT 1153
ID AAL07542 standard; DNA; 27118 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 10230.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 27118;
Best Local Similarity 75.4%; Pred. No. 6.4e-41;
RESULT 1154
ID ABA08223 standard; DNA; 27118 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1018.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 27118;
Best Local Similarity 75.4%; Pred. No. 6.4e-41;
RESULT 1155
ID ADS36464 standard; DNA; 27509 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1678.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 15.4%; Score 199.2; DB 13; Length 27509;
Best Local Similarity 79.9%; Pred. No. 6.4e-41;
RESULT 1156
ID AAK83970 standard; DNA; 31952 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2946.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 31952;
Best Local Similarity 79.9%; Pred. No. 6.9e-41;
RESULT 1157
ID AAF54723 standard; DNA; 35465 BP.
DE Nucleotide sequence of a human polynucleotide sequence.
PN WO200105422-A2.
PD 25-JAN-2001.
PA (INMR) BIOMERIEUX STELHYS.
Query Match 15.4%; Score 199.2; DB 4; Length 35465;
Best Local Similarity 78.1%; Pred. No. 7.2e-41;
RESULT 1158
ID ABT17380 standard; DNA; 35465 BP.
DE Human IG gene related nucleic acid SEQ ID No 6.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 15.4%; Score 199.2; DB 8; Length 35465;
Best Local Similarity 78.1%; Pred. No. 7.2e-41;
RESULT 1159
ID ABT17382 standard; DNA; 36991 BP.
DE Human IG gene related nucleic acid SEQ ID No 8.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 15.4%; Score 199.2; DB 8; Length 36991;
Best Local Similarity 78.1%; Pred. No. 7.3e-41;
RESULT 1160
ID AED18110 standard; DNA; 36991 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 361.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 15.4%; Score 199.2; DB 14; Length 36991;
Best Local Similarity 78.1%; Pred. No. 7.3e-41;
RESULT 1161

ID AEF75130 standard; DNA; 36991 BP.
DE Human polynucleotide #644.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (VISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 15.4%; Score 199.2; DB 15; Length 36991;
Best Local Similarity 78.1%; Pred. No. 7.3e-41;
RESULT 1162
ID AAK75029 standard; DNA; 49777 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29841.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 49777;
Best Local Similarity 82.1%; Pred. No. 8.3e-41;
RESULT 1163
ID AAK76214 standard; DNA; 49777 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31026.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 49777;
Best Local Similarity 82.1%; Pred. No. 8.3e-41;
RESULT 1164
ID AAK80495 standard; DNA; 55008 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35307.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199.2; DB 4; Length 55008;
Best Local Similarity 81.1%; Pred. No. 8.7e-41;
RESULT 1165
ID ADP45591 standard; DNA; 92500 BP.
DE Human intercellular adhesion molecule ICAM-1/ICAM-4/ICAM-5 gDNA.
Query Match 15.4%; Score 199.2; DB 12; Length 92500;
Best Local Similarity 79.9%; Pred. No. 1.1e-40;
RESULT 1166
Query Match 15.4%; Score 199.2; DB 6; Length 106286;
Best Local Similarity 83.4%; Pred. No. 1.2e-40;
RESULT 1167
Query Match 15.4%; Score 199.2; DB 6; Length 110000;
Best Local Similarity 83.4%; Pred. No. 1.2e-40;
RESULT 1168
Query Match 15.4%; Score 199.2; DB 12; Length 110000;
Best Local Similarity 83.2%; Pred. No. 1.2e-40;
RESULT 1169
Query Match 15.4%; Score 199.2; DB 12; Length 110000;
Best Local Similarity 83.2%; Pred. No. 1.2e-40;
RESULT 1170
Query Match 15.4%; Score 199.2; DB 14; Length 110000;
Best Local Similarity 83.4%; Pred. No. 1.2e-40;
RESULT 1171
Query Match 15.4%; Score 199.2; DB 8; Length 164702;
Best Local Similarity 81.1%; Pred. No. 1.4e-40;
RESULT 1172
ID ACF62730 standard; DNA; 164702 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:658.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 15.4%; Score 199.2; DB 8; Length 164702;
Best Local Similarity 81.1%; Pred. No. 1.4e-40;
RESULT 1173
ID ADB20845 standard; DNA; 164702 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:658.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 15.4%; Score 199.2; DB 8; Length 164702;
Best Local Similarity 81.1%; Pred. No. 1.4e-40;
RESULT 1174
ID ADB87934 standard; DNA; 164702 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28934.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

DE Human UGT1A1 gene sequence SEQ ID NO:658.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 15.4%; Score 199.2; DB 10; Length 164702;
Best Local Similarity 81.1%; Pred. No. 1.4e-40;
RESULT 1175
ID ADB96917 standard; DNA; 164702 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:658.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 15.4%; Score 199.2; DB 10; Length 164702;
Best Local Similarity 81.1%; Pred. No. 1.4e-40;
RESULT 1176
ID ADB92108 standard; DNA; 164702 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:658.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 15.4%; Score 199.2; DB 10; Length 164702;
Best Local Similarity 81.1%; Pred. No. 1.4e-40;
RESULT 1177
ID AEA61167 standard; DNA; 165097 BP.
DE Human FLJ10718 gene genomic sequence SEQ ID NO:77.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 15.4%; Score 199.2; DB 14; Length 165097;
Best Local Similarity 83.4%; Pred. No. 1.4e-40;
RESULT 1178
ID ABT11173 standard; DNA; 168174 BP.
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 15.4%; Score 199.2; DB 6; Length 168174;
Best Local Similarity 83.2%; Pred. No. 1.4e-40;
RESULT 1179
ID ABT11114 standard; DNA; 168273 BP.
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 15.4%; Score 199.2; DB 6; Length 168273;
Best Local Similarity 83.2%; Pred. No. 1.4e-40;
RESULT 1180
ID AEE05008 standard; DNA; 246386 BP.
DE Cancer-associated gene SEQ ID NO:326.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.4%; Score 199.2; DB 14; Length 246386;
Best Local Similarity 81.5%; Pred. No. 1.7e-40;
RESULT 1181
ID ADL08109 standard; DNA; 247682 BP.
DE Human gene associated with low HDL-C AT3.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 15.4%; Score 199.2; DB 12; Length 247682;
Best Local Similarity 83.2%; Pred. No. 1.7e-40;
RESULT 1182
ID ABS55200 standard; DNA; 341511 BP.
DE Genomic DNA encoding human transporter protein.
Query Match 15.4%; Score 199.2; DB 6; Length 341511;
Best Local Similarity 83.4%; Pred. No. 1.9e-40;
RESULT 1183
ID AAK74122 standard; DNA; 327 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28934.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 15.4%; Score 199; DB 4; Length 327;
Best Local Similarity 81.8%; Pred. No. 1e-41;
RESULT 1184
ID AAK83997 standard; DNA; 603 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38809.
PN W0200157182-A2.
PD .09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199; DB 4; Length 603;
Best Local Similarity 83.0%; Pred. No. 1.4e-41;
RESULT 1185
ID AAI96506 standard; cDNA; 793 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2581.
PN W0200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 15.4%; Score 199; DB 4; Length 793;
Best Local Similarity 63.1%; Pred. No. 1.5e-41;
RESULT 1186
ID ADF81627 standard; DNA; 6657 BP.
DE Leukaemia-related DNA sequence #2183.
PN W02003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFF-) HAERLACH T.
PA (SCHO-) SCHOCH C.
PA (KERN-) KERN W.
Query Match 15.4%; Score 199; DB 10; Length 6657;
Best Local Similarity 78.9%; Pred. No. 3.9e-41;
RESULT 1187
ID ADX05831 standard; DNA; 6657 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 396.
PN W02005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 15.4%; Score 199; DB 14; Length 6657;
Best Local Similarity 78.9%; Pred. No. 3.9e-41;
RESULT 1188
ID ABA20383 standard; DNA; 7074 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12714.
PN W0200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199; DB 5; Length 7074;
Best Local Similarity 84.2%; Pred. No. 4e-41;
RESULT 1189
ID AAI62714 standard; DNA; 7588 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 364.
PN W0200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199; DB 4; Length 7588;
Best Local Similarity 81.6%; Pred. No. 4.1e-41;
RESULT 1190
ID AAL07036 standard; DNA; 7588 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9724.
PN W0200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199; DB 4; Length 7588;
Best Local Similarity 81.6%; Pred. No. 4.1e-41;
RESULT 1191
ID ADH10009 standard; DNA; 8949 BP.
DE Human FUS II exon A and A1 DNA.
PN W02003093310-A1.
PD 13-NOV-2003.
PA (UYBR-) UNIV BREMEN.
Query Match 15.4%; Score 199; DB 10; Length 8949;
Best Local Similarity 84.2%; Pred. No. 4.4e-41;
RESULT 1192
ID ABA20382 standard; DNA; 10642 BP.

DE Human nervous system related polynucleotide SEQ ID NO 12713.
PN W0200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 199; DB 5; Length 10642;
Best Local Similarity 84.2%; Pred. No. 4.8e-41;
RESULT 1193
ID AEB32383 standard; DNA; 21043 BP.
DE Human genomic DNA #24.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 15.4%; Score 199; DB 14; Length 21043;
Best Local Similarity 80.7%; Pred. No. 6.5e-41;
RESULT 1194
ID AEB32390 standard; DNA; 21044 BP.
DE Human genomic DNA #31.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 15.4%; Score 199; DB 11; Length 26318;
Best Local Similarity 81.8%; Pred. No. 7.1e-41;
RESULT 1195
ID ACN44242 standard; DNA; 26318 BP.
DE Human genomic sequence hCG20537.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199; DB 11; Length 26318;
Best Local Similarity 81.8%; Pred. No. 7.1e-41;
RESULT 1196
ID ACN44866 standard; DNA; 27204 BP.
DE Human genomic sequence hCG23376.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 199; DB 11; Length 27204;
Best Local Similarity 81.8%; Pred. No. 7.2e-41;
RESULT 1197
ID ADZ12935 standard; DNA; 28320 BP.
DE Human cancer-associated genomic DNA #39.
PN W02005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.4%; Score 199; DB 14; Length 28320;
Best Local Similarity 81.8%; Pred. No. 7.4e-41;
RESULT 1198
ID ADJ12490 standard; DNA; 45698 BP.
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq344.
PN US2004010132-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (DUAN/) DUAN R D.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (GREE/) GREENE J M.
PA (YOUN/) YOUNG P E.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (FLOR/) FLORENCE C.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H.
Query Match 15.4%; Score 199; DB 12; Length 45698;
Best Local Similarity 83.0%; Pred. No. 9.1e-41;
RESULT 1199
ID ADR16283 standard; DNA; 47219 BP.
DE Human Cayman ataxia splice site mutant DNA.
PN US2004146900-A1.
PD 23-JUL-2004.
PA (UNMI) UNIV MICHIGAN.
Query Match 15.4%; Score 199; DB 13; Length 47219;
Best Local Similarity 77.4%; Pred. No. 9.2e-41;

RESULT 1200
ID ADJ10262 standard; DNA; 51001 BP.
DE Human geranylgeranyl diphosphate synthase 1 genomic DNA SeqID 11.
PN US2004005570-A1.
PD 08-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.4%; Score 199; DB 12; Length 51001;
Best Local Similarity 84.4%; Pred. No. 9.5e-41;
RESULT 1201
ID ADB85543 standard; DNA; 51256 BP.
DE Human sentrin-specific family-related protease genomic DNA sequence.
Query Match 15.4%; Score 199; DB 10; Length 51256;
Best Local Similarity 77.7%; Pred. No. 9.5e-41;
RESULT 1202
ID ADK66161 standard; DNA; 51256 BP.
DE Human protease gene.
Query Match 15.4%; Score 199; DB 10; Length 51256;
Best Local Similarity 77.7%; Pred. No. 9.5e-41;
RESULT 1203
ID ADR16284 standard; DNA; 59884 BP.
DE Human Cayman ataxia genomic DNA.
PN US2004146900-A1.
PD 29-JUL-2004.
PA (UNMI) UNIV MICHIGAN.
Query Match 15.4%; Score 199; DB 13; Length 59884;
Best Local Similarity 77.4%; Pred. No. 1e-40;
RESULT 1204
ID ADZ10962 standard; DNA; 74424 BP.
DE Human STAT3 DNA sequence - SEQ ID 153.
PN US2005074879-A1.
PD 07-APR-2005.
PA (KARR/) KARRAS J G.
Query Match 15.4%; Score 199; DB 14; Length 74424;
Best Local Similarity 84.2%; Pred. No. 1.1e-40;
RESULT 1205
ID ADM97422 standard; DNA; 76341 BP.
DE Prostate and breast cancer associated human gene SRD5A2.
PN WO2004028346-A2.
PD 08-APR-2004.
PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
Query Match 15.4%; Score 199; DB 12; Length 76341;
Best Local Similarity 85.5%; Pred. No. 1.1e-40;
RESULT 1206
ID ADZ13418 standard; DNA; 85920 BP.
DE Human cancer-associated genomic DNA #80.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.4%; Score 199; DB 14; Length 85920;
Best Local Similarity 83.0%; Pred. No. 1.2e-40;
RESULT 1207
ID ABD33291 standard; DNA; 99046 BP.
DE Human cancer-associated (CA) gene HD07-051.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 199; DB 13; Length 99046;
Best Local Similarity 83.0%; Pred. No. 1.3e-40;
RESULT 1208
ID ADZ13341 standard; DNA; 101513 BP.
DE Human cancer-associated genomic DNA #73.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.4%; Score 199; DB 14; Length 101513;
Best Local Similarity 83.0%; Pred. No. 1.3e-40;
RESULT 1209
Query Match 15.4%; Score 199; DB 11; Length 110000;
Best Local Similarity 78.6%; Pred. No. 1.3e-40;
RESULT 1210
ID AED34666 standard; DNA; 458207 BP.
DE ABL1 genomic DNA SEQ ID NO 2.
PN WO2005094291-A2.

PD 13-OCT-2005.
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
Query Match 15.4%; Score 199; DB 14; Length 110000;
Best Local Similarity 83.0%; Pred. No. 1.3e-40;
RESULT 1211
ID ADL13941 standard; DNA; 125515 BP.
DE Osteoarthritis-associated polymorphic nucleotide #473.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.4%; Score 199; DB 10; Length 125515;
Best Local Similarity 81.6%; Pred. No. 1.4e-40;
RESULT 1212
ID ABD33171 standard; DNA; 127508 BP.
DE Human cancer-associated (CA) gene HD07-024.
PN WO2004038146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 199; DB 13; Length 127508;
Best Local Similarity 84.2%; Pred. No. 1.4e-40;
RESULT 1213
ID AAD54634 standard; DNA; 142519 BP.
DE Human chromodomain helicase DNA binding protein (CHD) encoding DNA #9.
PN WO200298899-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 15.4%; Score 199; DB 10; Length 142519;
Best Local Similarity 80.3%; Pred. No. 1.5e-40;
RESULT 1214
ID ADQ97721 standard; DNA; 178024 BP.
DE Human cancer associated sequence HD10-033, SEQ ID 698.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 199; DB 12; Length 178024;
Best Local Similarity 81.8%; Pred. No. 1.6e-40;
RESULT 1215
ID AAK91003 standard; DNA; 310 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4579.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 310;
Best Local Similarity 83.4%; Pred. No. 1.1e-41;
RESULT 1216
ID AAK93270 standard; DNA; 310 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38082.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 310;
Best Local Similarity 83.4%; Pred. No. 1.1e-41;
RESULT 1217
ID AAI99645 standard; DNA; 310 BP.
DE Human expressed polynucleotide SEQ ID NO 66.
PN WO200155167-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 310;
Best Local Similarity 83.4%; Pred. No. 1.1e-41;
RESULT 1218
ID AAS32654 standard; DNA; 310 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 608.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 310;
Best Local Similarity 83.4%; Pred. No. 1.1e-41;
RESULT 1219
ID AAS32038 standard; DNA; 310 BP.
DE Human liver associated genomic DNA #212.
PN WO200155355-A1.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 198.8; DB 5; Length 310;
 Best Local Similarity 83.4%; Pred. No. 1.1e-41;
 RESULT 1220
 ID ABN90393 standard; DNA; 310 BP.
 DE Human liver antigen HLBDE09 genomic sequence, SEQ ID NO:514.
 PN US2002042096-A1.
 PD 11-APR-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 15.4%; Score 198.8; DB 6; Length 310;
 Best Local Similarity 83.4%; Pred. No. 1.1e-41;
 RESULT 1221
 ID ADJ15306 standard; DNA; 310 BP.
 DE Human liver-related genomic DNA - SEQ ID 514.
 PN US2003077602-A1.
 PD 24-APR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 198.8; DB 11; Length 310;
 Best Local Similarity 83.4%; Pred. No. 1.1e-41;
 RESULT 1222
 ID ADJ12817 standard; DNA; 310 BP.
 DE DNA fragment of a BAC clone that encodes a human secreted protein Seq671.
 PN US2004010132-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (BREW/) BREWER L A.
 PA (DUAN/) DUAN R D.
 PA (RUBE/) RUBEN S M.
 PA (FLOR/) FLORENCE K A.
 PA (GREE/) GREENE J M.
 PA (YOUN/) YOUNG P E.
 PA (FERR/) FERRIE A M.
 PA (YUGG/) YU G.
 PA (FLOR/) FLORENCE C.
 PA (EBNE/) EBNER R.
 PA (OLSE/) OLSEN H.
 Query Match 15.4%; Score 198.8; DB 12; Length 310;
 Best Local Similarity 83.4%; Pred. No. 1.1e-41;
 RESULT 1223
 ID ADM03523 standard; cDNA; 1935 BP.
 DE Human cDNA of the invention SEQ ID NO:2208.
 PN EPI347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.4%; Score 198.8; DB 11; Length 1935;
 Best Local Similarity 80.2%; Pred. No. 2.6e-41;
 RESULT 1224
 ID AEC86453 standard; cDNA; 1935 BP.
 DE Human cDNA clone THYMU20058070, SEQ ID 2208.
 PN EPI580263-A1.
 PD 28-SEP-2005.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.4%; Score 198.8; DB 14; Length 1935;
 Best Local Similarity 80.2%; Pred. No. 2.6e-41;
 RESULT 1225
 ID ADM03115 standard; cDNA; 2147 BP.
 DE Human cDNA of the invention SEQ ID NO:1800.
 PN EPI347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.4%; Score 198.8; DB 11; Length 2147;
 Best Local Similarity 83.7%; Pred. No. 2.7e-41;
 RESULT 1226
 ID AEC86045 standard; cDNA; 2147 BP.
 DE Human cDNA clone SPLEN20329240, SEQ ID 1800.
 PN EPI580263-A1.
 PD 28-SEP-2005.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.4%; Score 198.8; DB 14; Length 2147;
 Best Local Similarity 83.7%; Pred. No. 2.7e-41;
 RESULT 1227

ID ADB62815 standard; cDNA; 2477 BP.
 DE Human cDNA encoding clone NTONG20005310.
 PN EPI308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.4%; Score 198.8; DB 10; Length 2477;
 Best Local Similarity 83.7%; Pred. No. 2.9e-41;
 RESULT 1228
 ID AAK90223 standard; DNA; 3407 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3799.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 198.8; DB 4; Length 3407;
 Best Local Similarity 83.4%; Pred. No. 3.3e-41;
 RESULT 1229
 ID AAS39852 standard; DNA; 3407 BP.
 DE Genomic sequence #271 encoding human colon associated polypeptide.
 PN WO200155302-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 198.8; DB 5; Length 3407;
 Best Local Similarity 83.4%; Pred. No. 3.3e-41;
 RESULT 1230
 ID ADB32812 standard; DNA; 3407 BP.
 DE Human novel colon related polypeptide DNA SEQ ID NO 749.
 PN US2003050231-A1.
 PD 13-MAR-2003.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 15.4%; Score 198.8; DB 9; Length 3407;
 Best Local Similarity 83.4%; Pred. No. 3.3e-41;
 RESULT 1231
 ID ADQ63021 standard; cDNA; 4442 BP.
 DE Novel human cDNA sequence #182.
 PN EPI440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.4%; Score 198.8; DB 12; Length 4442;
 Best Local Similarity 80.9%; Pred. No. 3.7e-41;
 RESULT 1232
 ID AAK85164 standard; DNA; 5638 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39976.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 198.8; DB 4; Length 5638;
 Best Local Similarity 80.1%; Pred. No. 4.1e-41;
 RESULT 1233
 ID ABX63291 standard; cDNA; 5981 BP.
 DE Human cDNA #291 differentially expressed in activated vascular tissue.
 PN US2002137081-A1.
 PD 26-SEP-2002.
 PA (BAND/) BANDMAN O.
 Query Match 15.4%; Score 198.8; DB 8; Length 5981;
 Best Local Similarity 79.5%; Pred. No. 4.2e-41;
 RESULT 1234
 ID AAL07322 standard; DNA; 7566 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 10010.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.4%; Score 198.8; DB 4; Length 7566;
 Best Local Similarity 82.5%; Pred. No. 4.7e-41;
 RESULT 1235
 ID AAC66549 standard; DNA; 10884 BP.
 DE Human kinesin-like protein HKLP coding sequence contig SEQ ID NO: 2.
 PN WO200063375-A1.
 PD 26-OCT-2000.
 PA (GEST) GENSET.
 Query Match 15.4%; Score 198.8; DB 3; Length 10884;

Best Local Similarity 83.3%; Pred. No. 5.5e-41;
RESULT 1236
ID AAF97861 standard; DNA; 13864 BP.
DE Human neuroblastoma cell line NB-1 lp36 nucleotide sequence SEQ ID NO:75.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 15.4%; Score 198.8; DB 5; Length 13864;
Best Local Similarity 80.2%; Pred. No. 6.1e-41;
RESULT 1237
ID AAK72508 standard; DNA; 17181 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27320.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 17181;
Best Local Similarity 83.4%; Pred. No. 6.7e-41;
RESULT 1238
ID AAK84642 standard; DNA; 17181 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39454.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 17181;
Best Local Similarity 83.4%; Pred. No. 6.7e-41;
RESULT 1239
ID AAL03764 standard; DNA; 18820 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6452.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 18820;
Best Local Similarity 83.4%; Pred. No. 6.9e-41;
RESULT 1240
ID ABA07938 standard; DNA; 18820 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 733.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 18820;
Best Local Similarity 83.4%; Pred. No. 6.9e-41;
RESULT 1241
ID ADA66458 standard; DNA; 29000 BP.
DE Human Transforming Growth Factor-beta 3 coding sequence, SEQ ID 17.
PN WO2003008544-A2.
PD 30-JAN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.4%; Score 198.8; DB 10; Length 29000;
Best Local Similarity 81.3%; Pred. No. 8.4e-41;
RESULT 1242
ID AAK82628 standard; DNA; 48203 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37440.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 48203;
Best Local Similarity 83.4%; Pred. No. 1e-40;
RESULT 1243
ID AAK81663 standard; DNA; 48203 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36475.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 48203;
Best Local Similarity 83.4%; Pred. No. 1e-40;
RESULT 1244
ID AAK70161 standard; DNA; 48203 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24973.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 48203;
Best Local Similarity 83.3%; Pred. No. 5.5e-41;
RESULT 1245
ID AAK81666 standard; DNA; 48204 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36478.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 48204;
Best Local Similarity 83.4%; Pred. No. 1e-40;
RESULT 1246
ID AAK82630 standard; DNA; 48204 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37442.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 48204;
Best Local Similarity 83.4%; Pred. No. 1e-40;
RESULT 1247
ID AAK70164 standard; DNA; 48204 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24976.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.4%; Score 198.8; DB 4; Length 48204;
Best Local Similarity 83.4%; Pred. No. 1e-40;
RESULT 1248
ID ADQ97215 standard; DNA; 56018 BP.
DE Human cancer associated sequence HD08-014, SEQ ID 191.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 198.8; DB 12; Length 56018;
Best Local Similarity 80.5%; Pred. No. 1.1e-40;
RESULT 1249
ID ADA02576 standard; DNA; 87878 BP.
DE Human FKBPS carcinoma associated gene, SEQ ID NO:1094.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 198.8; DB 9; Length 87878;
Best Local Similarity 81.3%; Pred. No. 1.4e-40;
RESULT 1250
ID ADB72314 standard; DNA; 87878 BP.
DE Human FKBPS gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 198.8; DB 10; Length 87878;
Best Local Similarity 81.3%; Pred. No. 1.4e-40;
RESULT 1251
ID ADE95824 standard; DNA; 87878 BP.
DE Human FKBPS gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 198.8; DB 10; Length 87878;
Best Local Similarity 81.3%; Pred. No. 1.4e-40;
RESULT 1252
ID ADX98568 standard; DNA; 92600 BP.
DE Human intercellular adhesion molecule (ICAM1, ICAM4, ICAM5) genomic DNA.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 198.8; DB 13; Length 100608;
Best Local Similarity 82.5%; Pred. No. 1.4e-40;
RESULT 1254
ID ACN44926 standard; DNA; 108182 BP.
DE Human genomic sequence hCG14831.

PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 198.8; DB 11; Length 108182;
Best Local Similarity 78.1%; Pred. No. 1.5e-40;
RESULT 1255
Query Match 15.4%; Score 198.8; DB 4; Length 110000;
Best Local Similarity 82.5%; Pred. No. 1.5e-40;
RESULT 1256
Query Match 15.4%; Score 198.8; DB 4; Length 110000;
Best Local Similarity 82.5%; Pred. No. 1.5e-40;
RESULT 1257
Query Match 15.4%; Score 198.8; DB 6; Length 110000;
Best Local Similarity 82.5%; Pred. No. 1.5e-40;
RESULT 1258
Query Match 15.4%; Score 198.8; DB 6; Length 110000;
Best Local Similarity 82.3%; Pred. No. 1.5e-40;
RESULT 1259
Query Match 15.4%; Score 198.8; DB 6; Length 110000;
Best Local Similarity 82.5%; Pred. No. 1.5e-40;
RESULT 1260
ID ACN44150 standard; DNA; 439892 BP.
DE Human genomic sequence hCG27278.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 198.8; DB 11; Length 110000;
Best Local Similarity 83.7%; Pred. No. 1.5e-40;
RESULT 1261
Query Match 15.4%; Score 198.8; DB 11; Length 110000;
Best Local Similarity 83.7%; Pred. No. 1.5e-40;
RESULT 1262
Query Match 15.4%; Score 198.8; DB 11; Length 110000;
Best Local Similarity 82.5%; Pred. No. 1.5e-40;
RESULT 1263
Query Match 15.4%; Score 198.8; DB 12; Length 110000;
Best Local Similarity 82.5%; Pred. No. 1.5e-40;
RESULT 1264
Query Match 15.4%; Score 198.8; DB 12; Length 110000;
Best Local Similarity 82.3%; Pred. No. 1.5e-40;
RESULT 1265
Query Match 15.4%; Score 198.8; DB 12; Length 110000;
Best Local Similarity 82.3%; Pred. No. 1.5e-40;
RESULT 1266
Query Match 15.4%; Score 198.8; DB 12; Length 110000;
Best Local Similarity 82.3%; Pred. No. 1.5e-40;
RESULT 1267
Query Match 15.4%; Score 198.8; DB 14; Length 110000;
Best Local Similarity 82.3%; Pred. No. 1.5e-40;
RESULT 1268
ID AEF74559 standard; DNA; 113916 BP.
DE Human polynucleotide #73.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 15.4%; Score 198.8; DB 15; Length 113916;
Best Local Similarity 83.4%; Pred. No. 1.5e-40;
RESULT 1269
ID AD212943 standard; DNA; 126488 BP.
DE Human cancer-associated genomic DNA #40.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.4%; Score 198.8; DB 14; Length 126488;
Best Local Similarity 82.5%; Pred. No. 1.6e-40;
RESULT 1270
ID ABK83575 standard; cDNA; 136284 BP.
DE Human cDNA differentially expressed in granulocytic cells #146.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 15.4%; Score 198.8; DB 6; Length 136284;

Best Local Similarity 83.7%; Pred. No. 1.7e-40;
RESULT 1271
ID ADR52798 standard; DNA; 136284 BP.
DE Drug therapy altered expressed gene #149.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 15.4%; Score 198.8; DB 13; Length 136284;
Best Local Similarity 83.7%; Pred. No. 1.7e-40;
RESULT 1272
ID ACN44394 standard; DNA; 150130 BP.
DE Human genomic sequence hCG28278.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 198.8; DB 11; Length 150130;
Best Local Similarity 83.3%; Pred. No. 1.7e-40;
RESULT 1273
ID ADF65423 standard; DNA; 154068 BP.
DE Human sequence from clone RP11-363122 on chromosome 1, complete DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 15.4%; Score 198.8; DB 11; Length 154068;
Best Local Similarity 85.4%; Pred. No. 1.7e-40;
RESULT 1274
ID ABE04899 standard; DNA; 183558 BP.
DE Cancer-associated gene SEQ ID NO:217.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.4%; Score 198.8; DB 14; Length 183558;
Best Local Similarity 83.4%; Pred. No. 1.9e-40;
RESULT 1275
ID ADQ97397 standard; DNA; 225587 BP.
DE Human cancer associated sequence HD08-043, SEQ ID 374.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 198.8; DB 12; Length 225587;
Best Local Similarity 83.7%; Pred. No. 2.1e-40;
RESULT 1276
ID AD213715 standard; DNA; 234882 BP.
DE Human cancer-associated genomic DNA #106.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.4%; Score 198.8; DB 14; Length 234882;
Best Local Similarity 83.7%; Pred. No. 2.1e-40;
RESULT 1277
ID ADQ59422 standard; DNA; 246940 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:58.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.4%; Score 198.8; DB 12; Length 246940;
Best Local Similarity 83.7%; Pred. No. 2.1e-40;
RESULT 1278
ID ACN44514 standard; DNA; 256493 BP.
DE Human genomic sequence hCG17361.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.4%; Score 198.8; DB 11; Length 256493;
Best Local Similarity 83.7%; Pred. No. 2.2e-40;
RESULT 1279
ID ADC86940 standard; DNA; 349901 BP.
DE Human GPCR gene SEQ ID NO:1393.
PN EP1270724-A2.

PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.4%; Score 198.8; DB 10; Length 349901;
Best Local Similarity 77.9%; Pred. No. 2.5e-40;
RESULT 1280
ID ADC87621 standard; DNA; 349938 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2074.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.4%; Score 198.8; DB 10; Length 349938;
Best Local Similarity 77.9%; Pred. No. 2.5e-40;
RESULT 1281
ID AAK78857 standard; DNA; 358 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33669.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 4; Length 358;
Best Local Similarity 83.2%; Pred. No. 1.4e-41;
RESULT 1282
ID AAK78858 standard; DNA; 358 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33670.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 4; Length 358;
Best Local Similarity 83.2%; Pred. No. 1.4e-41;
RESULT 1283
ID ADA41567 standard; DNA; 1120 BP.
DE Human secreted protein related DNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 8; Length 1120;
Best Local Similarity 83.2%; Pred. No. 2.3e-41;
RESULT 1284
ID ACC50901 standard; cDNA; 1120 BP.
DE Human secreted protein BAC clone SEQ ID NO 1081.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 8; Length 1120;
Best Local Similarity 83.2%; Pred. No. 2.3e-41;
RESULT 1285
ID RAH14255 standard; cDNA; 2396 BP.
DE Human cDNA sequence SEQ ID NO:11564.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 15.3%; Score 198.6; DB 4; Length 2396;
Best Local Similarity 83.2%; Pred. No. 3.2e-41;
RESULT 1286
ID ADG90947 standard; DNA; 3297 BP.
DE Hepatic specific nucleic acid encoding sequence #136.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 15.3%; Score 198.6; DB 10; Length 3297;
Best Local Similarity 78.8%; Pred. No. 3.6e-41;
RESULT 1287
ID ADQ86476 standard; cDNA; 3496 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3348.
PN WO2004050270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 15.3%; Score 198.6; DB 13; Length 3496;
Best Local Similarity 75.7%; Pred. No. 3.7e-41;
RESULT 1288

ID ACN39458 standard; cDNA; 3496 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325672, SEQ ID NO:3608.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 15.3%; Score 198.6; DB 13; Length 3496;
Best Local Similarity 75.7%; Pred. No. 3.7e-41;
RESULT 1289
ID ADQ84379 standard; cDNA; 3726 BP.
DE Novel human cDNA sequence #1540.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.3%; Score 198.6; DB 12; Length 3726;
Best Local Similarity 87.3%; Pred. No. 3.8e-41;
RESULT 1290
ID AAK87418 standard; DNA; 4026 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42230.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 4; Length 4026;
Best Local Similarity 84.4%; Pred. No. 4e-41;
RESULT 1291
ID AAK67156 standard; DNA; 4094 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21968.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 4; Length 4094;
Best Local Similarity 80.7%; Pred. No. 4e-41;
RESULT 1292
ID AAK70463 standard; DNA; 4094 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25275.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 4; Length 4094;
Best Local Similarity 80.7%; Pred. No. 4e-41;
RESULT 1293
ID ADQ63041 standard; cDNA; 4161 BP.
DE Novel human cDNA sequence #202.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.3%; Score 198.6; DB 12; Length 4161;
Best Local Similarity 83.2%; Pred. No. 4e-41;
RESULT 1294
ID ABA20591 standard; DNA; 6515 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12922.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 5; Length 6515;
Best Local Similarity 79.6%; Pred. No. 4.9e-41;
RESULT 1295
ID AAK73722 standard; DNA; 14085 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28534.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 4; Length 14085;
Best Local Similarity 79.8%; Pred. No. 6.9e-41;
RESULT 1296
ID AEB96529 standard; DNA; 20001 BP.
DE Human SUL2B1 gene, SEQ ID 13.
PN JP2005204549-A.
PD 04-AUG-2005.
PA (HYUB-) HYUBITTO GENOMICS KK.
PA (KAWA/) KAWADA Y.
Query Match 15.3%; Score 198.6; DB 14; Length 20001;
Best Local Similarity 80.9%; Pred. No. 8e-41;
RESULT 1297

ID ADQ97840 standard; DNA; 23852 BP.
DE Human cancer associated sequence HD11-009, SEQ ID 817.
FN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.3%; Score 198.6; DB 12; Length 23852;
Best Local Similarity 84.4%; Pred. No. 8.7e-41;
RESULT 1298
ID AD212506 standard; DNA; 24244 BP.
DE Human cancer-associated genomic DNA #4.
FN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.3%; Score 198.6; DB 14; Length 24244;
Best Local Similarity 82.0%; Pred. No. 8.7e-41;
RESULT 1299
ID ADP77125 standard; DNA; 27848 BP.
DE Type II diabetes gene SEQ ID NO 2.
FN WO2004084797-A2.
PD 07-OCT-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (DAIM/) DAIMON M.
PA (KATO/) KATO T.
Query Match 15.3%; Score 198.6; DB 13; Length 27848;
Best Local Similarity 79.6%; Pred. No. 9.3e-41;
RESULT 1300
ID AAK89452 standard; DNA; 32192 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3028.
FN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.6; DB 4; Length 32192;
Best Local Similarity 78.6%; Pred. No. 9.9e-41;
RESULT 1301
ID ACN37240 standard; DNA; 34796 BP.
DE Human periodontal disease related gene PLOD SEQ ID NO:150.
FN WO2004042054-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (KAMO/) KAMO I K.
Query Match 15.3%; Score 198.6; DB 13; Length 34796;
Best Local Similarity 83.2%; Pred. No. 1e-40;
RESULT 1302
ID ABL68824 standard; DNA; 38374 BP.
DE Kidney cancer related gene sequence SEQ ID NO:7161.
FN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 15.3%; Score 198.6; DB 6; Length 38374;
Best Local Similarity 79.6%; Pred. No. 1.1e-40;
RESULT 1303
ID ABL68363 standard; DNA; 38374 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6700.
FN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 15.3%; Score 198.6; DB 6; Length 38374;
Best Local Similarity 79.6%; Pred. No. 1.1e-40;
RESULT 1304
ID ABL68364 standard; DNA; 38374 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6701.
FN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 15.3%; Score 198.6; DB 6; Length 38374;
Best Local Similarity 79.6%; Pred. No. 1.1e-40;
RESULT 1305
ID ABN96966 standard; DNA; 38374 BP.
DE Gene #3464 used to diagnose liver cancer.
FN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 15.3%; Score 198.6; DB 6; Length 38374;

Best Local Similarity 79.6%; Pred. No. 1.1e-40;
RESULT 1306
ID ADW42340 standard; DNA; 49620 BP.
DE Human chromosome 3 region containing the DDX36 gene.
FN WO2005001031-A2.
PD 06-JAN-2005.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.3%; Score 198.6; DB 14; Length 49620;
Best Local Similarity 82.7%; Pred. No. 1.2e-40;
RESULT 1307
ID ACN45102 standard; DNA; 69611 BP.
DE Human genomic sequence hCG24168.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.6; DB 11; Length 69611;
Best Local Similarity 83.0%; Pred. No. 1.4e-40;
RESULT 1308
ID ACN44774 standard; DNA; 95960 BP.
DE Human genomic sequence hCG21354.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.6; DB 11; Length 95960;
Best Local Similarity 83.2%; Pred. No. 1.6e-40;
RESULT 1309
ID ACN44770 standard; DNA; 95960 BP.
DE Human genomic sequence hCG21354.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.6; DB 11; Length 95960;
Best Local Similarity 83.2%; Pred. No. 1.6e-40;
RESULT 1310
ID ADX06943 standard; DNA; 103738 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1508.
FN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 15.3%; Score 198.6; DB 14; Length 103738;
Best Local Similarity 78.6%; Pred. No. 1.7e-40;
RESULT 1311
Query Match 15.3%; Score 198.6; DB 13; Length 110000;
Best Local Similarity 83.2%; Pred. No. 1.7e-40;
RESULT 1312
Query Match 15.3%; Score 198.6; DB 13; Length 110000;
Best Local Similarity 83.2%; Pred. No. 1.7e-40;
RESULT 1313
Query Match 15.3%; Score 198.6; DB 14; Length 110000;
Best Local Similarity 83.2%; Pred. No. 1.7e-40;
RESULT 1314
ID ADX06911 standard; DNA; 131078 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1476.
FN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 15.3%; Score 198.6; DB 14; Length 131078;
Best Local Similarity 84.4%; Pred. No. 1.8e-40;
RESULT 1315
ID AED89414 standard; DNA; 150450 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 54.
FN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.3%; Score 198.6; DB 14; Length 150450;
Best Local Similarity 80.7%; Pred. No. 1.9e-40;
RESULT 1316
ID ADE82948 standard; DNA; 167163 BP.
DE Human PVT1 genomic DNA sequence.
FN WO2003080808-A2.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.6; DB 10; Length 167163;

Best Local Similarity 80.9%; Pred. No. 2e-40;
RESULT 1317
ID AED89413 standard; DNA; 191343 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 53.
PD WO2005106044-A1.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.3%; Score 198.6; DB 14; Length 191343;
Best Local Similarity 80.7%; Pred. No. 2.2e-40;
RESULT 1318
ID ACN44126 standard; DNA; 209484 BP.
DE Human genomic sequence hCG16187.
PD WO2003073826-A2.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.6; DB 11; Length 209484;
Best Local Similarity 77.7%; Pred. No. 2.3e-40;
RESULT 1319
ID ABZ80229 standard; DNA; 249999 BP.
DE Human tramodrin gene region genomic DNA SEQ ID NO:26.
PD WO2003016502-A2.
PA (MCLA-) MCLAUGHLIN RES INST.
Query Match 15.3%; Score 198.6; DB 8; Length 249999;
Best Local Similarity 83.2%; Pred. No. 2.4e-40;
RESULT 1320
ID AED76155 standard; DNA; 261108 BP.
DE Human CA genomic DNA sequence-ID hD25-006.
PD WO2005104810-A2.
PD 10-NOV-2005.
PA (SAGR-) SAGRES DISCOVERY INC.
PA (LAI/A/) LAI A.
PA (FATT/) FATTAY A.
Query Match 15.3%; Score 198.6; DB 14; Length 261108;
Best Local Similarity 83.2%; Pred. No. 2.5e-40;
RESULT 1321
ID ADS93537 standard; DNA; 322885 BP.
DE Human MRCK2 gene genomic sequence SeqID3.
Query Match 15.3%; Score 198.6; DB 13; Length 322885;
Best Local Similarity 79.6%; Pred. No. 2.7e-40;
RESULT 1322
ID RAT94758 standard; DNA; 320 BP.
DE Alu insertion sequence which can mutate human progesterone receptor.
PD US5683885-A.
PD 04-NOV-1997.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 15.3%; Score 198.4; DB 2; Length 320;
Best Local Similarity 83.7%; Pred. No. 1.5e-41;
RESULT 1323
ID AAT84749 standard; DNA; 320 BP.
DE Human progesterone receptor Alu insertion.
PD US5645995-A.
PD 08-JUL-1997.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 15.3%; Score 198.4; DB 2; Length 320;
Best Local Similarity 83.7%; Pred. No. 1.5e-41;
RESULT 1324
ID AAK66695 standard; DNA; 457 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21507.
PD WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.4; DB 4; Length 457;
Best Local Similarity 81.3%; Pred. No. 1.7e-41;
RESULT 1325
ID AAK6266 standard; DNA; 1655 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21078.
PD WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.4; DB 4; Length 1655;
Best Local Similarity 83.7%; Pred. No. 3e-41;
RESULT 1326

ID AAK66148 standard; DNA; 2331 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20960.
PD WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.4; DB 4; Length 2331;
Best Local Similarity 79.2%; Pred. No. 3.5e-41;
RESULT 1327
ID AAK80792 standard; DNA; 3227 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35604.
PD WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.4; DB 4; Length 3227;
Best Local Similarity 81.5%; Pred. No. 4.1e-41;
RESULT 1328
ID AAK80791 standard; DNA; 3227 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35603.
PD WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.4; DB 4; Length 3227;
Best Local Similarity 81.5%; Pred. No. 4.1e-41;
RESULT 1329
ID ADR10439 standard; cDNA; 3513 BP.
DE Full length human cDNA useful for treating neurological disease Seq 3945.
PD EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.3%; Score 198.4; DB 13; Length 3513;
Best Local Similarity 85.2%; Pred. No. 4.2e-41;
RESULT 1330
ID ACC85702 standard; DNA; 5023 BP.
DE Human protease MPTS9 related DNA sequence SEQ ID NO: 17.
PD WO2004001047-A1.
PD 31-DEC-2003.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 15.3%; Score 198.4; DB 12; Length 5023;
Best Local Similarity 78.2%; Pred. No. 4.9e-41;
RESULT 1331
ID AAZ60888 standard; DNA; 17131 BP.
DE DNA encoding a human geranylgeranyl pyrophosphate synthetase (hGGPPS).
PD WO200005382-A2.
PD 03-FEB-2000.
PA (GEST) GENSET.
Query Match 15.3%; Score 198.4; DB 3; Length 17131;
Best Local Similarity 81.3%; Pred. No. 8.5e-41;
RESULT 1332
ID AAD46552 standard; DNA; 29844 BP.
DE Human GMOAT Gene #2.
PD WO200272888-A2.
PD 19-SEP-2002.
PA (ASTR) ASTRAZENECA AB.
Query Match 15.3%; Score 198.4; DB 6; Length 29844;
Best Local Similarity 80.6%; Pred. No. 1.1e-40;
RESULT 1333
ID ADJ10262 standard; DNA; 51001 BP.
DE Human geranylgeranyl diphosphate synthase 1 genomic DNA SeqID 11.
PD US2004005570-A1.
PD 08-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.3%; Score 198.4; DB 12; Length 51001;
Best Local Similarity 81.3%; Pred. No. 1.4e-40;
RESULT 1334
ID ADQ97864 standard; DNA; 60729 BP.
DE Human cancer associated sequence HD11-014, SEQ ID 841.
PD WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.3%; Score 198.4; DB 12; Length 60729;
Best Local Similarity 77.5%; Pred. No. 1.5e-40;
RESULT 1335

ID ADQ97563 standard; DNA; 79084 BP.
DE Human cancer associated sequence HD09-014, SEQ ID 540.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.3%; Score 198.4; DB 12; Length 79084;
Best Local Similarity 83.8%; Pred. No. 1.7e-40;
RESULT 1336
Query Match 15.3%; Score 198.4; DB 14; Length 83432;
Best Local Similarity 78.1%; Pred. No. 1.7e-40;
RESULT 1337
ID ADF45593 standard; DNA; 147300 BP.
DE Human Rho family guanine-nucleotide exchange factor KIAA0861 gDNA.
PN WO2004047623-A2.
PD 10-JUN-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 15.3%; Score 198.4; DB 12; Length 147300;
Best Local Similarity 82.7%; Pred. No. 2.2e-40;
RESULT 1338
ID ADX98570 standard; DNA; 147700 BP.
DE Human guanine-nucleotide exchange factor KIAA0861 genomic DNA.
Query Match 15.3%; Score 198.4; DB 14; Length 147700;
Best Local Similarity 82.7%; Pred. No. 2.2e-40;
RESULT 1339
ID ASE96613 standard; DNA; 147700 BP.
DE KIAA0861 genomic DNA sequence, SEQ ID NO:1.
PN WO2005118856-A1.
PD 15-DEC-2005.
PA (SEQU-) SEQUENOM INC.
Query Match 15.3%; Score 198.4; DB 15; Length 147700;
Best Local Similarity 82.7%; Pred. No. 2.2e-40;
RESULT 1340
ID ASK84797 standard; cDNA; 149671 BP.
DE Human cDNA differentially expressed in granulocytic cells #1368.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 15.3%; Score 198.4; DB 6; Length 149671;
Best Local Similarity 83.7%; Pred. No. 2.2e-40;
RESULT 1341
ID ADB70361 standard; cDNA; 149671 BP.
DE Moesin cDNA SEQ ID NO:53.
PN WO2003021229-A2.
PD 13-MAR-2003.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 15.3%; Score 198.4; DB 9; Length 149671;
Best Local Similarity 83.7%; Pred. No. 2.2e-40;
RESULT 1342
ID ADJ37140 standard; cDNA; 149671 BP.
DE Human malignant pleural mesothelioma (MPM) cDNA #23.
PN US2003219760-A1.
PD 27-NOV-2003.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 15.3%; Score 198.4; DB 12; Length 149671;
Best Local Similarity 83.7%; Pred. No. 2.2e-40;
RESULT 1343
ID ADL13904 standard; DNA; 164772 BP.
DE Osteoarthritis-associated polymorphic nucleotide #436.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.3%; Score 198.4; DB 10; Length 164772;
Best Local Similarity 80.2%; Pred. No. 2.3e-40;
RESULT 1344
ID ACN44626 standard; DNA; 175077 BP.
DE Human genomic sequence hCG19724.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.4; DB 11; Length 175077;
Best Local Similarity 76.4%; Pred. No. 2.3e-40;
RESULT 1345
ID ADF69167 standard; cDNA; 216215 BP.

DE Human MP53 nucleotide sequence SEQ ID NO:25.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 15.3%; Score 198.4; DB 10; Length 216215;
Best Local Similarity 83.9%; Pred. No. 2.6e-40;
RESULT 1346
ID ADX80720 standard; DNA; 221600 BP.
DE Human neurophilin 1 (NRP1) genomic DNA.
Query Match 15.3%; Score 198.4; DB 14; Length 221600;
Best Local Similarity 79.4%; Pred. No. 2.6e-40;
RESULT 1347
ID ACN45146 standard; DNA; 226215 BP.
DE Human genomic sequence hCG1639824.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.4; DB 11; Length 226215;
Best Local Similarity 85.2%; Pred. No. 2.6e-40;
RESULT 1348
ID ASD32598 standard; DNA; 290547 BP.
DE Human cancer-associated genomic DNA HD7-220.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.3%; Score 198.4; DB 13; Length 290547;
Best Local Similarity 81.5%; Pred. No. 2.9e-40;
RESULT 1349
ID ADC86916 standard; DNA; 349989 BP.
DE Human GPCR gene SEQ ID NO:1369.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.3%; Score 198.4; DB 10; Length 349989;
Best Local Similarity 83.7%; Pred. No. 3.2e-40;
RESULT 1350
ID AAS44682 standard; DNA; 642 BP.
DE Human full-length polynucleotide sequence #107.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.3%; Score 198.2; DB 4; Length 642;
Best Local Similarity 81.8%; Pred. No. 2.3e-41;
RESULT 1351
ID AAK85658 standard; DNA; 963 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40470.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198.2; DB 4; Length 963;
Best Local Similarity 82.2%; Pred. No. 2.7e-41;
RESULT 1352
ID ABL61322 standard; cDNA; 2224 BP.
DE Human Pur-alpha 13.13 cDNA.
PN CN1331170-A.
PD 16-JAN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 15.3%; Score 198.2; DB 6; Length 2224;
Best Local Similarity 82.0%; Pred. No. 3.9e-41;
RESULT 1353
ID AAH18302 standard; cDNA; 2533 BP.
DE Human cDNA sequence SEQ ID NO:18295.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 15.3%; Score 198.2; DB 4; Length 2533;
Best Local Similarity 78.8%; Pred. No. 4.1e-41;
RESULT 1354
ID ADB63187 standard; cDNA; 2817 BP.
DE Human cDNA encoding clone SPLEN20108000.
PN EP1308459-A2.
PD 07-MAY-2003.

PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 15.3%; Score 198.2; DB 10; Length 2817;
 Best Local Similarity 78.8%; Pred. No. 4.3e-41;
 RESULT 1355
 ID ADE28226 standard; DNA; 3100 BP.
 DE Human MDDT DNA - SEQ ID 76.
 PN WO2003046152-A2.
 PD 05-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 15.3%; Score 198.2; DB 10; Length 3100;
 Best Local Similarity 80.9%; Pred. No. 4.5e-41;
 RESULT 1356
 ID ADJ1471 standard; DNA; 5834 BP.
 DE DNA fragment of a BAC clone that encodes a human secreted protein Seq325.
 PN US2004010132-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (BREW/) BREWER L A.
 PA (DUAN/) DUAN R D.
 PA (RUBE/) RUBEN S M.
 PA (FLOR/) FLORENCE K A.
 PA (GREE/) GREENE J M.
 PA (YOUN/) YOUNG P E.
 PA (FERR/) FERRIE A M.
 PA (YUGG/) YU G.
 PA (FLOR/) FLORENCE C.
 PA (EBNE/) EBNER R.
 PA (OLSE/) OLSEN H.
 Query Match 15.3%; Score 198.2; DB 12; Length 5834;
 Best Local Similarity 79.8%; Pred. No. 6e-41;
 RESULT 1357
 ID AAL04675 standard; DNA; 5862 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7363.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 4; Length 5862;
 Best Local Similarity 76.2%; Pred. No. 6e-41;
 RESULT 1358
 ID ABL97582 standard; DNA; 5862 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2234.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 4; Length 5862;
 Best Local Similarity 76.2%; Pred. No. 6e-41;
 RESULT 1359
 ID AAS18802 standard; cDNA; 6145 BP.
 DE DNA encoding cancer and neurogenesis associated gene, variant 5G-3V1.
 PN WO200190354-A1.
 PD 29-NOV-2001.
 PA (UYLS-) UNIV LEEDS.
 Query Match 15.3%; Score 198.2; DB 6; Length 6145;
 Best Local Similarity 82.9%; Pred. No. 6.1e-41;
 RESULT 1360
 ID ABA20982 standard; DNA; 11472 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 13313.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 5; Length 11472;
 Best Local Similarity 83.0%; Pred. No. 8e-41;
 RESULT 1361
 ID AAK66710 standard; DNA; 14781 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21522.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 4; Length 14781;
 Best Local Similarity 79.0%; Pred. No. 9e-41;
 RESULT 1362
 ID ABQ80004 standard; cDNA; 15957 BP.

DE Secreted human protein gene.
 PN WO2003002138-A1.
 PD 09-JAN-2003.
 PA (PEKE) PE CORP NY.
 Query Match 15.3%; Score 198.2; DB 8; Length 15957;
 Best Local Similarity 80.6%; Pred. No. 9.3e-41;
 RESULT 1363
 ID ABK42246 standard; DNA; 17809 BP.
 DE Genomic sequence #145 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 4; Length 17809;
 Best Local Similarity 83.9%; Pred. No. 9.7e-41;
 RESULT 1364
 ID ADB60402 standard; DNA; 17809 BP.
 DE Connective tissue related genomic DNA #145.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 9; Length 17809;
 Best Local Similarity 83.9%; Pred. No. 9.7e-41;
 RESULT 1365
 ID AAK90363 standard; DNA; 21358 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3939.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 4; Length 21358;
 Best Local Similarity 78.0%; Pred. No. 1.1e-40;
 RESULT 1366
 ID AAK73090 standard; DNA; 21358 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27902.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 4; Length 21358;
 Best Local Similarity 78.0%; Pred. No. 1.1e-40;
 RESULT 1367
 ID AAK87446 standard; DNA; 21358 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42258.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 4; Length 21358;
 Best Local Similarity 78.0%; Pred. No. 1.1e-40;
 RESULT 1368
 ID AAK87558 standard; DNA; 21358 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42370.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 4; Length 21358;
 Best Local Similarity 78.0%; Pred. No. 1.1e-40;
 RESULT 1369
 ID AAL06419 standard; DNA; 21358 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9107.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 4; Length 21358;
 Best Local Similarity 78.0%; Pred. No. 1.1e-40;
 RESULT 1370
 ID AAS39919 standard; DNA; 21358 BP.
 DE Genomic sequence #338 encoding human colon associated polypeptide.
 PN WO200155302-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 15.3%; Score 198.2; DB 5; Length 21358;
 Best Local Similarity 78.0%; Pred. No. 1.1e-40;
 RESULT 1371
 ID ADB32879 standard; DNA; 21358 BP.
 DE Human novel colon related polypeptide DNA SEQ ID NO 816.

PN US2003050231-A1.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 9; Length 21358;
Result 1372 78.0%; Pred. No. 1.1e-40;
ID ADN41667 standard; DNA; 21358 BP.
DE Novel human secreted protein polynucleotide seqid 789.
PN US2004044191-A1.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 12; Length 21358;
Result 1373 78.0%; Pred. No. 1.1e-40;
ID AAK90362 standard; DNA; 21676 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3938.
PN WO200155314-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 4; Length 21676;
Result 1374 78.0%; Pred. No. 1.1e-40;
ID AAK87549 standard; DNA; 21676 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42361.
PN WO200157182-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 4; Length 21676;
Result 1375 78.0%; Pred. No. 1.1e-40;
ID AAK73081 standard; DNA; 21676 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27893.
PN WO200157182-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 4; Length 21676;
Result 1376 78.0%; Pred. No. 1.1e-40;
ID AAK87445 standard; DNA; 21676 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42257.
PN WO200157182-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 4; Length 21676;
Result 1377 78.0%; Pred. No. 1.1e-40;
ID AAL06418 standard; DNA; 21676 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9106.
PN WO200155320-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 4; Length 21676;
Result 1378 78.0%; Pred. No. 1.1e-40;
ID AAS39918 standard; DNA; 21676 BP.
DE Genomic sequence #337 encoding human colon associated polypeptide.
PN WO200155302-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 5; Length 21676;
Result 1379 78.0%; Pred. No. 1.1e-40;
ID AOB32878 standard; DNA; 21676 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 815.
PN US2003050231-A1.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 9; Length 21676;
Result 1380 78.0%; Pred. No. 1.1e-40;
ID ADN41670 standard; DNA; 21676 BP.
DE Novel human secreted protein polynucleotide seqid 792.
PN US2004044191-A1.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 12; Length 21676;
Result 1381 78.0%; Pred. No. 1.1e-40;
ID AAL03558 standard; DNA; 32173 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6246.
PN WO200155320-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 4; Length 32173;
Result 1382 84.6%; Pred. No. 1.3e-40;
ID ABA07767 standard; DNA; 32173 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 562.
PN WO200155325-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 4; Length 32173;
Result 1383 84.6%; Pred. No. 1.3e-40;
ID AAK60452 standard; DNA; 38928 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23264.
PN WO200157182-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 4; Length 38928;
Result 1384 84.6%; Pred. No. 1.4e-40;
ID ADO61194 standard; DNA; 48001 BP.
DE Human PPAR binding protein DNA.
PN US2004101855-A1.
PA (ISIS-) ISIS PHARM INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 12; Length 48001;
Result 1385 83.4%; Pred. No. 1.5e-40;
ID ABS67634 standard; DNA; 63000 BP.
DE Human casein kinase-2 genomic DNA.
PN WO200262818-A2.
PA (ISIS-) ISIS PHARM INC.
Query Match
Best Local Similarity 15.3%; Score 198.2; DB 6; Length 63000;
Result 1386 83.4%; Pred. No. 1.7e-40;

ID AD212791 standard; DNA; 64700 BP.
DE Human cancer-associated genomic DNA #27.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.3%; Score 198.2; DB 14; Length 64700;
Best Local Similarity 78.0%; Pred. No. 1.7e-40;
RESULT 1387
ID ACN44402 standard; DNA; 65621 BP.
DE Human genomic sequence hCG21253.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.2; DB 11; Length 65621;
Best Local Similarity 83.9%; Pred. No. 1.7e-40;
RESULT 1388
ID ABD33325 standard; DNA; 84675 BP.
DE Human cancer-associated (CA) gene HD07-058.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.3%; Score 198.2; DB 13; Length 84675;
Best Local Similarity 83.0%; Pred. No. 1.9e-40;
RESULT 1389
ID ADE95902 standard; DNA; 94719 BP.
DE Human STAT5B gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.2; DB 10; Length 94719;
Best Local Similarity 83.4%; Pred. No. 2e-40;
RESULT 1390
ID ADA02654 standard; DNA; 94720 BP.
DE Human STAT5B carcinoma associated gene, SEQ ID NO:1172.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.2; DB 9; Length 94720;
Best Local Similarity 83.4%; Pred. No. 2e-40;
RESULT 1391
ID ADB72392 standard; DNA; 94720 BP.
DE Human STAT5B gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198.2; DB 10; Length 94720;
Best Local Similarity 83.4%; Pred. No. 2e-40;
RESULT 1392
ID AEB96542 standard; DNA; 104932 BP.
DE Human STAT5A gene, SEQ ID 26.
Query Match 15.3%; Score 198.2; DB 14; Length 104932;
Best Local Similarity 83.4%; Pred. No. 2.1e-40;
RESULT 1393
ID ADC87336 standard; DNA; 108316 BP.
DE Human GPCR gene SEQ ID NO:1789.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.3%; Score 198.2; DB 10; Length 108316;
Best Local Similarity 81.1%; Pred. No. 2.1e-40;
RESULT 1394
Query Match 15.3%; Score 198.2; DB 13; Length 110000;
Best Local Similarity 79.6%; Pred. No. 2.2e-40;
RESULT 1395
ID RAX90201 standard; DNA; 119950 BP.
DE Human yeast gene.
PN WO9935290-A1.
PD 15-JUL-1999.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 15.3%; Score 198.2; DB 2; Length 119950;
Best Local Similarity 83.4%; Pred. No. 2.2e-40;
RESULT 1396

ID ADQ80254 standard; cDNA; 127145 BP.
DE Hermansky-Pudlak syndrome associated cDNA.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 15.3%; Score 198.2; DB 13; Length 127145;
Best Local Similarity 83.1%; Pred. No. 2.3e-40;
RESULT 1397
ID ADC87620 standard; DNA; 144792 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2073.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.3%; Score 198.2; DB 10; Length 144792;
Best Local Similarity 83.2%; Pred. No. 2.4e-40;
RESULT 1398
ID ADP65423 standard; DNA; 154068 BP.
DE Human sequence from clone RP11-363122 on chromosome 1, complete DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 15.3%; Score 198.2; DB 11; Length 154068;
Best Local Similarity 78.0%; Pred. No. 2.5e-40;
RESULT 1399
ID ABN83124 standard; DNA; 172637 BP.
DE Human voltage-activated ion channel transporter protein gene.
Query Match 15.3%; Score 198.2; DB 6; Length 172637;
Best Local Similarity 83.0%; Pred. No. 2.6e-40;
RESULT 1400
ID AEB80195 standard; DNA; 172637 BP.
DE Human transporter genomic DNA.
Query Match 15.3%; Score 198.2; DB 14; Length 172637;
Best Local Similarity 83.0%; Pred. No. 2.6e-40;
RESULT 1401
ID ADQ97721 standard; DNA; 178024 BP.
DE Human cancer associated sequence HD10-033, SEQ ID 698.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.3%; Score 198.2; DB 12; Length 178024;
Best Local Similarity 80.9%; Pred. No. 2.7e-40;
RESULT 1402
ID ABQ88146 standard; cDNA; 178896 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 53.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 15.3%; Score 198.2; DB 6; Length 178896;
Best Local Similarity 81.1%; Pred. No. 2.7e-40;
RESULT 1403
ID ABQ75562 standard; DNA; 188888 BP.
DE Human related CYP 27C1 clone RP11-30F3 SEQ ID NO:21.
PN WO200264765-A2.
PD 22-AUG-2002.
PA (CYTO-) CYTOCHROMA INC.
Query Match 15.3%; Score 198.2; DB 6; Length 188888;
Best Local Similarity 80.9%; Pred. No. 2.7e-40;
RESULT 1404
ID ADY94258 standard; DNA; 190276 BP.
DE BRAF protein kinase gene DNA sequence.
PN WO2005027710-A2.
PD 31-MAR-2005.
PA (SEQU-) SEQUENOM INC.
Query Match 15.3%; Score 198.2; DB 14; Length 190276;
Best Local Similarity 80.9%; Pred. No. 2.7e-40;
RESULT 1405
ID ADL13684 standard; DNA; 247509 BP.
DE Osteoarthritis-associated polymorphic nucleotide #216.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 15.3%; Score 198.2; DB 10; Length 247509;
Best Local Similarity 79.0%; Pred. No. 3.1e-40;
RESULT 1406
ID ABA07247 standard; DNA; 317 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 566.
PN W0200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 4; Length 317;
Best Local Similarity 84.1%; Pred. No. 1.9e-41;
RESULT 1407
ID AAK89888 standard; DNA; 317 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3464.
PN W0200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 4; Length 317;
Best Local Similarity 84.1%; Pred. No. 1.9e-41;
RESULT 1408
ID ABA19006 standard; DNA; 336 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11337.
PN W0200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 5; Length 336;
Best Local Similarity 83.7%; Pred. No. 1.9e-41;
RESULT 1409
ID ABZ73926 standard; DNA; 336 BP.
DE Secreted protein gene 105 genomic fragment HE8SG96, SEQ ID NO:1073.
PN W0200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 8; Length 336;
Best Local Similarity 83.7%; Pred. No. 1.9e-41;
RESULT 1410
ID ADC20676 standard; DNA; 336 BP.
DE Human secreted protein-related DNA sequence #94.
PN W0200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 10; Length 336;
Best Local Similarity 83.7%; Pred. No. 1.9e-41;
RESULT 1411
ID ABZ67514 standard; DNA; 336 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1037.
PN W0200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 10; Length 336;
Best Local Similarity 83.7%; Pred. No. 1.9e-41;
RESULT 1412
ID ABA15628 standard; DNA; 566 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7959.
PN W0200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 5; Length 506;
Best Local Similarity 77.6%; Pred. No. 2.3e-41;
RESULT 1413
ID ADL43619 standard; DNA; 552 BP.
DE Human ovarian cancer DNA marker #17509.
PN W0200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.3%; Score 198; DB 5; Length 552;
Best Local Similarity 78.1%; Pred. No. 2.4e-41;
RESULT 1414
ID ABV21912 standard; cDNA; 1221 BP.
DE Human prostate expression marker cDNA 21903.
PN W0200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.3%; Score 198; DB 5; Length 1221;

Best Local Similarity 79.6%; Pred. No. 3.4e-41;
RESULT 1415
ID ABV27744 standard; cDNA; 1221 BP.
DE Human prostate expression marker cDNA 27735.
PN W0200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.3%; Score 198; DB 5; Length 1221;
Best Local Similarity 79.6%; Pred. No. 3.4e-41;
RESULT 1416
ID ADM14253 standard; DNA; 2252 BP.
DE Glucose and Insulin Responsive Element DNA, SEQ ID 1.
PN CN1454900-A.
PD 12-NOV-2003.
PA (FUDA-) FUDAN SHENHUI GENE SCI & TECHNOLOGY CO L.
Query Match 15.3%; Score 198; DB 13; Length 2252;
Best Local Similarity 81.3%; Pred. No. 4.4e-41;
RESULT 1417
ID AAH19185 standard; cDNA; 3224 BP.
DE Human secreted protein-encoding gene 16 cDNA clone HNGAV54, SEQ ID NO:26.
PN W0200132910-A2.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 4; Length 3224;
Best Local Similarity 67.9%; Pred. No. 5.2e-41;
RESULT 1418
ID ABZ74266 standard; DNA; 5131 BP.
DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1413.
PN W0200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 8; Length 5131;
Best Local Similarity 79.6%; Pred. No. 6.4e-41;
RESULT 1419
ID ADA98795 standard; DNA; 5131 BP.
DE Human secreted protein-related DNA sequence #388.
PN W02003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 8; Length 5131;
Best Local Similarity 79.6%; Pred. No. 6.4e-41;
RESULT 1420
ID ABZ67832 standard; DNA; 5131 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1355.
PN W0200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 10; Length 5131;
Best Local Similarity 79.6%; Pred. No. 6.4e-41;
RESULT 1421
ID ABK42275 standard; DNA; 5629 BP.
DE Genomic sequence #174 encoding novel human connective tissue polypeptide.
PN W0200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 4; Length 5629;
Best Local Similarity 84.1%; Pred. No. 6.6e-41;
RESULT 1422
ID ADB60431 standard; DNA; 5629 BP.
DE Connective tissue related genomic DNA #174.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 9; Length 5629;
Best Local Similarity 84.1%; Pred. No. 6.6e-41;
RESULT 1423
ID ABK42274 standard; DNA; 6265 BP.
DE Genomic sequence #173 encoding novel human connective tissue polypeptide.
PN W0200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 4; Length 6265;
Best Local Similarity 84.1%; Pred. No. 6.9e-41;

RESULT 1424
ID ADB6430 standard; DNA; 6265 BP.
DE Connective tissue related genomic DNA #173.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 9; Length 6265;
Best Local Similarity 84.1%; Pred. No. 6.9e-41;
RESULT 1425
ID ADM77463 standard; DNA; 9731 BP.
DE Human fibrocytin (PKHD1) gene - intron 61.
PN WO2003062453-A2.
PD 31-JUL-2003.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 15.3%; Score 198; DB 11; Length 9731;
Best Local Similarity 80.4%; Pred. No. 8.4e-41;
RESULT 1426
ID ADP74371 standard; DNA; 19300 BP.
DE Human X chromosome nucleotides 469701-489000.
PN US2004110156-A1.
PD 10-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.3%; Score 198; DB 12; Length 19300;
Best Local Similarity 81.7%; Pred. No. 1.1e-40;
RESULT 1427
ID AAK75098 standard; DNA; 20752 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29910.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 4; Length 20752;
Best Local Similarity 82.7%; Pred. No. 1.2e-40;
RESULT 1428
ID ADJ46536 standard; DNA; 22111 BP.
DE Human reguim DNA #2.
PN US2004023385-A1.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 15.3%; Score 198; DB 12; Length 22111;
Best Local Similarity 83.0%; Pred. No. 1.2e-40;
RESULT 1429
ID AAS27687 standard; DNA; 24757 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1347.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 4; Length 24757;
Best Local Similarity 82.9%; Pred. No. 1.3e-40;
RESULT 1430
ID AAS33481 standard; DNA; 24757 BP.
DE DNA encoding human secreted protein, Seq ID No 764.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 4; Length 24757;
Best Local Similarity 82.9%; Pred. No. 1.3e-40;
RESULT 1431
ID ADB94490 standard; DNA; 24757 BP.
DE Novel human protein DNA #99.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.3%; Score 198; DB 10; Length 24757;
Best Local Similarity 82.9%; Pred. No. 1.3e-40;
RESULT 1432
ID ADZ48481 standard; DNA; 31970 BP.
DE Human caspase 9 gene sequence SEQ ID NO:33.
PN CN1548554-A.
PD 24-NOV-2004.
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
Query Match 15.3%; Score 198; DB 14; Length 31970;

Best Local Similarity 75.7%; Pred. No. 1.4e-40;
RESULT 1433
ID ABZ74034 standard; DNA; 39119 BP.
DE Secreted protein gene 163 genomic fragment HJPC08, SEQ ID NO:1181.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 8; Length 39119;
Best Local Similarity 85.4%; Pred. No. 1.5e-40;
RESULT 1434
ID ADA98641 standard; DNA; 39119 BP.
DE Human secreted protein-related DNA sequence #234.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 8; Length 39119;
Best Local Similarity 85.4%; Pred. No. 1.5e-40;
RESULT 1435
ID ADC20764 standard; DNA; 39119 BP.
DE Human secreted protein-related DNA sequence #182.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 10; Length 39119;
Best Local Similarity 85.4%; Pred. No. 1.5e-40;
RESULT 1436
ID ABZ67621 standard; DNA; 39119 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1144.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 198; DB 10; Length 39119;
Best Local Similarity 85.4%; Pred. No. 1.5e-40;
RESULT 1437
ID ABS56200 standard; DNA; 42450 BP.
DE Gene encoding human lanosterol synthase-like enzyme protein.
Query Match 15.3%; Score 198; DB 10; Length 42450;
Best Local Similarity 82.7%; Pred. No. 1.6e-40;
RESULT 1438
ID ADS16411 standard; DNA; 42450 BP.
DE Human lanosterol synthase gene.
Query Match 15.3%; Score 198; DB 13; Length 42450;
Best Local Similarity 82.7%; Pred. No. 1.6e-40;
RESULT 1439
ID AEB96536 standard; DNA; 49942 BP.
DE Human LTPB2 gene, SEQ ID 20.
Query Match 15.3%; Score 198; DB 14; Length 49942;
Best Local Similarity 78.4%; Pred. No. 1.7e-40;
RESULT 1440
ID ADC86870 standard; DNA; 69770 BP.
DE Human GPCR gene SEQ ID NO:1323.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NABD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.3%; Score 198; DB 10; Length 69770;
Best Local Similarity 83.0%; Pred. No. 2e-40;
RESULT 1441
ID ACN44450 standard; DNA; 75252 BP.
DE Human genomic sequence hCG27772.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198; DB 11; Length 75252;
Best Local Similarity 84.1%; Pred. No. 2.1e-40;
RESULT 1442
ID AAC95559 standard; DNA; 80331 BP.
DE Human histone deacetylase HDAC-C coding sequence.
PN WO200071703-A2.
PD 30-NOV-2000.
PA (METH-) METHYLENE INC.
Query Match 15.3%; Score 198; DB 4; Length 80331;
Best Local Similarity 82.9%; Pred. No. 2.1e-40;

RESULT 1443
ID AD048535 standard; DNA; 91000 BP.
DE Human neuropilin 1 (NRPI) genomic DNA sequence #1.
Query Match 15.3%; Score 198; DB 12; Length 91000;
Best Local Similarity 79.1%; Pred. No. 2.2e-40;
RESULT 1444
Query Match 15.3%; Score 198; DB 9; Length 110000;
Best Local Similarity 81.7%; Pred. No. 2.4e-40;
RESULT 1445
Query Match 15.3%; Score 198; DB 12; Length 110000;
Best Local Similarity 82.9%; Pred. No. 2.4e-40;
RESULT 1446
Query Match 15.3%; Score 198; DB 14; Length 110000;
Best Local Similarity 77.8%; Pred. No. 2.4e-40;
ID ACN45054 standard; DNA; 133632 BP.
DE Human genomic sequence hCG28560.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198; DB 11; Length 133632;
Best Local Similarity 79.0%; Pred. No. 2.7e-40;
RESULT 1448
ID AD213285 standard; DNA; 133642 BP.
DE Human cancer-associated genomic DNA #66.
PN W02005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 15.3%; Score 198; DB 14; Length 133642;
Best Local Similarity 79.0%; Pred. No. 2.7e-40;
ID AQ080324 standard; cDNA; 138251 BP.
DE Human PAC clone RP5-855D21 cDNA.
PN W02004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 15.3%; Score 198; DB 13; Length 138251;
Best Local Similarity 81.3%; Pred. No. 2.7e-40;
RESULT 1450
ID ACA64961 standard; DNA; 152141 BP.
DE Human BCR DNA corresponding to U07000.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHOARRAY GMBH.
Query Match 15.3%; Score 198; DB 8; Length 152141;
Best Local Similarity 82.9%; Pred. No. 2.8e-40;
RESULT 1451
ID ACN44010 standard; DNA; 198522 BP.
DE Human genomic sequence hCG1643869.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 198; DB 11; Length 198522;
Best Local Similarity 77.6%; Pred. No. 3.2e-40;
RESULT 1452
ID AQ097421 standard; DNA; 228835 BP.
DE Human cancer associated sequence HD08-046, SEQ ID 398.
PN W02004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.3%; Score 198; DB 12; Length 228835;
Best Local Similarity 81.7%; Pred. No. 3.4e-40;
RESULT 1453
ID AB223704 standard; cDNA; 254366 BP.
DE Human phosphatase genomic DNA #SEQ ID 3.
Query Match 15.3%; Score 198; DB 8; Length 254366;
Best Local Similarity 76.6%; Pred. No. 3.5e-40;
RESULT 1454
ID ACN44046 standard; DNA; 260027 BP.
DE Human genomic sequence hCG1735292.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 15.3%; Score 198; DB 11; Length 260027;
Best Local Similarity 82.9%; Pred. No. 3.6e-40;
RESULT 1455
ID ABD32730 standard; DNA; 260803 BP.
DE Human cancer-associated genomic DNA HD15-016.
PN W02004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.3%; Score 198; DB 13; Length 260803;
Best Local Similarity 81.7%; Pred. No. 3.6e-40;
RESULT 1456
ID AEE06394 standard; DNA; 267966 BP.
DE Glycogen synthase kinase-3beta (GSK-3beta) gene.
PN W02005108582-A1.
PD 17-NOV-2005.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 15.3%; Score 198; DB 14; Length 267966;
Best Local Similarity 83.1%; Pred. No. 3.6e-40;
RESULT 1457
ID AAH71089 standard; cDNA; 366 BP.
DE Human cervical cancer marker nucleic acid 2363.
PN W0200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 15.3%; Score 197.8; DB 4; Length 366;
Best Local Similarity 82.4%; Pred. No. 2.3e-41;
RESULT 1458
ID AAK78061 standard; DNA; 745 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32873.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 4; Length 745;
Best Local Similarity 83.6%; Pred. No. 3.1e-41;
RESULT 1459
ID AAK78060 standard; DNA; 745 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32872.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 4; Length 745;
Best Local Similarity 83.6%; Pred. No. 3.1e-41;
RESULT 1460
ID ADB63773 standard; cDNA; 2400 BP.
DE Human cDNA encoding clone UTERU20045200.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 15.3%; Score 197.8; DB 10; Length 2400;
Best Local Similarity 83.4%; Pred. No. 5.1e-41;
RESULT 1461
ID ABK42678 standard; DNA; 3818 BP.
DE Genomic sequence #577 encoding novel human connective tissue polypeptide.
PN W0200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 4; Length 3818;
Best Local Similarity 83.4%; Pred. No. 6.3e-41;
RESULT 1462
ID ADB60834 standard; DNA; 3818 BP.
DE Connective tissue related genomic DNA #577.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 9; Length 3818;
Best Local Similarity 83.4%; Pred. No. 6.3e-41;
RESULT 1463
ID ABK42328 standard; DNA; 5304 BP.
DE Genomic sequence #227 encoding novel human connective tissue polypeptide.
PN W0200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 15.3%; Score 197.8; DB 4; Length 5304;
Best Local Similarity 84.9%; Pred. No. 7.3e-41;
RESULT 1464
ID ABK42327 standard; DNA; 5304 BP.
DE Genomic sequence #226 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 4; Length 5304;
Best Local Similarity 84.9%; Pred. No. 7.3e-41;
RESULT 1465
ID ADB60483 standard; DNA; 5304 BP.
DE Connective tissue related genomic DNA #226.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 9; Length 5304;
Best Local Similarity 84.9%; Pred. No. 7.3e-41;
RESULT 1466
ID ADB60484 standard; DNA; 5304 BP.
DE Connective tissue related genomic DNA #227.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 9; Length 5304;
Best Local Similarity 84.9%; Pred. No. 7.3e-41;
RESULT 1467
ID AAK72826 standard; DNA; 5576 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27638.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 4; Length 5576;
Best Local Similarity 83.4%; Pred. No. 7.4e-41;
RESULT 1468
ID AAK72901 standard; DNA; 5576 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27713.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 4; Length 5576;
Best Local Similarity 83.4%; Pred. No. 7.4e-41;
RESULT 1469
ID ABT16305 standard; DNA; 22400 BP.
DE Zinc finger protein 9 (ZNF9) DNA SEQ ID NO 1.
PN WO200292763-A2.
PD 21-NOV-2002.
PA (MINU) UNIV MINNESOTA.
PA (RANU) RANUM L P W.
PA (DAYJ) DAY J W.
PA (LIQU) LIQUORI C.
Query Match 15.3%; Score 197.8; DB 8; Length 22400;
Best Local Similarity 81.1%; Pred. No. 1.4e-40;
RESULT 1470
ID ACN45138 standard; DNA; 23694 BP.
DE Human genomic sequence hCG17175.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 197.8; DB 11; Length 23694;
Best Local Similarity 75.3%; Pred. No. 1.4e-40;
RESULT 1471
ID AAL39687 standard; DNA; 31352 BP.
DE Genomic DNA encoding the human smoothened Drosophila homologue (SMOH).
PN WO200229004-A2.
PD 11-APR-2002.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 15.3%; Score 197.8; DB 6; Length 31352;
Best Local Similarity 83.2%; Pred. No. 1.6e-40;
RESULT 1472
ID AAK70686 standard; DNA; 34917 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25498.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.8; DB 4; Length 34917;
Best Local Similarity 81.3%; Pred. No. 1.7e-40;
RESULT 1473
ID ABK85018 standard; DNA; 43545 BP.
DE Human cadherin-like asymmetry protein-2 (CLASP-2) genomic DNA.
PN WO200231117-A2.
PD 18-APR-2002.
PA (ARBO-) ARBOR VITA CORP.
PA (GARM) GARMAN J D.
PA (CAND) CANDIA A F.
Query Match 15.3%; Score 197.8; DB 6; Length 43545;
Best Local Similarity 78.5%; Pred. No. 1.8e-40;
RESULT 1474
ID ADC87426 standard; DNA; 59588 BP.
DE Human GPCR gene SEQ ID NO:1879.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 15.3%; Score 197.8; DB 10; Length 59588;
Best Local Similarity 78.0%; Pred. No. 2.1e-40;
RESULT 1475
ID ABD32800 standard; DNA; 68196 BP.
DE Human cancer-associated genomic DNA HD16-049.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 15.3%; Score 197.8; DB 13; Length 68196;
Best Local Similarity 81.3%; Pred. No. 2.2e-40;
RESULT 1476
ID ACN45026 standard; DNA; 87749 BP.
DE Human genomic sequence hCG25055.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 197.8; DB 11; Length 87749;
Best Local Similarity 85.1%; Pred. No. 2.5e-40;
RESULT 1477
ID ABQ88139 standard; CDNA; 103747 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 46.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 15.3%; Score 197.8; DB 6; Length 103747;
Best Local Similarity 83.4%; Pred. No. 2.7e-40;
RESULT 1478
ID AAD08215 standard; DNA; 114793 BP.
DE Human genome from BAC clone, hbm168.
PN WO200142434-A1.
PD 14-JUN-2001.
PA (MERI) MERCK & CO INC.
Query Match 15.3%; Score 197.8; DB 4; Length 114793;
Best Local Similarity 82.2%; Pred. No. 2.8e-40;
RESULT 1479
ID ABX56555 standard; DNA; 118384 BP.
DE Human autoimmune disease related protein PAT1 gene region #1.
PN WO200280842-A2.
PD 17-OCT-2002.
PA (ESTE-) ESTETECON AB.
Query Match 15.3%; Score 197.8; DB 10; Length 118384;
Best Local Similarity 83.4%; Pred. No. 2.8e-40;
RESULT 1480
ID ACN44074 standard; DNA; 128668 BP.
DE Human genomic sequence hCG40471.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 15.3%; Score 197.8; DB 11; Length 128668;
Best Local Similarity 83.4%; Pred. No. 2.9e-40;
RESULT 1481

ID ABQ88198 standard; cDNA; 154902 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 105.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 15.3%; Score 197.8; DB 6; Length 154902;
Best Local Similarity 83.7%; Pred. No. 3.2e-40;
RESULT 1482
ID AED89421 standard; DNA; 159497 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 61.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.3%; Score 197.8; DB 14; Length 159497;
Best Local Similarity 83.6%; Pred. No. 3.2e-40;
RESULT 1483
ID AEF92730 standard; DNA; 163218 BP.
DE Human chromosome 17 sequence, clone hRPK.318_A_15.
PN WO2006020269-A2.
PD 23-FEB-2006.
PA (UYRP) UNIV ROCHESTER.
Query Match 15.3%; Score 197.8; DB 15; Length 163218;
Best Local Similarity 80.2%; Pred. No. 3.3e-40;
RESULT 1484
ID AED89420 standard; DNA; 171427 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 60.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 15.3%; Score 197.8; DB 14; Length 171427;
Best Local Similarity 83.6%; Pred. No. 3.3e-40;
RESULT 1485
ID ASF19127 standard; DNA; 188056 BP.
DE Human NIPBL genomic sequence.
PN US2006003354-A1.
PD 05-JAN-2006.
PA (KRAN/) KRANTZ I D.
PA (JACK/) JACKSON L G.
Query Match 15.3%; Score 197.8; DB 15; Length 188056;
Best Local Similarity 81.7%; Pred. No. 3.5e-40;
RESULT 1486
ID AEA17302 standard; DNA; 197140 BP.
DE Human GNAI gene locus Seq 12.
PN WO2005047318-A1.
PD 26-MAY-2005.
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
Query Match 15.3%; Score 197.8; DB 14; Length 197140;
Best Local Similarity 78.2%; Pred. No. 3.5e-40;
RESULT 1487
ID ABK84798 standard; cDNA; 220895 BP.
DE Human cDNA differentially expressed in granulocytic cells #1369.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 15.3%; Score 197.8; DB 6; Length 220895;
Best Local Similarity 81.3%; Pred. No. 3.7e-40;
RESULT 1488
ID ADR52737 standard; DNA; 220895 BP.
DE Drug therapy altered expressed gene #88.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AWHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 15.3%; Score 197.8; DB 13; Length 220895;
Best Local Similarity 81.3%; Pred. No. 3.7e-40;
RESULT 1489
ID AAK85653 standard; DNA; 1992 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40465.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.6; DB 4; Length 1992;
Best Local Similarity 82.9%; Pred. No. 5.3e-41;
RESULT 1490
ID AAK85652 standard; DNA; 1995 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40464.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.6; DB 4; Length 1995;
Best Local Similarity 82.9%; Pred. No. 5.3e-41;
RESULT 1491
ID ADO55218 standard; cDNA; 3144 BP.
DE Human bladder cancer-associated BIG-2 gene, SEQ ID NO:3.
PN WO2004010848-A2.
PD 05-FEB-2004.
PA (DIOM-) DIOMEDA LIFE SCI INC.
Query Match 15.3%; Score 197.6; DB 12; Length 3144;
Best Local Similarity 82.9%; Pred. No. 6.5e-41;
RESULT 1492
ID AAL36960 standard; DNA; 3813 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3325.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.6; DB 4; Length 3813;
Best Local Similarity 82.7%; Pred. No. 7.1e-41;
RESULT 1493
ID ABX59948 standard; cDNA; 3813 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2292.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 15.3%; Score 197.6; DB 8; Length 3813;
Best Local Similarity 82.7%; Pred. No. 7.1e-41;
RESULT 1494
ID ADJ30698 standard; DNA; 3813 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3325.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.6; DB 12; Length 3813;
Best Local Similarity 82.7%; Pred. No. 7.1e-41;
RESULT 1495
ID AAK81320 standard; DNA; 5021 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36132.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.6; DB 4; Length 5021;
Best Local Similarity 82.9%; Pred. No. 8e-41;
RESULT 1496
ID ABA93753 standard; cDNA; 5282 BP.
DE Human transcription factor cDNA clone tes3_18n14.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GERH-) GERMAN HUMAN GENOME PROJECT.
Query Match 15.3%; Score 197.6; DB 6; Length 5282;
Best Local Similarity 84.4%; Pred. No. 8.2e-41;
RESULT 1497
ID ABA15148 standard; DNA; 6031 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7479.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.6; DB 5; Length 6031;
Best Local Similarity 80.8%; Pred. No. 8.7e-41;
RESULT 1498
ID ADM20191 standard; cDNA; 6491 BP.

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DE Alternative nucleotide for novel channel/transporter cDNA #212.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.6; DB 5; Length 6491;
Best Local Similarity 83.1%; Pred. No. 9e-41;
RESULT 1499
ID ADO17010 standard; DNA; 11763 BP.
DE Human LIPIN3 genomic DNA.
PN US2004018497-A1.
PD 29-JAN-2004.
PA (WARD/) WARDEN C H.
Query Match 15.3%; Score 197.6; DB 12; Length 11763;
Best Local Similarity 84.4%; Pred. No. 1.2e-40;
RESULT 1500
ID ABK42692 standard; DNA; 12822 BP.
DE Genomic sequence #591 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 15.3%; Score 197.6; DB 4; Length 12822;
Best Local Similarity 81.7%; Pred. No. 1.2e-40;

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2006, 19:35:40 ; Search time 258 Seconds
(without alignments)
9391.806 Million cell updates/sec

Title: US-10-785-221-8

Perfect score: 1295

Sequence: 1 ccagaagtccaaggccccc.....ataaatagcttgatattc 1295

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued Patents NA:*

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- 6: /EMC Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC Celerra_SIDS3/ptodata/2/ina/PTUS COMB.seq:*
- 8: /EMC Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC Celerra_SIDS3/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1295	100.0	1295	3	US-09-902-775A-63
5	1295	100.0	1295	3	US-09-906-700-63
6	1295	100.0	1295	3	US-09-903-603A-63
7	1295	100.0	1295	3	US-09-904-520A-63
8	1295	100.0	1295	3	US-09-909-064-63
9	1295	100.0	1295	3	US-09-905-381A-63
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11	1295	100.0	1295	3	US-09-953-499-8
12	1295	100.0	1295	3	US-09-906-646-63
13	1295	100.0	1295	3	US-09-904-462-63
14	1295	100.0	1295	3	US-09-902-736A-63
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22	922.4	71.2	1022	3	US-09-853-161-35
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Sequence 15273, A
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c 104	205.4	15.9	60304	3	US-09-949-016-11995	Sequence 11995, A	C 177	204	15.8	101981	3	US-09-949-016-15195	Sequence 15195, A
105	205.4	15.9	60304	3	US-09-949-016-17264	Sequence 17264, A	C 178	204	15.8	101982	3	US-09-949-016-15590	Sequence 15590, A
106	205.4	15.9	135476	3	US-09-949-016-12611	Sequence 12611, A	C 179	203.8	15.7	601	3	US-09-949-016-176091	Sequence 176091, A
107	205.4	15.9	135476	3	US-09-949-016-14413	Sequence 14413, A	C 180	203.8	15.7	601	3	US-09-949-016-195308	Sequence 195308, A
c 108	205.2	15.8	601	3	US-09-949-016-168945	Sequence 168945, A	181	203.8	15.7	10427	3	US-09-949-016-15785	Sequence 15785, A
109	205.2	15.8	112132	3	US-09-741-150-3	Sequence 3, Appli	182	203.8	15.7	20901	3	US-09-949-016-11866	Sequence 11866, A
110	205.2	15.8	112132	3	US-10-160-187-3	Sequence 3, Appli	183	203.8	15.7	31823	3	US-09-949-016-15945	Sequence 15945, A
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115	205	15.8	117937	3	US-09-949-016-15775	Sequence 15775, A	C 188	203.6	15.7	84761	3	US-09-949-016-11919	Sequence 11919, A
c 116	205	15.8	133358	3	US-09-949-016-16964	Sequence 16964, A	C 189	203.6	15.7	84763	3	US-09-949-016-13914	Sequence 13914, A
c 117	205	15.8	133360	3	US-09-949-016-12651	Sequence 12651, A	C 190	203.6	15.7	141589	5	US-09-543-678A-2480	Sequence 2480, Ap
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c 122	204.6	15.8	85963	3	US-09-949-016-13804	Sequence 13804, A	C 195	203.6	15.7	209274	5	US-09-543-679A-3004	Sequence 3004, Ap
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138	204.6	15.8	818128	3	US-09-949-016-14549	Sequence 14549, A	C 211	203	15.7	601	3	US-09-949-016-17674	Sequence 17674, A
139	204.6	15.8	818128	3	US-09-949-016-14550	Sequence 14550, A	C 212	203	15.7	601	3	US-09-949-016-39305	Sequence 39305, A
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141	204.6	15.8	818128	3	US-09-949-016-14552	Sequence 14552, A	C 214	203	15.7	601	3	US-09-949-016-39369	Sequence 39369, A
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144	204.6	15.8	818128	3	US-09-949-016-14555	Sequence 14555, A	C 217	203	15.7	601	3	US-09-949-016-114202	Sequence 114202, A
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148	204.6	15.8	818128	3	US-09-949-016-14559	Sequence 14559, A	C 221	203	15.7	601	3	US-09-949-016-114874	Sequence 114874, A
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156	204.4	15.8	12899	3	US-09-949-016-16149	Sequence 16149, A	C 229	203	15.7	38368	3	US-09-949-016-12958	Sequence 12958, A
c 157	204.4	15.8	96845	3	US-09-949-016-13558	Sequence 13558, A	C 230	203	15.7	41941	3	US-09-949-016-17380	Sequence 17380, A
c 158	204.4	15.8	101951	3	US-09-949-016-15648	Sequence 15648, A	C 231	203	15.7	88240	3	US-09-949-016-16279	Sequence 16279, A
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c 161	204.2	15.8	52530	3	US-09-949-016-12343	Sequence 12343, A	C 234	202.8	15.7	601	3	US-09-949-016-87815	Sequence 87815, A
c 162	204.2	15.8	52530	3	US-09-949-016-13948	Sequence 13948, A	C 235	202.8	15.7	601	3	US-09-949-016-13000	Sequence 13000, A
c 163	204.2	15.8	87629	3	US-09-949-016-15862	Sequence 15862, A	C 236	202.8	15.7	31208	3	US-09-949-016-17380	Sequence 17380, A
c 164	204.2	15.8	87629	3	US-09-949-016-15263	Sequence 15263, A	C 237	202.8	15.7	31208	3	US-09-949-016-16279	Sequence 16279, A
c 165	204.2	15.8	87629	3	US-09-949-016-15264	Sequence 15264, A	C 238	202.8	15.7	46347	3	US-09-949-016-13469	Sequence 13469, A
c 166	204.2	15.8	87629	3	US-09-949-016-15265	Sequence 15265, A	C 239	202.8	15.7	70770	3	US-09-949-016-16938	Sequence 16938, A
c 167	204.2	15.8	157822	3	US-09-949-016-16723	Sequence 16723, A	C 240	202.8	15.7	118923	3	US-09-949-016-13227	Sequence 13227, A
168	204	15.8	601	3	US-09-949-016-87814	Sequence 87814, A	C 241	202.8	15.7	235452	3	US-09-949-016-13675	Sequence 13675, A
c 169	204	15.8	601	3	US-09-949-016-131800	Sequence 131800, A	C 242	202.8	15.7	255679	3	US-09-949-016-17189	Sequence 17189, A

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c 244	202.6	15.6	601	3	US-09-949-016-68039	Sequence 68039, A	c 317	201.8	15.6	601	3	US-09-949-016-114704	Sequence 114704,
c 245	202.6	15.6	601	3	US-09-949-016-68099	Sequence 68099, A	c 318	201.8	15.6	601	3	US-09-949-016-114705	Sequence 114705,
c 246	202.6	15.6	601	3	US-09-949-016-115288	Sequence 115288, A	c 319	201.8	15.6	601	3	US-09-949-016-114872	Sequence 114872,
c 247	202.6	15.6	601	3	US-09-949-016-200329	Sequence 200329, A	c 320	201.8	15.6	601	3	US-09-949-016-114873	Sequence 114873,
c 248	202.6	15.6	601	3	US-09-949-002-2584	Sequence 2584, Ap	c 321	201.8	15.6	601	3	US-09-949-016-115040	Sequence 115040,
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c 250	202.6	15.6	5934	3	US-09-949-016-14235	Sequence 14235, A	c 323	201.8	15.6	601	3	US-09-949-016-115041	Sequence 115041,
c 251	202.6	15.6	10344	3	US-09-949-016-14208	Sequence 14208, A	c 324	201.8	15.6	601	3	US-09-949-002-1536	Sequence 1536, Ap
c 252	202.6	15.6	14084	3	US-09-949-016-14288	Sequence 14288, A	c 325	201.8	15.6	601	3	US-09-949-002-10805	Sequence 10805, A
c 253	202.6	15.6	24214	3	US-09-949-016-15551	Sequence 15551, A	c 326	201.8	15.6	20481	3	US-09-949-016-12093	Sequence 12093, A
c 254	202.6	15.6	38052	3	US-09-949-016-13825	Sequence 13825, A	c 327	201.8	15.6	20482	3	US-09-949-016-13660	Sequence 13660, A
c 255	202.6	15.6	63783	3	US-09-949-016-13576	Sequence 13576, A	c 328	201.8	15.6	71879	3	US-09-949-016-17465	Sequence 17465, A
c 256	202.6	15.6	94133	3	US-09-949-016-11901	Sequence 11901, A	c 329	201.8	15.6	90472	3	US-09-949-016-14038	Sequence 14038, A
c 257	202.6	15.6	94133	3	US-09-949-016-12713	Sequence 12713, A	c 330	201.8	15.6	110096	4	US-09-880-107-1542	Sequence 1542, Ap
c 258	202.6	15.6	94135	3	US-09-949-016-15934	Sequence 15934, A	c 331	201.8	15.6	111677	3	US-09-949-016-16946	Sequence 16946, A
c 259	202.6	15.6	94135	3	US-09-949-016-15935	Sequence 15935, A	c 332	201.8	15.6	115677	3	US-09-949-016-16946	Sequence 16946, A
c 260	202.6	15.6	94135	3	US-09-949-016-15936	Sequence 15936, A	c 333	201.8	15.6	146307	3	US-09-949-016-14881	Sequence 14881, A
c 261	202.6	15.6	94135	3	US-09-949-016-15937	Sequence 15937, A	c 334	201.8	15.6	146307	3	US-09-949-016-14882	Sequence 14882, A
c 262	202.6	15.6	134292	3	US-09-949-016-12158	Sequence 12158, A	c 335	201.8	15.6	146307	3	US-09-949-016-14883	Sequence 14883, A
c 263	202.4	15.6	601	3	US-09-949-016-38229	Sequence 38229, A	c 336	201.8	15.6	146307	3	US-09-949-016-14884	Sequence 14884, A
c 264	202.4	15.6	601	3	US-09-949-016-51144	Sequence 51144, A	c 337	201.8	15.6	146307	3	US-09-949-016-14885	Sequence 14885, A
c 265	202.4	15.6	601	3	US-09-949-016-65931	Sequence 65931, A	c 338	201.8	15.6	146307	3	US-09-949-016-14886	Sequence 14886, A
c 266	202.4	15.6	601	3	US-09-949-016-113085	Sequence 113085, A	c 339	201.8	15.6	146307	3	US-09-949-016-14887	Sequence 14887, A
c 267	202.4	15.6	601	3	US-09-949-016-175089	Sequence 175089, A	c 340	201.8	15.6	146307	3	US-09-949-016-14888	Sequence 14888, A
c 268	202.4	15.6	7292	3	US-09-949-016-14862	Sequence 14862, A	c 341	201.8	15.6	148405	3	US-09-949-016-11747	Sequence 11747, A
c 269	202.4	15.6	12928	3	US-09-949-016-14862	Sequence 12772, A	c 342	201.8	15.6	148405	3	US-09-949-016-11747	Sequence 12835, A
c 270	202.4	15.6	12929	3	US-09-949-016-16702	Sequence 16702, A	c 343	201.8	15.6	148405	3	US-09-949-016-12836	Sequence 12836, A
c 271	202.4	15.6	40631	3	US-09-949-002-618	Sequence 618, App	c 344	201.8	15.6	148405	3	US-09-949-016-12837	Sequence 12837, A
c 272	202.4	15.6	40632	3	US-09-949-002-770	Sequence 770, App	c 345	201.8	15.6	205044	3	US-09-949-016-15851	Sequence 15851, A
c 273	202.4	15.6	62908	3	US-09-949-016-17554	Sequence 17554, A	c 346	201.8	15.6	205044	3	US-09-949-016-15852	Sequence 15852, A
c 274	202.4	15.6	300402	3	US-09-949-016-13632	Sequence 13632, A	c 347	201.8	15.6	205044	3	US-09-949-016-15853	Sequence 15853, A
c 275	202.2	15.6	601	3	US-09-949-016-38813	Sequence 38813, A	c 348	201.8	15.6	223471	3	US-09-949-016-12387	Sequence 12387, A
c 276	202.2	15.6	601	3	US-09-949-016-47035	Sequence 47035, A	c 349	201.8	15.6	223471	3	US-09-949-016-12387	Sequence 12724, A
c 277	202.2	15.6	601	3	US-09-949-016-181415	Sequence 181415, A	c 350	201.8	15.6	223471	3	US-09-949-016-12724	Sequence 12725, A
c 278	202.2	15.6	6257	5	US-09-984-429-381	Sequence 381, App	c 351	201.6	15.6	601	3	US-09-949-016-24985	Sequence 24985, A
c 279	202.2	15.6	14781	3	US-09-949-016-15917	Sequence 15917, A	c 352	201.6	15.6	601	3	US-09-949-016-50796	Sequence 50796, A
c 280	202.2	15.6	14781	3	US-09-949-016-15918	Sequence 15918, A	c 353	201.6	15.6	601	3	US-09-949-016-50797	Sequence 50797, A
c 281	202.2	15.6	29628	3	US-09-949-016-16483	Sequence 16483, A	c 354	201.6	15.6	601	3	US-09-949-016-50797	Sequence 50797, A
c 282	202.2	15.6	30172	3	US-09-949-002-660	Sequence 660, App	c 355	201.6	15.6	601	3	US-09-949-016-50797	Sequence 50797, A
c 283	202.2	15.6	34408	3	US-09-949-016-14010	Sequence 14010, A	c 356	201.6	15.6	17901	3	US-09-949-016-94322	Sequence 94322, A
c 284	202.2	15.6	40168	3	US-09-949-016-13225	Sequence 13225, A	c 357	201.6	15.6	24221	3	US-09-949-016-13213	Sequence 13213, A
c 285	202.2	15.6	40546	3	US-09-949-016-12847	Sequence 12847, A	c 358	201.6	15.6	46050	3	US-09-949-016-14964	Sequence 14964, A
c 286	202.2	15.6	40546	3	US-09-949-016-12847	Sequence 12847, A	c 359	201.6	15.6	58397	3	US-09-949-016-14469	Sequence 3, Appli
c 287	202.2	15.6	47883	3	US-09-949-016-11886	Sequence 11886, A	c 360	201.6	15.6	59076	3	US-09-949-016-15097	Sequence 15097, A
c 288	202.2	15.6	47883	3	US-09-949-016-17213	Sequence 17213, A	c 361	201.6	15.6	93894	3	US-09-949-016-13629	Sequence 13629, A
c 289	202.2	15.6	58782	3	US-09-949-016-16851	Sequence 16851, A	c 362	201.6	15.6	96690	3	US-09-949-016-17103	Sequence 17103, A
c 290	202.2	15.6	168174	3	US-10-071-411A-63	Sequence 63, Appli	c 363	201.6	15.6	105210	3	US-09-949-016-14158	Sequence 14158, A
c 291	202.2	15.6	168273	3	US-10-071-411A-63	Sequence 2, Appli	c 364	201.6	15.6	211049	3	US-09-949-016-15770	Sequence 15770, A
c 292	202	15.6	601	3	US-09-949-016-186879	Sequence 186879, A	c 365	201.6	15.6	312470	3	US-09-949-016-14043	Sequence 14043, A
c 293	202	15.6	24482	3	US-09-949-016-13391	Sequence 13391, A	c 366	201.6	15.6	336024	3	US-09-949-016-12373	Sequence 12373, A
c 294	202	15.6	45365	3	US-09-949-016-11893	Sequence 11893, A	c 367	201.4	15.6	601	3	US-09-949-016-181472	Sequence 181472, A
c 295	202	15.6	45456	3	US-09-949-016-17007	Sequence 17007, A	c 368	201.4	15.6	601	3	US-09-949-016-181473	Sequence 181473, A
c 296	202	15.6	83697	3	US-09-949-016-16040	Sequence 16040, A	c 369	201.4	15.6	601	3	US-09-949-016-181474	Sequence 181474, A
c 297	202	15.6	117807	3	US-09-949-016-15525	Sequence 15525, A	c 370	201.4	15.6	601	3	US-09-949-016-181475	Sequence 181475, A
c 298	202	15.6	225127	3	US-09-949-016-16480	Sequence 16480, A	c 371	201.4	15.6	601	3	US-09-949-016-182210	Sequence 182210, A
c 299	201.8	15.6	601	3	US-09-949-016-17672	Sequence 17672, A	c 372	201.4	15.6	24553	3	US-09-949-016-16901	Sequence 16901, A
c 300	201.8	15.6	601	3	US-09-949-016-17673	Sequence 17673, A	c 373	201.4	15.6	38374	4	US-09-880-107-3463	Sequence 3463, Ap
c 301	201.8	15.6	601	3	US-09-949-016-39303	Sequence 39303, A	c 374	201.4	15.6	47493	3	US-09-949-016-13241	Sequence 13241, A
c 302	201.8	15.6	601	3	US-09-949-016-39304	Sequence 39304, A	c 375	201.4	15.6	50368	3	US-09-949-016-13256	Sequence 13256, A
c 303	201.8	15.6	601	3	US-09-949-016-39335	Sequence 39335, A	c 376	201.4	15.6	54286	3	US-09-949-016-837	Sequence 837, App
c 304	201.8	15.6	601	3	US-09-949-016-39336	Sequence 39336, A	c 377	201.4	15.6	60194	3	US-09-949-002-656	Sequence 656, App
c 305	201.8	15.6	601	3	US-09-949-016-39367	Sequence 39367, A	c 378	201.4	15.6	60195	3	US-09-949-002-697	Sequence 697, App
c 306	201.8	15.6	601	3	US-09-949-016-39368	Sequence 39368, A	c 379	201.4	15.6	66955	3	US-09-949-002-642	Sequence 642, App
c 307	201.8	15.6	601	3	US-09-949-016-113864	Sequence 113864, A	c 380	201.4	15.6	72992	3	US-09-949-016-17592	Sequence 17592, A
c 308	201.8	15.6	601	3	US-09-949-016-113865	Sequence 113865, A	c 381	201.4	15.6	80246	3	US-09-078-294-4	Sequence 4, Appli
c 309	201.8	15.6	601	3	US-09-949-016-114032	Sequence 114032, A	c 382	201.4	15.6	80595	3	US-09-078-294-3	Sequence 3, Appli
c 310	201.8	15.6	601	3	US-09-949-016-114033	Sequence 114033, A	c 383	201.4	15.6	87648	3	US-09-949-016-13655	Sequence 13655, A
c 311	201.8	15.6	601	3	US-09-949-016-114200	Sequence 114200, A	c 384	201.4	15.6	96878	3	US-09-949-016-12551	Sequence 12551, A
c 312	201.8	15.6	601	3	US-09-949-016-114201	Sequence 114201, A	c 385	201.4	15.6	98828	3	US-09-949-016-16630	Sequence 16630, A
c 313	201.8	15.6	601	3	US-09-949-016-114368	Sequence 114368, A	c 386	201.4	15.6	123513	3	US-09-949-016-15794	Sequence 15794, A
c 314	201.8	15.6	601	3	US-09-949-016-114369	Sequence 114369, A	c 387	201.2	15.5	601	3	US-09-949-016-65855	Sequence 65855, A
c 315	201.8	15.6	601	3	US-09-949-016-114536	Sequence 114536, A	c 388	201.2	15.5	601	3	US-09-949-016-80058	Sequence 80058, A

389	201.2	15.5	601	3	US-09-949-016-94321	Sequence 94321, A	C 462	200.6	15.5	40333	3	US-09-949-016-11821	Sequence 11821, A
390	201.2	15.5	601	3	US-09-949-016-115287	Sequence 115287, A	C 463	200.6	15.5	40342	3	US-09-949-016-13982	Sequence 13982, A
391	201.2	15.5	601	3	US-09-949-016-148948	Sequence 148948, A	464	200.4	15.5	601	3	US-09-949-016-47257	Sequence 47257, A
392	201.2	15.5	601	3	US-09-949-016-149015	Sequence 149015, A	465	200.4	15.5	601	3	US-09-949-016-60624	Sequence 60624, A
393	201.2	15.5	601	3	US-09-949-016-149082	Sequence 149082, A	466	200.4	15.5	601	3	US-09-949-016-78602	Sequence 78602, A
394	201.2	15.5	601	3	US-09-949-016-149149	Sequence 149149, A	467	200.4	15.5	601	3	US-09-949-016-154657	Sequence 154657, A
C 395	201.2	15.5	1701	3	US-08-078-294-9	Sequence 9, Appli	468	200.4	15.5	601	3	US-09-949-016-166340	Sequence 166340, A
396	201.2	15.5	27579	3	US-09-949-016-13465	Sequence 13465, A	C 469	200.4	15.5	14084	3	US-09-949-016-13889	Sequence 13889, A
C 397	201.2	15.5	29433	3	US-09-949-016-15740	Sequence 15740, A	470	200.4	15.5	43577	3	US-09-949-016-16694	Sequence 16694, A
398	201.2	15.5	38657	3	US-09-949-016-14567	Sequence 14567, A	C 471	200.4	15.5	47698	3	US-09-949-016-13514	Sequence 13514, A
C 399	201.2	15.5	46725	3	US-09-949-016-15680	Sequence 15680, A	C 472	200.4	15.5	73757	3	US-09-949-016-13514	Sequence 13514, A
400	201.2	15.5	49848	3	US-09-949-016-15675	Sequence 15675, A	C 473	200.4	15.5	87562	3	US-09-949-016-13685	Sequence 13685, A
401	201.2	15.5	56109	4	US-08-080-107-3768	Sequence 3768, Ap	C 474	200.4	15.5	275110	3	US-09-949-016-12706	Sequence 12706, A
C 402	201.2	15.5	76553	3	US-09-949-016-13432	Sequence 13432, A	C 475	200.4	15.5	275110	3	US-09-949-016-16070	Sequence 16070, A
403	201.2	15.5	112112	3	US-09-949-016-15639	Sequence 15639, A	C 476	200.4	15.5	285478	3	US-09-949-016-13362	Sequence 13362, A
404	201.2	15.5	128470	3	US-09-949-016-13765	Sequence 13765, A	C 477	200.2	15.5	412	4	US-09-880-107-1164	Sequence 1164, Ap
405	201.2	15.5	181429	3	US-09-949-016-12372	Sequence 12372, A	C 478	200.2	15.5	601	3	US-09-949-016-79784	Sequence 79784, A
406	201.2	15.5	181430	3	US-09-949-016-15772	Sequence 15772, A	C 479	200.2	15.5	601	3	US-09-949-016-125477	Sequence 125477, A
407	201.2	15.5	198285	4	US-08-080-107-3814	Sequence 3814, Ap	C 480	200.2	15.5	24984	3	US-09-949-016-14950	Sequence 14950, A
C 408	201.2	15.5	200663	3	US-09-949-016-12569	Sequence 12569, A	481	200.2	15.5	26433	3	US-09-949-016-15401	Sequence 15401, A
409	201.2	15.5	246240	2	US-08-724-394A-20	Sequence 20, Appl	C 482	200.2	15.5	37565	3	US-09-949-016-15847	Sequence 15847, A
410	201.2	15.5	246240	2	US-08-724-394A-21	Sequence 21, Appl	483	200.2	15.5	38983	3	US-09-949-016-15700	Sequence 15700, A
411	201.2	15.5	246240	2	US-08-724-394A-22	Sequence 22, Appl	484	200.2	15.5	40168	3	US-09-949-016-13225	Sequence 13225, A
C 412	201.2	15.5	325791	3	US-09-768-185A-1	Sequence 1, Appli	485	200.2	15.5	44378	3	US-09-949-016-13650	Sequence 13650, A
413	201	15.5	601	3	US-09-949-016-115289	Sequence 115289, A	C 486	200.2	15.5	44430	3	US-09-949-016-12468	Sequence 12468, A
414	201	15.5	601	3	US-09-949-016-146875	Sequence 146875, A	C 487	200.2	15.5	44431	3	US-09-949-016-15882	Sequence 15882, A
C 415	201	15.5	2412	3	US-10-104-047-1714	Sequence 1714, Ap	488	200.2	15.5	74550	3	US-09-949-016-12310	Sequence 12310, A
C 416	201	15.5	25659	3	US-09-949-016-15052	Sequence 15052, A	489	200.2	15.5	74550	3	US-09-949-016-12764	Sequence 12764, A
C 417	201	15.5	35058	3	US-09-949-016-12607	Sequence 12607, A	490	200.2	15.5	74550	3	US-09-949-016-13649	Sequence 13649, A
C 418	201	15.5	35059	3	US-09-949-016-13931	Sequence 13931, A	491	200.2	15.5	74550	3	US-09-949-016-13650	Sequence 13650, A
C 419	201	15.5	50000	3	US-08-146-053-3	Sequence 3, Appli	C 492	200.2	15.5	83938	3	US-09-949-016-16068	Sequence 16068, A
C 420	201	15.5	84587	3	US-09-949-016-15733	Sequence 15733, A	C 493	200.2	15.5	198942	3	US-09-949-016-13209	Sequence 13209, A
C 421	201	15.5	107800	3	US-09-949-016-13118	Sequence 13118, A	C 494	200.2	15.5	234884	3	US-09-949-016-16420	Sequence 16420, A
C 422	201	15.5	112623	3	US-09-949-016-14374	Sequence 14374, A	C 495	200.2	15.5	601	3	US-09-949-016-15520	Sequence 15520, A
C 423	201	15.5	116425	3	US-09-949-016-11809	Sequence 11809, A	C 496	200	15.4	601	3	US-09-949-016-163719	Sequence 163719, A
C 424	201	15.5	134890	3	US-09-949-016-15502	Sequence 15502, A	C 497	200	15.4	13193	3	US-09-949-016-17515	Sequence 17515, A
C 425	200.8	15.5	601	3	US-09-949-016-139302	Sequence 139302, A	498	200	15.4	14079	3	US-09-949-016-11993	Sequence 11993, A
C 426	200.8	15.5	601	3	US-09-949-016-168342	Sequence 168342, A	499	200	15.4	28819	3	US-09-949-016-15806	Sequence 15806, A
C 427	200.8	15.5	1697	4	US-10-094-749-513	Sequence 513, App	C 500	200	15.4	32725	3	US-09-949-016-15239	Sequence 15239, A
C 428	200.8	15.5	7697	3	US-09-949-016-12628	Sequence 12628, A	C 501	200	15.4	43537	3	US-09-949-016-13458	Sequence 13458, A
C 429	200.8	15.5	7697	3	US-09-949-016-16343	Sequence 16343, A	C 502	200	15.4	49136	3	US-09-422-869-1	Sequence 1, Appli
C 430	200.8	15.5	12797	3	US-09-949-016-13123	Sequence 13123, A	C 503	200	15.4	50810	3	US-09-949-016-16039	Sequence 16039, A
C 431	200.8	15.5	14241	3	US-08-949-016-13869	Sequence 13869, A	C 504	200	15.4	66213	3	US-09-949-016-11803	Sequence 11803, A
C 432	200.8	15.5	29889	3	US-09-949-016-13682	Sequence 13682, A	C 505	200	15.4	66213	3	US-09-949-016-16739	Sequence 16739, A
C 433	200.8	15.5	40908	3	US-09-949-002-845	Sequence 845, App	C 506	200	15.4	87523	3	US-09-949-016-12670	Sequence 12670, A
C 434	200.8	15.5	40944	3	US-09-949-002-603	Sequence 603, App	C 507	200	15.4	87523	3	US-09-949-016-15047	Sequence 15047, A
C 435	200.8	15.5	51671	3	US-09-949-016-12068	Sequence 12068, A	C 508	200	15.4	87523	3	US-09-949-016-15048	Sequence 15048, A
C 436	200.8	15.5	51671	3	US-09-949-016-15962	Sequence 15962, A	C 509	200	15.4	87523	3	US-09-949-016-15049	Sequence 15049, A
C 437	200.8	15.5	57507	3	US-09-949-016-15019	Sequence 15019, A	C 510	200	15.4	87869	3	US-09-949-016-11744	Sequence 11744, A
C 438	200.8	15.5	103987	3	US-09-949-016-12513	Sequence 12513, A	C 511	200	15.4	87869	3	US-09-949-016-15044	Sequence 15044, A
C 439	200.8	15.5	103988	3	US-09-949-016-17050	Sequence 17050, A	C 512	200	15.4	87869	3	US-09-949-016-15045	Sequence 15045, A
C 440	200.8	15.5	123463	3	US-09-949-016-17078	Sequence 17078, A	C 513	200	15.4	87869	3	US-09-949-016-15046	Sequence 15046, A
441	200.8	15.5	152481	3	US-09-949-016-12521	Sequence 12521, A	C 514	200	15.4	89992	3	US-09-949-016-15367	Sequence 15367, A
442	200.8	15.5	152798	3	US-09-949-016-12775	Sequence 12775, A	C 515	200	15.4	107421	3	US-09-949-016-15532	Sequence 15532, A
443	200.8	15.5	152822	3	US-09-949-016-17518	Sequence 17518, A	C 516	200	15.4	111454	3	US-09-949-016-14196	Sequence 14196, A
444	200.8	15.5	152822	3	US-09-949-016-17519	Sequence 17519, A	C 517	200	15.4	111459	3	US-09-949-016-13337	Sequence 12337, A
445	200.8	15.5	225127	3	US-09-949-016-16480	Sequence 16480, A	C 518	200	15.4	113538	3	US-09-949-016-16329	Sequence 16329, A
446	200.8	15.5	283536	3	US-09-949-016-13506	Sequence 13506, A	C 519	200	15.4	235452	3	US-09-949-016-13675	Sequence 13675, A
447	200.8	15.5	636591	3	US-09-949-016-11808	Sequence 11808, A	C 520	199.8	15.4	601	3	US-09-949-016-32182	Sequence 32182, A
448	200.8	15.5	636591	3	US-09-949-016-13388	Sequence 13388, A	C 521	199.8	15.4	601	3	US-09-949-016-125474	Sequence 125474, A
449	200.8	15.5	784019	3	US-09-949-016-14033	Sequence 14033, A	C 522	199.8	15.4	601	3	US-09-949-016-140625	Sequence 140625, A
450	200.8	15.5	828152	3	US-09-949-016-12777	Sequence 12777, A	C 523	199.8	15.4	601	3	US-09-949-016-147535	Sequence 147535, A
C 451	200.6	15.5	601	3	US-09-949-016-124962	Sequence 124962, A	C 524	199.8	15.4	601	3	US-09-949-016-153071	Sequence 153071, A
C 452	200.6	15.5	601	3	US-09-949-016-149962	Sequence 149962, A	C 525	199.8	15.4	601	3	US-09-949-016-199993	Sequence 199993, A
C 453	200.6	15.5	601	3	US-09-949-016-163720	Sequence 163720, A	C 526	199.8	15.4	9779	3	US-09-949-016-15370	Sequence 15370, A
C 454	200.6	15.5	10932	3	US-09-949-016-14480	Sequence 14480, A	C 527	199.8	15.4	26852	3	US-09-949-016-12736	Sequence 12736, A
C 455	200.6	15.5	11200	3	US-09-949-016-13580	Sequence 13580, A	C 528	199.8	15.4	26852	3	US-09-949-016-15823	Sequence 15823, A
C 456	200.6	15.5	12797	3	US-09-949-016-13123	Sequence 13123, A	C 529	199.8	15.4	26867	3	US-09-949-016-16332	Sequence 16332, A
C 457	200.6	15.5	18417	3	US-09-949-016-13389	Sequence 13389, A	C 530	199.8	15.4	34047	3	US-09-949-016-16333	Sequence 16333, A
C 458	200.6	15.5	30146	3	US-09-949-002-599	Sequence 599, App	C 531	199.8	15.4	37059	3	US-09-949-016-17555	Sequence 17555, A
C 459	200.6	15.5	30146	3	US-09-949-002-858	Sequence 858, App	C 532	199.8	15.4	45427	3	US-09-949-016-15865	Sequence 15865, A
460	200.6	15.5	31797	3	US-09-949-016-17188	Sequence 17188, A	C 533	199.8	15.4	45427	3	US-09-949-016-16243	Sequence 16243, A
C 461	200.6	15.5	33624	3	US-09-949-016-15301	Sequence 15301, A	C 534	199.8	15.4	66933	3	US-09-544-398B-11	Sequence 11, Appl

c 535	199.8	15.4	66933	3	US-09-543-771B-11	Sequence 11, Appl	608	199.4	15.4	601	3	US-09-949-016-100477	Sequence 100477,
c 536	199.8	15.4	72049	3	US-09-544-398B-9	Sequence 9, Appl	609	199.4	15.4	601	3	US-09-949-016-100743	Sequence 100743,
c 537	199.8	15.4	72049	3	US-09-543-771B-9	Sequence 9, Appl	610	199.4	15.4	601	3	US-09-949-016-101047	Sequence 101047,
c 538	199.8	15.4	99014	4	US-09-880-107-3428	Sequence 3428, Ap	611	199.4	15.4	601	3	US-09-949-016-101133	Sequence 101133,
c 539	199.8	15.4	118868	3	US-09-949-016-15746	Sequence 15746, A	612	199.4	15.4	601	3	US-09-949-016-101579	Sequence 101579,
c 540	199.8	15.4	140844	3	US-09-949-016-14199	Sequence 14199, A	613	199.4	15.4	601	3	US-09-949-016-101845	Sequence 101845,
c 541	199.8	15.4	678533	3	US-09-949-016-14577	Sequence 14577, A	c 614	199.4	15.4	601	3	US-09-949-016-124679	Sequence 124679,
c 542	199.8	15.4	678533	3	US-09-949-016-14578	Sequence 14578, A	c 615	199.4	15.4	601	3	US-09-949-016-124701	Sequence 124701,
c 543	199.8	15.4	818128	3	US-09-949-016-14546	Sequence 14546, A	c 616	199.4	15.4	601	3	US-09-949-016-124723	Sequence 124723,
c 544	199.8	15.4	818128	3	US-09-949-016-14547	Sequence 14547, A	c 617	199.4	15.4	601	3	US-09-949-016-124745	Sequence 124745,
c 545	199.8	15.4	818128	3	US-09-949-016-14548	Sequence 14548, A	c 618	199.4	15.4	601	3	US-09-949-016-168338	Sequence 168338,
c 546	199.8	15.4	818128	3	US-09-949-016-14549	Sequence 14549, A	c 619	199.4	15.4	601	3	US-09-949-016-196191	Sequence 196191,
c 547	199.8	15.4	818128	3	US-09-949-016-14550	Sequence 14550, A	c 620	199.4	15.4	601	3	US-09-949-016-196193	Sequence 196193,
c 548	199.8	15.4	818128	3	US-09-949-016-14551	Sequence 14551, A	c 621	199.4	15.4	601	3	US-09-949-016-196194	Sequence 196194,
c 549	199.8	15.4	818128	3	US-09-949-016-14552	Sequence 14552, A	c 622	199.4	15.4	2091	3	US-10-104-047-300	Sequence 300, App
c 550	199.8	15.4	818128	3	US-09-949-016-14553	Sequence 14553, A	c 623	199.4	15.4	7855	3	US-09-949-016-12431	Sequence 12431, A
c 551	199.8	15.4	818128	3	US-09-949-016-14554	Sequence 14554, A	624	199.4	15.4	16410	3	US-09-949-016-11781	Sequence 1781, A
c 552	199.8	15.4	818128	3	US-09-949-016-14555	Sequence 14555, A	625	199.4	15.4	16411	3	US-09-949-016-16770	Sequence 16770, A
c 553	199.8	15.4	818128	3	US-09-949-016-14556	Sequence 14556, A	626	199.4	15.4	32211	3	US-09-949-016-16307	Sequence 16307, A
c 554	199.8	15.4	818128	3	US-09-949-016-14557	Sequence 14557, A	627	199.4	15.4	32669	3	US-09-949-016-17250	Sequence 17250, A
c 555	199.8	15.4	818128	3	US-09-949-016-14558	Sequence 14558, A	628	199.4	15.4	47781	3	US-09-949-016-16492	Sequence 16492, A
c 556	199.8	15.4	818128	3	US-09-949-016-14559	Sequence 14559, A	629	199.4	15.4	47781	3	US-09-949-016-16493	Sequence 16493, A
c 557	199.8	15.4	818128	3	US-09-949-016-14560	Sequence 14560, A	c 630	199.4	15.4	47781	3	US-09-949-016-16494	Sequence 16494, A
c 558	199.8	15.4	818128	3	US-09-949-016-14561	Sequence 14561, A	c 631	199.4	15.4	50950	3	US-09-949-016-16659	Sequence 16659, A
c 559	199.8	15.4	818128	3	US-09-949-016-14562	Sequence 14562, A	632	199.4	15.4	60417	3	US-09-949-016-13312	Sequence 13312, A
c 560	199.8	15.4	818128	3	US-09-949-016-14563	Sequence 14563, A	c 633	199.4	15.4	61664	3	US-09-949-016-13308	Sequence 13308, A
c 561	199.8	15.4	818128	3	US-09-949-016-14564	Sequence 14564, A	c 634	199.4	15.4	85675	3	US-09-949-016-12333	Sequence 12333, A
c 562	199.8	15.4	818128	3	US-09-949-016-14565	Sequence 14565, A	c 635	199.4	15.4	85675	3	US-09-949-016-15956	Sequence 15956, A
c 563	199.8	15.4	818128	3	US-09-949-016-14566	Sequence 14566, A	c 636	199.4	15.4	87470	3	US-09-949-016-15881	Sequence 15881, A
c 564	199.6	15.4	601	3	US-09-949-016-163718	Sequence 163718, A	c 637	199.4	15.4	121970	3	US-09-949-016-17216	Sequence 17216, A
c 565	199.6	15.4	16672	3	US-09-949-016-12322	Sequence 12322, A	c 638	199.4	15.4	131332	3	US-09-949-016-15535	Sequence 15535, A
c 566	199.6	15.4	16672	3	US-09-949-016-12880	Sequence 12880, A	639	199.2	15.4	601	3	US-09-949-016-64990	Sequence 64990, A
c 567	199.6	15.4	16672	3	US-09-949-016-13104	Sequence 13104, A	640	199.2	15.4	601	3	US-09-949-016-96453	Sequence 96453, A
c 568	199.6	15.4	16672	3	US-09-949-016-13105	Sequence 13105, A	641	199.2	15.4	601	3	US-09-949-016-96719	Sequence 96719, A
c 569	199.6	15.4	16672	3	US-09-949-016-14818	Sequence 14818, A	642	199.2	15.4	601	3	US-09-949-016-96985	Sequence 96985, A
c 570	199.6	15.4	16672	3	US-09-949-016-14819	Sequence 14819, A	643	199.2	15.4	601	3	US-09-949-016-97251	Sequence 97251, A
c 571	199.6	15.4	28791	3	US-09-949-016-15396	Sequence 15396, A	644	199.2	15.4	601	3	US-09-949-016-97517	Sequence 97517, A
c 572	199.6	15.4	39480	3	US-09-949-016-13634	Sequence 13634, A	645	199.2	15.4	601	3	US-09-949-016-97783	Sequence 97783, A
c 573	199.6	15.4	49315	3	US-09-949-016-13016	Sequence 13016, A	646	199.2	15.4	601	3	US-09-949-016-98049	Sequence 98049, A
c 574	199.6	15.4	53442	3	US-09-949-016-11921	Sequence 11921, A	647	199.2	15.4	601	3	US-09-949-016-98315	Sequence 98315, A
c 575	199.6	15.4	53453	3	US-09-949-016-13370	Sequence 13370, A	648	199.2	15.4	601	3	US-09-949-016-98581	Sequence 98581, A
c 576	199.6	15.4	56326	3	US-09-949-016-16468	Sequence 16468, A	649	199.2	15.4	601	3	US-09-949-016-98847	Sequence 98847, A
c 577	199.6	15.4	88268	3	US-09-949-016-14178	Sequence 14178, A	650	199.2	15.4	601	3	US-09-949-016-99113	Sequence 99113, A
c 578	199.6	15.4	97423	3	US-09-949-016-12742	Sequence 12742, A	651	199.2	15.4	601	3	US-09-949-016-99379	Sequence 99379, A
c 579	199.6	15.4	97424	3	US-09-949-016-15576	Sequence 15576, A	652	199.2	15.4	601	3	US-09-949-016-99645	Sequence 99645, A
c 580	199.6	15.4	97500	3	US-09-798-096-10	Sequence 10, Appl	653	199.2	15.4	601	3	US-09-949-016-99911	Sequence 99911, A
c 581	199.6	15.4	174170	3	US-09-949-016-14810	Sequence 14810, A	654	199.2	15.4	601	3	US-09-949-016-100177	Sequence 100177, A
c 582	199.6	15.4	174170	3	US-09-949-016-14811	Sequence 14811, A	655	199.2	15.4	601	3	US-09-949-016-100443	Sequence 100443, A
c 583	199.6	15.4	174318	3	US-09-949-016-11880	Sequence 11880, A	656	199.2	15.4	601	3	US-09-949-016-100709	Sequence 100709, A
c 584	199.6	15.4	174318	3	US-09-949-016-14812	Sequence 14812, A	657	199.2	15.4	601	3	US-09-949-016-101013	Sequence 101013, A
c 585	199.6	15.4	174318	3	US-09-949-016-14813	Sequence 14813, A	658	199.2	15.4	601	3	US-09-949-016-101279	Sequence 101279, A
c 586	199.6	15.4	187136	3	US-09-949-016-17231	Sequence 17231, A	659	199.2	15.4	601	3	US-09-949-016-101545	Sequence 101545, A
c 587	199.6	15.4	193169	3	US-09-949-016-15091	Sequence 15091, A	660	199.2	15.4	601	3	US-09-949-016-101811	Sequence 101811, A
c 588	199.6	15.4	212449	3	US-09-949-016-15419	Sequence 15419, A	661	199.2	15.4	601	3	US-09-949-016-130177	Sequence 130177, A
c 589	199.6	15.4	227390	3	US-09-949-016-12201	Sequence 12201, A	662	199.2	15.4	601	3	US-09-949-016-136481	Sequence 136481, A
c 590	199.6	15.4	227390	3	US-09-949-016-13365	Sequence 13365, A	663	199.2	15.4	601	3	US-09-949-016-136482	Sequence 136482, A
c 591	199.6	15.4	238815	3	US-09-949-016-16274	Sequence 16274, A	664	199.2	15.4	601	3	US-09-949-016-146876	Sequence 146876, A
c 592	199.4	15.4	601	3	US-09-949-016-34568	Sequence 34568, A	665	199.2	15.4	601	3	US-09-949-016-168341	Sequence 168341, A
c 593	199.4	15.4	601	3	US-09-949-016-96487	Sequence 96487, A	666	199.2	15.4	34328	3	US-09-949-016-14933	Sequence 14933, A
c 594	199.4	15.4	601	3	US-09-949-016-96753	Sequence 96753, A	667	199.2	15.4	36580	3	US-09-949-016-14136	Sequence 14136, A
c 595	199.4	15.4	601	3	US-09-949-016-97019	Sequence 97019, A	668	199.2	15.4	38805	3	US-09-949-016-14932	Sequence 14932, A
c 596	199.4	15.4	601	3	US-09-949-016-97285	Sequence 97285, A	669	199.2	15.4	50368	3	US-09-949-016-13256	Sequence 13256, A
c 597	199.4	15.4	601	3	US-09-949-016-97551	Sequence 97551, A	c 670	199.2	15.4	71278	3	US-09-949-016-11851	Sequence 11851, A
c 598	199.4	15.4	601	3	US-09-949-016-97817	Sequence 97817, A	c 671	199.2	15.4	71278	3	US-09-949-016-17563	Sequence 17563, A
c 599	199.4	15.4	601	3	US-09-949-016-98083	Sequence 98083, A	672	199.2	15.4	76264	3	US-09-949-016-15773	Sequence 15773, A
c 600	199.4	15.4	601	3	US-09-949-016-98349	Sequence 98349, A	673	199.2	15.4	81433	3	US-09-949-016-11941	Sequence 11941, A
c 601	199.4	15.4	601	3	US-09-949-016-98615	Sequence 98615, A	674	199.2	15.4	84227	3	US-09-949-016-17374	Sequence 17374, A
c 602	199.4	15.4	601	3	US-09-949-016-98881	Sequence 98881, A	675	199.2	15.4	104428	3	US-09-949-016-12737	Sequence 12737, A
c 603	199.4	15.4	601	3	US-09-949-016-99147	Sequence 99147, A	676	199.2	15.4	104429	3	US-09-949-016-13814	Sequence 13814, A
c 604	199.4	15.4	601	3	US-09-949-016-99413	Sequence 99413, A	c 677	199.2	15.4	110243	3	US-09-949-016-13698	Sequence 13698, A
c 605	199.4	15.4	601	3	US-09-949-016-99679	Sequence 99679, A	678	199.2	15.4	156698	3	US-09-949-016-16038	Sequence 16038, A
c 606	199.4	15.4	601	3	US-09-949-016-99945	Sequence 99945, A	679	199.2	15.4	168174	3	US-10-071-411A-63	Sequence 63, Appl
c 607	199.4	15.4	601	3	US-09-949-016-100211	Sequence 100211, A	680	199.2	15.4	168273	3	US-10-071-411A-2	Sequence 2, Appl

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683	199.2	15.4	194915	3	US-09-949-016-15584	Sequence 15584, A	C 756	198.4	15.3	320	2	US-08-629-933-5	Sequence 5, Appl1
684	199.2	15.4	247781	3	US-09-949-016-14193	Sequence 14193, A	C 757	198.4	15.3	320	2	US-08-759-873-5	Sequence 5, Appl1
685	199.2	15.4	256171	3	US-09-949-016-12822	Sequence 12822, A	C 758	198.4	15.3	601	3	US-09-949-016-41965	Sequence 41965, A
686	199.2	15.4	256176	3	US-09-949-016-12822	Sequence 12822, A	C 759	198.4	15.3	22206	3	US-09-949-016-13901	Sequence 13901, A
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696	199	15.4	33489	3	US-09-949-016-15620	Sequence 15620, A	C 769	198.2	15.3	346112	3	US-09-949-016-37003	Sequence 37003, A
697	199	15.4	37385	3	US-09-949-002-654	Sequence 654, App	C 770	198.2	15.3	601	3	US-09-949-016-37003	Sequence 37003, A
698	199	15.4	42094	3	US-09-949-016-15354	Sequence 15354, A	C 771	198.2	15.3	601	3	US-09-949-016-46268	Sequence 46268, A
699	199	15.4	45698	5	US-09-949-016-16445	Sequence 16445, A	C 772	198.2	15.3	601	3	US-09-949-016-70230	Sequence 70230, A
700	199	15.4	45913	3	US-08-984-429-344	Sequence 344, App	C 773	198.2	15.3	601	3	US-09-949-016-70291	Sequence 70291, A
701	199	15.4	54711	3	US-09-949-002-655	Sequence 655, App	C 774	198.2	15.3	601	3	US-09-949-016-122240	Sequence 12240, A
702	199	15.4	77618	3	US-09-949-016-17489	Sequence 17489, A	C 775	198.2	15.3	601	3	US-09-949-016-135168	Sequence 135168, A
703	199	15.4	79858	3	US-09-949-016-11768	Sequence 11768, A	C 776	198.2	15.3	601	3	US-09-949-016-140482	Sequence 140482, A
704	199	15.4	81335	3	US-09-949-016-16080	Sequence 16080, A	C 777	198.2	15.3	601	3	US-09-949-016-140483	Sequence 140483, A
705	199	15.4	83707	3	US-09-949-002-709	Sequence 709, App	C 778	198.2	15.3	601	3	US-09-949-016-195150	Sequence 195150, A
706	199	15.4	85894	3	US-09-949-002-595	Sequence 595, App	C 779	198.2	15.3	601	3	US-09-949-002-1244	Sequence 1244, Ap
707	199	15.4	187916	3	US-09-949-016-12908	Sequence 12908, A	C 780	198.2	15.3	601	3	US-09-949-002-8882	Sequence 8882, Ap
708	198.8	15.4	310	5	US-09-949-016-12980	Sequence 12980, A	C 781	198.2	15.3	2817	3	US-10-104-047-1341	Sequence 1341, Ap
709	198.8	15.4	601	3	US-09-984-429-671	Sequence 671, App	C 782	198.2	15.3	5834	5	US-09-984-429-325	Sequence 325, App
710	198.8	15.4	601	3	US-09-949-016-86951	Sequence 86951, A	C 783	198.2	15.3	8534	3	US-09-949-016-14723	Sequence 14723, A
711	198.8	15.4	601	3	US-09-949-016-86951	Sequence 86951, A	C 784	198.2	15.3	10958	3	US-09-949-016-14762	Sequence 14762, A
712	198.8	15.4	2477	3	US-10-104-047-969	Sequence 969, App	C 785	198.2	15.3	10958	3	US-09-949-016-14763	Sequence 14763, A
713	198.8	15.4	21360	3	US-09-949-016-12857	Sequence 12857, A	C 786	198.2	15.3	15615	3	US-09-949-016-17221	Sequence 17221, A
714	198.8	15.4	21361	3	US-09-949-016-16245	Sequence 16245, A	C 787	198.2	15.3	17198	3	US-09-949-016-13776	Sequence 13776, A
715	198.8	15.4	29000	3	US-09-949-016-17	Sequence 17, Appl	C 788	198.2	15.3	21358	3	US-09-973-278-789	Sequence 789, App
716	198.8	15.4	36720	3	US-09-949-016-13476	Sequence 13476, A	C 789	198.2	15.3	21676	3	US-09-973-278-792	Sequence 792, App
717	198.8	15.4	39686	3	US-09-949-016-13633	Sequence 13633, A	C 790	198.2	15.3	26244	3	US-09-949-016-13369	Sequence 13369, A
718	198.8	15.4	49144	3	US-09-949-016-15343	Sequence 15343, A	C 791	198.2	15.3	28257	3	US-09-949-016-13076	Sequence 13076, A
719	198.8	15.4	49487	3	US-09-949-016-11770	Sequence 11770, A	C 792	198.2	15.3	43086	3	US-09-949-016-13059	Sequence 13059, A
720	198.8	15.4	50217	3	US-09-949-016-16067	Sequence 16067, A	C 793	198.2	15.3	51539	3	US-09-949-002-677	Sequence 677, App
721	198.8	15.4	62873	3	US-09-949-016-15676	Sequence 15676, A	C 794	198.2	15.3	51540	3	US-09-949-002-819	Sequence 819, App
722	198.8	15.4	71251	3	US-09-949-016-15332	Sequence 15332, A	C 795	198.2	15.3	63000	3	US-09-780-172-18	Sequence 16473, A
723	198.8	15.4	71879	3	US-09-949-016-17465	Sequence 17465, A	C 796	198.2	15.3	63266	3	US-09-949-016-12011	Sequence 12011, A
724	198.8	15.4	75216	3	US-09-949-016-16061	Sequence 16061, A	C 797	198.2	15.3	78720	3	US-09-949-016-12710	Sequence 12710, A
725	198.8	15.4	250958	3	US-09-949-016-16061	Sequence 16061, A	C 798	198.2	15.3	78720	3	US-09-949-016-12710	Sequence 12710, A
726	198.8	15.4	462589	3	US-09-949-016-12900	Sequence 12900, A	C 799	198.2	15.3	84525	3	US-09-949-016-12830	Sequence 12830, A
727	198.8	15.4	476044	3	US-09-949-016-12412	Sequence 12412, A	C 800	198.2	15.3	109025	3	US-09-949-016-12678	Sequence 12678, A
728	198.6	15.3	509	3	US-09-949-016-12966	Sequence 12966, A	C 801	198.2	15.3	109025	3	US-09-949-016-12609	Sequence 12609, A
729	198.6	15.3	601	3	US-09-949-016-65854	Sequence 65854, A	C 802	198.2	15.3	109025	3	US-09-949-016-17567	Sequence 17567, A
730	198.6	15.3	601	3	US-09-949-016-159210	Sequence 159210, A	C 803	198.2	15.3	134434	3	US-09-949-016-17362	Sequence 17362, A
731	198.6	15.3	11145	3	US-09-949-016-12471	Sequence 12471, A	C 804	198.2	15.3	135010	3	US-09-949-016-17234	Sequence 17234, A
732	198.6	15.3	12840	3	US-09-949-016-15720	Sequence 15720, A	C 805	198.2	15.3	148156	3	US-09-949-016-11776	Sequence 11776, A
733	198.6	15.3	21308	3	US-09-949-002-584	Sequence 584, App	C 806	198.2	15.3	173791	3	US-09-949-016-12542	Sequence 12542, A
734	198.6	15.3	21407	3	US-09-949-002-784	Sequence 784, App	C 807	198.2	15.3	173791	3	US-09-949-016-17302	Sequence 17302, A
735	198.6	15.3	25951	3	US-08-949-016-16194	Sequence 16194, App	C 808	198.2	15.3	276687	3	US-09-949-016-13840	Sequence 13840, A
736	198.6	15.3	37215	3	US-09-949-016-15326	Sequence 15326, A	C 809	198	15.3	601	3	US-09-949-016-23347	Sequence 23347, A
737	198.6	15.3	38374	4	US-09-949-016-15326	Sequence 15326, A	C 810	198	15.3	601	3	US-09-949-016-34646	Sequence 34646, A
738	198.6	15.3	43463	3	US-09-949-016-16341	Sequence 16341, A	C 811	198	15.3	601	3	US-09-949-016-94044	Sequence 94044, A
739	198.6	15.3	44789	3	US-09-949-016-13909	Sequence 13909, A	C 812	198	15.3	601	3	US-09-949-016-145453	Sequence 145453, A
740	198.6	15.3	50622	3	US-09-949-016-13809	Sequence 13809, A	C 813	198	15.3	601	3	US-09-949-016-145454	Sequence 145454, A
741	198.6	15.3	54711	3	US-09-949-016-17489	Sequence 17489, A	C 814	198	15.3	601	3	US-09-949-016-155144	Sequence 155144, A
742	198.6	15.3	55328	3	US-09-949-016-12747	Sequence 12747, A	C 815	198	15.3	601	3	US-09-949-016-159123	Sequence 159123, A
743	198.6	15.3	55330	3	US-09-949-016-17146	Sequence 17146, A	C 816	198	15.3	601	3	US-09-949-016-16084	Sequence 16084, A
744	198.6	15.3	60194	3	US-09-949-002-656	Sequence 656, App	C 817	198	15.3	601	3	US-09-949-016-170260	Sequence 170260, A
745	198.6	15.3	60195	3	US-09-949-002-697	Sequence 697, App	C 818	198	15.3	190599	3	US-09-949-016-175478	Sequence 175478, A
746	198.6	15.3	71815	3	US-09-949-016-12501	Sequence 12501, A	C 819	198	15.3	190599	3	US-09-949-016-13061	Sequence 13061, A
747	198.6	15.3	72128	3	US-09-949-016-16018	Sequence 16018, A	C 820	198	15.3	19577	3	US-09-949-016-17427	Sequence 17427, A
748	198.6	15.3	81927	3	US-09-949-016-15623	Sequence 15623, A	C 821	198	15.3	20316	3	US-09-949-016-14360	Sequence 14360, A
749	198.6	15.3	108310	3	US-09-949-016-16366	Sequence 16366, A	C 822	198	15.3	23108	3	US-09-949-016-13659	Sequence 13659, A
750	198.6	15.3	146428	3	US-09-949-016-12620	Sequence 12620, A	C 823	198	15.3	23533	3	US-09-949-016-12582	Sequence 12582, A
751	198.6	15.3	146438	3	US-09-949-016-12081	Sequence 12081, A	C 824	198	15.3	30851	3	US-09-949-016-15377	Sequence 15377, A
752	198.6	15.3	192956	3	US-09-949-016-14382	Sequence 14382, A	C 825	198	15.3	32010	3	US-09-949-016-17418	Sequence 17418, A
753	198.6	15.3	237241	3	US-09-949-016-16101	Sequence 16101, A	C 826	198	15.3	33885	3	US-09-949-016-13127	Sequence 13127, A
												US-09-949-016-16081	Sequence 16081, A

c 827	198	15.3	37297	3	US-09-949-016-12133	Sequence 12133, A	900	197.6	15.3	76164	3	US-09-949-016-12288	Sequence 12288, A
c 828	198	15.3	42450	3	US-09-815-048-3	Sequence 3, Appl1	901	197.6	15.3	76165	3	US-09-949-016-16003	Sequence 14005, A
c 829	198	15.3	52502	3	US-09-949-016-12150	Sequence 12150, A	c 902	197.6	15.3	82612	3	US-09-949-016-16823	Sequence 16823, A
c 830	198	15.3	52522	3	US-09-949-016-15374	Sequence 15374, A	903	197.6	15.3	83851	3	US-09-949-016-13847	Sequence 13847, A
c 831	198	15.3	83450	3	US-09-949-016-15848	Sequence 15848, A	c 904	197.6	15.3	84252	3	US-09-949-016-17315	Sequence 17315, A
c 832	198	15.3	107827	3	US-09-949-016-15790	Sequence 15790, A	905	197.6	15.3	93493	3	US-09-949-016-12063	Sequence 12063, A
c 833	198	15.3	132150	3	US-09-949-016-17398	Sequence 17398, A	906	197.6	15.3	95020	3	US-09-949-016-13272	Sequence 13272, A
c 834	198	15.3	132577	3	US-09-949-016-12879	Sequence 12879, A	907	197.6	15.3	129127	3	US-09-949-016-13481	Sequence 13481, A
c 835	198	15.3	173992	3	US-09-949-016-13379	Sequence 13379, A	908	197.6	15.3	145287	3	US-09-949-016-13530	Sequence 13530, A
c 836	198	15.3	201529	3	US-09-949-016-12740	Sequence 12740, A	909	197.6	15.3	145287	3	US-09-949-016-13531	Sequence 13531, A
c 837	198	15.3	254366	3	US-08-822-871-3	Sequence 3, Appl1	c 910	197.6	15.3	125254	3	US-08-949-016-12683	Sequence 12683, A
c 838	197.8	15.3	601	3	US-09-949-016-46056	Sequence 46056, A	c 911	197.6	15.3	125254	3	US-09-949-016-13194	Sequence 13194, A
c 839	197.8	15.3	601	3	US-09-949-016-52871	Sequence 52871, A	912	197.6	15.3	187169	3	US-09-949-016-12776	Sequence 12776, A
c 840	197.8	15.3	601	3	US-09-949-016-128356	Sequence 128356, A	913	197.6	15.3	190078	3	US-09-949-016-12707	Sequence 12707, A
c 841	197.8	15.3	601	3	US-09-949-016-146465	Sequence 146465, A	914	197.6	15.3	190078	3	US-09-949-016-17026	Sequence 17026, A
c 842	197.8	15.3	601	3	US-09-949-016-167238	Sequence 167238, A	915	197.6	15.3	191569	3	US-09-949-016-15940	Sequence 15940, A
c 843	197.8	15.3	601	3	US-08-949-016-196192	Sequence 196192, A	c 916	197.6	15.3	30890	3	US-09-949-016-14720	Sequence 14720, A
c 844	197.8	15.3	601	3	US-09-949-016-206339	Sequence 206339, A	c 917	197.6	15.3	451924	3	US-09-949-016-12896	Sequence 12896, A
c 845	197.8	15.3	2400	3	US-10-104-047-1927	Sequence 1927, Ap	c 918	197.6	15.3	451925	3	US-09-949-016-17305	Sequence 17305, A
c 846	197.8	15.3	8909	3	US-09-949-016-13348	Sequence 13348, A	919	197.4	15.2	601	3	US-09-949-016-56992	Sequence 56992, A
c 847	197.8	15.3	22400	3	US-10-143-266-1	Sequence 1, Appl1	c 920	197.4	15.2	601	3	US-09-949-016-115156	Sequence 115156, A
c 848	197.8	15.3	24415	3	US-09-949-016-15855	Sequence 15855, A	921	197.4	15.2	601	3	US-09-949-016-123834	Sequence 123834, A
c 849	197.8	15.3	24942	3	US-08-949-016-13318	Sequence 13318, A	c 922	197.4	15.2	601	3	US-09-949-016-138588	Sequence 138588, A
c 850	197.8	15.3	36759	3	US-09-949-016-12216	Sequence 12216, A	c 923	197.4	15.2	601	3	US-09-949-016-145744	Sequence 145744, A
c 851	197.8	15.3	36760	3	US-09-949-016-14021	Sequence 14021, A	c 924	197.4	15.2	601	3	US-09-949-016-146012	Sequence 146012, A
c 852	197.8	15.3	44019	3	US-09-949-016-14902	Sequence 14902, A	c 925	197.4	15.2	601	3	US-09-949-016-146280	Sequence 146280, A
c 853	197.8	15.3	49848	3	US-09-949-016-15675	Sequence 15675, A	c 926	197.4	15.2	601	3	US-09-949-016-146464	Sequence 146464, A
c 854	197.8	15.3	50229	3	US-09-949-016-15499	Sequence 15499, A	927	197.4	15.2	601	3	US-09-949-016-168474	Sequence 168474, A
c 855	197.8	15.3	51620	3	US-09-949-016-12848	Sequence 12848, A	928	197.4	15.2	601	3	US-09-949-016-168522	Sequence 168522, A
c 856	197.8	15.3	51621	3	US-09-949-016-16503	Sequence 16503, A	929	197.4	15.2	601	3	US-09-949-016-168570	Sequence 168570, A
c 857	197.8	15.3	58397	3	US-09-949-016-14469	Sequence 14469, A	930	197.4	15.2	601	3	US-09-949-016-168867	Sequence 168867, A
c 858	197.8	15.3	74804	3	US-09-949-016-15118	Sequence 15118, A	931	197.4	15.2	601	3	US-09-949-016-171183	Sequence 171183, A
c 859	197.8	15.3	75799	3	US-09-949-016-15231	Sequence 15231, A	932	197.4	15.2	601	3	US-09-949-016-171313	Sequence 171313, A
c 860	197.8	15.3	77626	3	US-08-949-016-12608	Sequence 12608, A	933	197.4	15.2	601	3	US-09-949-016-189347	Sequence 189347, A
c 861	197.8	15.3	93493	3	US-09-949-016-12063	Sequence 12063, A	934	197.4	15.2	601	3	US-09-949-016-193085	Sequence 193085, A
c 862	197.8	15.3	95020	3	US-09-949-016-13272	Sequence 13272, A	935	197.4	15.2	601	3	US-09-949-016-193178	Sequence 193178, A
c 863	197.8	15.3	112507	3	US-09-949-016-12420	Sequence 12420, A	936	197.4	15.2	601	3	US-09-949-016-193271	Sequence 193271, A
c 864	197.8	15.3	112507	3	US-09-949-016-12794	Sequence 12794, A	937	197.4	15.2	601	3	US-09-949-016-193364	Sequence 193364, A
c 865	197.8	15.3	112508	3	US-09-949-016-16589	Sequence 16589, A	938	197.4	15.2	601	3	US-09-949-002-2468	Sequence 2468, Ap
c 866	197.8	15.3	112508	3	US-09-949-016-16590	Sequence 16590, A	939	197.4	15.2	601	3	US-09-949-002-5101	Sequence 5101, Ap
c 867	197.8	15.3	14793	3	US-10-148-806-3	Sequence 3, Appl1	c 940	197.4	15.2	700	3	US-09-735-271-344	Sequence 344, App
c 868	197.8	15.3	121384	3	US-09-949-016-16944	Sequence 16944, A	941	197.4	15.2	12690	3	US-09-949-016-13799	Sequence 13799, A
c 869	197.8	15.3	135030	3	US-09-949-016-14896	Sequence 14896, A	942	197.4	15.2	15849	3	US-09-054-272-50	Sequence 50, Appl1
c 870	197.8	15.3	161124	3	US-09-949-016-11760	Sequence 11760, A	943	197.4	15.2	15849	4	US-09-880-107-2362	Sequence 2362, Ap
c 871	197.8	15.3	193169	3	US-09-949-016-15091	Sequence 15091, A	c 944	197.4	15.2	20441	3	US-09-949-016-13052	Sequence 13052, A
c 872	197.6	15.3	601	3	US-09-949-016-48015	Sequence 48015, A	945	197.4	15.2	29615	3	US-09-949-016-14590	Sequence 14590, A
c 873	197.6	15.3	601	3	US-09-949-016-51670	Sequence 51670, A	946	197.4	15.2	29742	3	US-09-949-016-15650	Sequence 15650, A
c 874	197.6	15.3	601	3	US-09-949-016-56264	Sequence 56264, A	c 947	197.4	15.2	46626	3	US-09-949-016-13390	Sequence 13390, A
c 875	197.6	15.3	601	3	US-09-949-016-83152	Sequence 83152, A	c 948	197.4	15.2	57638	3	US-09-949-016-17000	Sequence 17000, A
c 876	197.6	15.3	601	3	US-09-949-016-83244	Sequence 83244, A	949	197.4	15.2	62804	3	US-09-800-960-3	Sequence 3, Appl1
c 877	197.6	15.3	601	3	US-09-949-016-103424	Sequence 103424, A	950	197.4	15.2	62804	3	US-10-096-960-3	Sequence 3, Appl1
c 878	197.6	15.3	601	3	US-09-949-016-115352	Sequence 115352, A	951	197.4	15.2	78846	3	US-09-949-016-12396	Sequence 12396, A
c 879	197.6	15.3	601	3	US-09-949-016-135170	Sequence 135170, A	952	197.4	15.2	78846	3	US-09-949-016-12791	Sequence 12791, A
c 880	197.6	15.3	601	3	US-09-949-016-174706	Sequence 174706, A	953	197.4	15.2	78846	3	US-09-949-016-12792	Sequence 12792, A
c 881	197.6	15.3	601	3	US-09-949-002-5384	Sequence 5384, Ap	954	197.4	15.2	78846	3	US-09-949-016-12793	Sequence 12793, A
c 882	197.6	15.3	18955	3	US-09-949-016-13343	Sequence 13343, A	955	197.4	15.2	78850	3	US-09-949-016-16013	Sequence 16013, A
c 883	197.6	15.3	19791	3	US-09-949-016-14607	Sequence 14607, A	956	197.4	15.2	78850	3	US-09-949-016-16014	Sequence 16014, A
c 884	197.6	15.3	23015	3	US-09-949-002-726	Sequence 726, App	957	197.4	15.2	78850	3	US-09-949-016-16015	Sequence 16015, A
c 885	197.6	15.3	27160	3	US-09-949-016-17378	Sequence 17378, A	958	197.4	15.2	78850	3	US-09-949-016-16016	Sequence 16016, A
c 886	197.6	15.3	30678	3	US-09-949-016-12818	Sequence 12818, A	959	197.4	15.2	78850	3	US-09-949-016-16201	Sequence 16201, A
c 887	197.6	15.3	30973	3	US-09-949-016-11971	Sequence 11971, A	960	197.4	15.2	78850	3	US-09-949-016-16202	Sequence 16202, A
c 888	197.6	15.3	30974	3	US-09-949-016-16628	Sequence 16628, A	961	197.4	15.2	78850	3	US-09-949-016-16203	Sequence 16203, A
c 889	197.6	15.3	34725	3	US-09-949-016-15797	Sequence 15797, A	962	197.4	15.2	78850	3	US-09-949-016-16204	Sequence 16204, A
c 890	197.6	15.3	34765	3	US-09-949-016-12808	Sequence 12808, A	963	197.4	15.2	78850	3	US-09-949-016-17547	Sequence 17547, A
c 891	197.6	15.3	38969	3	US-09-949-016-14051	Sequence 14051, A	964	197.4	15.2	92074	3	US-09-949-016-17163	Sequence 17163, A
c 892	197.6	15.3	42954	3	US-09-949-016-17123	Sequence 17123, A	c 965	197.4	15.2	93364	3	US-09-949-016-14890	Sequence 14890, A
c 893	197.6	15.3	42954	3	US-09-949-016-17124	Sequence 17124, A	c 966	197.4	15.2	120609	3	US-09-949-016-14890	Sequence 14890, A
c 894	197.6	15.3	47115	3	US-09-949-016-12278	Sequence 12278, A	c 967	197.4	15.2	152019	3	US-09-949-016-13915	Sequence 13915, A
c 895	197.6	15.3	47122	3	US-08-949-016-16520	Sequence 16520, A	c 968	197.4	15.2	163022	3	US-09-949-016-16029	Sequence 16029, A
c 896	197.6	15.3	47284	3	US-09-949-016-17029	Sequence 17029, A	c 969	197.4	15.2	166698	3	US-09-949-016-16038	Sequence 16038, A
c 897	197.6	15.3	58133	3	US-09-949-016-16464	Sequence 16464, A	c 970	197.4	15.2	166698	3	US-09-949-016-14172	Sequence 14172, A
c 898	197.6	15.3	64319	3	US-09-949-016-12804	Sequence 12804, A	c 971	197.4	15.2	219964	3	US-09-949-016-15086	Sequence 15086, A
c 899	197.6	15.3	73295	3	US-09-949-016-15151	Sequence 15151, A	972	197.4	15.2	395136	3	US-09-949-016-16073	Sequence 16073, A

c 973	197.2	15.2	601	3	US-09-949-016-47134	Sequence 47134, A	1046	197	15.2	161607	3	US-09-949-016-12210	Sequence 12210, A
974	197.2	15.2	601	3	US-09-949-016-103423	Sequence 103423, A	c1047	197	15.2	197336	3	US-09-949-016-12881	Sequence 12881, A
c 975	197.2	15.2	601	3	US-09-949-016-109555	Sequence 109555, A	c1048	197	15.2	197337	3	US-09-949-016-14376	Sequence 14376, A
c 976	197.2	15.2	601	3	US-09-949-016-145741	Sequence 145741, A	c1049	197	15.2	197337	3	US-09-949-002-738	Sequence 738, App
c 977	197.2	15.2	601	3	US-09-949-016-146009	Sequence 146009, A	c1050	197	15.2	209210	3	US-09-949-016-15094	Sequence 15094, A
c 978	197.2	15.2	601	3	US-09-949-016-146277	Sequence 146277, A	c1051	197	15.2	234287	3	US-09-949-002-687	Sequence 687, App
979	197.2	15.2	601	3	US-09-949-016-177754	Sequence 177754, A	c1052	197	15.2	234287	3	US-09-949-016-17272	Sequence 17272, A
c 980	197.2	15.2	601	3	US-09-949-016-179930	Sequence 179930, A	c1053	197	15.2	234288	3	US-09-949-002-841	Sequence 841, App
c 981	197.2	15.2	601	3	US-09-949-016-206619	Sequence 206619, A	c1054	197	15.2	237326	5	US-08-852-495C-2	Sequence 2, Appli
c 982	197.2	15.2	601	3	US-09-949-016-206620	Sequence 206620, A	c1055	197	15.2	316068	3	US-09-949-016-113173	Sequence 13173, A
c 983	197.2	15.2	601	3	US-09-949-002-5385	Sequence 5385, App	c1056	197	15.2	360470	3	US-09-949-016-16923	Sequence 16923, A
c 984	197.2	15.2	1834	3	US-08-836-7348-3	Sequence 3, Appli	c1057	197	15.2	390416	3	US-09-949-016-14033	Sequence 14033, A
c 985	197.2	15.2	11437	3	US-09-949-002-587	Sequence 587, App	c1058	197	15.2	784019	3	US-09-949-016-14033	Sequence 12777, A
986	197.2	15.2	11589	3	US-09-949-002-826	Sequence 826, App	c1059	197	15.2	828152	3	US-09-949-016-12777	Sequence 67120, A
c 987	197.2	15.2	11730	3	US-09-949-016-14991	Sequence 14991, A	c1060	196.8	15.2	601	3	US-09-949-016-67120	Sequence 82345, A
c 988	197.2	15.2	18264	3	US-09-949-016-13030	Sequence 13030, A	c1061	196.8	15.2	601	3	US-09-949-016-82315	Sequence 142801, A
c 989	197.2	15.2	30364	3	US-09-949-016-15620	Sequence 15620, A	c1062	196.8	15.2	601	3	US-09-949-016-142801	Sequence 187485, A
c 990	197.2	15.2	31469	3	US-09-949-016-13722	Sequence 13722, A	c1063	196.8	15.2	601	3	US-09-949-016-187485	Sequence 8905, App
c 991	197.2	15.2	37155	3	US-09-949-016-16945	Sequence 16945, A	c1064	196.8	15.2	601	3	US-09-949-002-8905	Sequence 8, Appli
c 992	197.2	15.2	37412	3	US-09-949-016-17566	Sequence 17566, A	c1065	196.8	15.2	5426	3	US-09-949-016-13931	Sequence 13931, A
c 993	197.2	15.2	58782	3	US-09-949-016-17851	Sequence 17851, A	c1066	196.8	15.2	15415	3	US-09-949-016-13932	Sequence 13932, A
c 994	197.2	15.2	60593	3	US-09-949-016-13779	Sequence 13779, A	c1067	196.8	15.2	15415	3	US-09-949-016-16211	Sequence 16211, A
c 995	197.2	15.2	71863	3	US-09-949-016-15112	Sequence 15112, A	c1068	196.8	15.2	16056	3	US-09-949-016-16212	Sequence 16212, A
c 996	197.2	15.2	71863	3	US-09-949-016-15112	Sequence 15112, A	c1069	196.8	15.2	16056	3	US-09-949-016-16212	Sequence 15361, A
c 997	197.2	15.2	76610	3	US-09-949-016-15521	Sequence 15521, A	c1070	196.8	15.2	17132	2	US-07-906-871-15	Sequence 15, Appli
c 998	197.2	15.2	106256	3	US-09-949-016-16858	Sequence 16858, A	c1071	196.8	15.2	17327	2	US-09-949-016-1438	Sequence 12438, A
c 999	197.2	15.2	209631	3	US-09-949-002-574	Sequence 574, App	c1072	196.8	15.2	24150	3	US-09-949-016-12438	Sequence 18, Appli
c 1000	197.2	15.2	209632	3	US-09-949-002-802	Sequence 802, App	c1073	196.8	15.2	27377	3	US-09-949-016-17107	Sequence 12710, A
c1001	197.2	15.2	209632	3	US-09-949-002-802	Sequence 802, App	c1074	196.8	15.2	41454	3	US-09-949-016-12271	Sequence 12271, A
c1002	197.2	15.2	209632	3	US-09-949-016-13506	Sequence 13506, A	c1075	196.8	15.2	47471	3	US-09-949-016-12271	Sequence 12598, A
c1003	197.2	15.2	283538	3	US-09-949-016-12008	Sequence 12008, A	c1076	196.8	15.2	47555	3	US-09-949-016-16549	Sequence 12598, A
c1004	197.2	15.2	331814	3	US-09-949-016-17056	Sequence 17056, A	c1077	196.8	15.2	49673	3	US-09-949-016-13598	Sequence 14868, A
c1005	197.2	15.2	331814	3	US-09-949-016-17056	Sequence 17056, A	c1078	196.8	15.2	52874	3	US-09-949-016-14868	Sequence 837, App
1006	197	15.2	601	3	US-09-949-016-18350	Sequence 18350, A	c1079	196.8	15.2	54286	3	US-09-949-002-837	Sequence 15594, A
1007	197	15.2	601	3	US-09-949-016-22191	Sequence 22191, A	c1080	196.8	15.2	59948	3	US-09-949-016-15594	Sequence 642, App
1008	197	15.2	601	3	US-09-949-016-56993	Sequence 56993, A	c1081	196.8	15.2	66955	3	US-09-949-016-12467	Sequence 12467, A
1009	197	15.2	601	3	US-09-949-016-58013	Sequence 58013, A	c1082	196.8	15.2	79350	3	US-09-949-016-12467	Sequence 16275, A
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c1011	197	15.2	601	3	US-09-949-016-115157	Sequence 115157, A	c1084	196.8	15.2	79988	3	US-09-949-016-12274	Sequence 16254, A
1012	197	15.2	601	3	US-09-949-016-127884	Sequence 127884, A	c1085	196.8	15.2	79988	3	US-09-949-016-12274	Sequence 15777, A
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1014	197	15.2	601	3	US-09-949-016-186577	Sequence 186577, A	c1087	196.8	15.2	86947	3	US-09-949-016-11930	Sequence 12005, A
1015	197	15.2	601	3	US-09-949-016-195549	Sequence 195549, A	c1088	196.8	15.2	101894	3	US-09-949-016-12005	Sequence 14450, A
1016	197	15.2	14305	3	US-09-949-016-15348	Sequence 15348, A	c1089	196.8	15.2	103894	3	US-09-949-016-14450	Sequence 13427, A
c1017	197	15.2	16082	3	US-09-949-016-16220	Sequence 16220, A	c1090	196.8	15.2	110385	3	US-09-949-016-13427	Sequence 16976, A
c1018	197	15.2	16871	3	US-09-949-016-12718	Sequence 12718, A	c1091	196.8	15.2	113283	3	US-09-949-016-16977	Sequence 16977, A
1019	197	15.2	16874	3	US-09-949-016-15176	Sequence 15176, A	c1092	196.8	15.2	113283	3	US-09-949-016-16977	Sequence 12537, A
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c1021	197	15.2	17743	3	US-09-949-016-17293	Sequence 17293, A	c1094	196.8	15.2	130724	3	US-09-949-016-16192	Sequence 16192, A
c1022	197	15.2	18396	3	US-09-949-002-763	Sequence 763, App	c1095	196.8	15.2	165841	3	US-09-949-016-16192	Sequence 16192, A
c1023	197	15.2	18595	3	US-09-949-016-11779	Sequence 11779, A	c1096	196.8	15.2	165841	3	US-09-949-016-16192	Sequence 15546, A
1024	197	15.2	37116	3	US-09-949-016-11996	Sequence 11996, A	c1097	196.8	15.2	187595	3	US-09-949-016-15546	Sequence 15868, A
1025	197	15.2	37117	3	US-09-949-016-14262	Sequence 14262, A	c1098	196.8	15.2	374159	3	US-09-949-016-15868	Sequence 18349, A
c1026	197	15.2	47677	3	US-09-949-002-668	Sequence 668, App	c1099	196.6	15.2	601	3	US-09-949-016-18349	Sequence 23223, A
1027	197	15.2	57331	3	US-09-949-016-17277	Sequence 17277, A	c1100	196.6	15.2	601	3	US-09-949-016-23223	Sequence 32540, A
1028	197	15.2	76563	3	US-09-949-016-17099	Sequence 17099, A	c1101	196.6	15.2	601	3	US-09-949-016-32540	Sequence 88813, A
c1030	197	15.2	78269	3	US-09-949-016-12497	Sequence 12497, A	c1102	196.6	15.2	601	3	US-09-949-016-88813	Sequence 91548, A
c1031	197	15.2	81001	3	US-09-750-580-1	Sequence 1, Appli	c1103	196.6	15.2	601	3	US-09-949-016-91548	Sequence 128222, A
c1032	197	15.2	84571	3	US-09-949-016-17420	Sequence 17420, A	c1104	196.6	15.2	601	3	US-09-949-016-127885	Sequence 128222, A
c1033	197	15.2	96074	3	US-09-949-016-12761	Sequence 12760, A	c1105	196.6	15.2	601	3	US-09-949-016-140618	Sequence 140618, A
1034	197	15.2	105210	3	US-09-949-016-13511	Sequence 13511, A	c1106	196.6	15.2	601	3	US-09-949-016-140618	Sequence 179611, A
c1035	197	15.2	106199	3	US-09-949-016-14158	Sequence 14158, A	c1107	196.6	15.2	601	3	US-09-949-016-179611	Sequence 179612, A
1036	197	15.2	107980	3	US-09-949-016-12393	Sequence 12393, A	c1108	196.6	15.2	601	3	US-09-949-016-179612	Sequence 187461, A
c1037	197	15.2	107980	3	US-09-949-016-14370	Sequence 14370, A	c1109	196.6	15.2	601	3	US-09-949-016-187461	Sequence 191414, A
1038	197	15.2	107980	3	US-09-949-016-14370	Sequence 14370, A	c1110	196.6	15.2	601	3	US-09-949-016-191414	Sequence 195548, A
c1039	197	15.2	112114	3	US-09-949-016-17292	Sequence 17292, A	c1111	196.6	15.2	601	3	US-09-949-016-195548	Sequence 195548, A
c1040	197	15.2	118067	3	US-08-497-855A-32	Sequence 32, Appli	c1112	196.6	15.2	601	3	US-09-949-002-6962	Sequence 6962, App
c1041	197	15.2	118382	3	US-09-949-016-15396	Sequence 15396, A	c1113	196.6	15.2	11111	3	US-09-949-016-14960	Sequence 14960, A
1042	197	15.2	132871	3	US-09-949-016-15997	Sequence 15997, A	c1114	196.6	15.2	17972	3	US-09-949-016-17214	Sequence 17214, A
1043	197	15.2	132871	3	US-09-949-016-13863	Sequence 13863, A	c1115	196.6	15.2	19762	3	US-09-949-016-14236	Sequence 14236, A
1044	197	15.2	154605	3	US-09-949-016-16240	Sequence 16240, A	c1116	196.6	15.2	21164	3	US-09-949-016-12814	Sequence 12814, A
1045	197	15.2	154605	3	US-09-949-016-11894	Sequence 11894, A	c1117	196.6	15.2	21164	3	US-09-949-016-16457	Sequence 16457, A
	197	15.2	156324	3	US-09-949-016-13749	Sequence 13749, A	c1118	196.6	15.2	25131	3	US-09-949-016-12385	Sequence 12385, A

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1120	196.6	15.2	26423	3	US-09-949-016-15459	Sequence 15459, A	1193	196.4	15.2	62354	3	US-09-949-016-16188	Sequence 16188, A
cl1121	196.6	15.2	17412	3	US-09-949-016-17025	Sequence 17025, A	1194	196.4	15.2	66988	3	US-09-949-016-11942	Sequence 11942, A
1122	196.6	15.2	27923	3	US-09-949-016-13371	Sequence 13371, A	1195	196.4	15.2	66989	3	US-09-949-016-16063	Sequence 16063, A
cl1123	196.6	15.2	22067	3	US-09-949-016-12535	Sequence 12535, A	1196	196.4	15.2	68778	3	US-09-949-016-16406	Sequence 16406, A
cl1124	196.6	15.2	23093	3	US-09-949-016-17476	Sequence 17476, A	cl1197	196.4	15.2	74545	3	US-09-949-002-606	Sequence 606, App
cl1125	196.6	15.2	26886	3	US-09-949-016-16379	Sequence 16379, A	1198	196.4	15.2	83462	3	US-09-949-016-15116	Sequence 15116, A
cl1126	196.6	15.2	36899	3	US-09-949-016-13566	Sequence 13566, A	1199	196.4	15.2	85963	3	US-09-949-016-13804	Sequence 13804, A
1127	196.6	15.2	47787	3	US-09-949-016-11969	Sequence 11969, A	cl1200	196.4	15.2	96739	3	US-09-949-016-15606	Sequence 15606, A
cl1128	196.6	15.2	48691	3	US-09-949-016-16308	Sequence 16308, A	cl1201	196.4	15.2	97195	3	US-09-949-016-12212	Sequence 12212, A
cl1129	196.6	15.2	53140	3	US-09-949-016-16023	Sequence 16023, A	cl1202	196.4	15.2	97196	3	US-09-949-016-16971	Sequence 16971, A
1130	196.6	15.2	65424	3	US-09-949-016-12426	Sequence 12426, A	1203	196.4	15.2	106315	3	US-09-949-016-16613	Sequence 16613, A
cl1131	196.6	15.2	67620	3	US-09-949-016-16939	Sequence 16939, A	cl1204	196.4	15.2	108060	3	US-09-949-016-13159	Sequence 13159, A
1132	196.6	15.2	75395	3	Sequence 3, Appl1	Sequence 3, Appl1	cl1205	196.4	15.2	121234	3	US-09-949-016-14142	Sequence 14142, A
cl1133	196.6	15.2	75395	3	US-10-274-194-3	Sequence 3, Appl1	cl1206	196.4	15.2	131860	3	US-09-949-002-730	Sequence 730, App
1134	196.6	15.2	75395	3	US-10-760-407-3	Sequence 3, Appl1	1207	196.4	15.2	137000	3	US-10-172-911-11	Sequence 11, Appl
1135	196.6	15.2	76221	3	US-09-949-016-12009	Sequence 12009, A	cl1208	196.4	15.2	140315	3	US-09-949-016-14141	Sequence 14141, A
1136	196.6	15.2	76221	3	US-09-949-016-17053	Sequence 17053, A	cl1209	196.4	15.2	146095	3	US-09-949-016-12872	Sequence 12872, A
cl1137	196.6	15.2	78846	3	US-09-949-016-12396	Sequence 12396, A	cl1210	196.4	15.2	146104	3	US-09-949-016-13239	Sequence 13239, A
cl1138	196.6	15.2	78846	3	US-09-949-016-12791	Sequence 12791, A	cl1211	196.4	15.2	150032	3	US-09-949-016-14321	Sequence 14321, A
cl1139	196.6	15.2	78846	3	US-09-949-016-12792	Sequence 12792, A	cl1212	196.4	15.2	232024	3	US-09-949-016-13477	Sequence 13477, A
cl1140	196.6	15.2	78846	3	US-09-949-016-12793	Sequence 12793, A	cl1213	196.4	15.2	236474	3	US-09-949-016-13418	Sequence 13418, A
cl1141	196.6	15.2	78850	3	US-09-949-016-16013	Sequence 16013, A	cl1214	196.4	15.2	237863	3	US-09-949-016-13404	Sequence 13404, A
cl1142	196.6	15.2	78850	3	US-09-949-016-16014	Sequence 16014, A	1215	196.2	15.2	601	3	US-09-949-016-128355	Sequence 128355, A
cl1143	196.6	15.2	78850	3	US-09-949-016-16015	Sequence 16015, A	1216	196.2	15.2	601	3	US-09-949-016-128271	Sequence 128271, A
cl1144	196.6	15.2	78850	3	US-09-949-016-16016	Sequence 16016, A	1217	196.2	15.2	601	3	US-09-949-016-129342	Sequence 129342, A
cl1145	196.6	15.2	78850	3	US-09-949-016-16201	Sequence 16201, A	1218	196.2	15.2	601	3	US-09-949-016-129413	Sequence 129413, A
cl1146	196.6	15.2	78850	3	US-09-949-016-16202	Sequence 16202, A	1219	196.2	15.2	601	3	US-09-949-016-129484	Sequence 129484, A
cl1147	196.6	15.2	78850	3	US-09-949-016-16203	Sequence 16203, A	1220	196.2	15.2	601	3	US-09-949-016-129555	Sequence 129555, A
cl1148	196.6	15.2	78850	3	US-09-949-016-16204	Sequence 16204, A	1221	196.2	15.2	601	3	US-09-949-016-129626	Sequence 129626, A
cl1149	196.6	15.2	83516	3	US-09-949-016-15378	Sequence 15378, A	1222	196.2	15.2	601	3	US-09-949-016-129697	Sequence 129697, A
cl1150	196.6	15.2	110096	4	US-09-880-107-1542	Sequence 1542, Ap	1223	196.2	15.2	601	3	US-09-949-016-129768	Sequence 129768, A
cl1151	196.6	15.2	113042	3	US-09-949-016-12343	Sequence 12343, A	1224	196.2	15.2	601	3	US-09-949-016-129839	Sequence 129839, A
cl1152	196.6	15.2	113042	3	US-09-949-016-15246	Sequence 15246, A	1225	196.2	15.2	601	3	US-09-949-016-129910	Sequence 129910, A
cl1153	196.6	15.2	145287	3	US-09-949-016-13530	Sequence 13530, A	1226	196.2	15.2	601	3	US-09-949-016-129981	Sequence 129981, A
cl1154	196.6	15.2	145287	3	US-09-949-016-13531	Sequence 13531, A	1227	196.2	15.2	601	3	US-09-949-016-130052	Sequence 130052, A
1155	196.6	15.2	193303	3	US-09-497-855A-37	Sequence 37, Appl1	1228	196.2	15.2	601	3	US-09-949-016-131905	Sequence 131905, A
1156	196.6	15.2	193303	3	US-09-497-855A-44	Sequence 44, Appl1	1229	196.2	15.2	601	3	US-09-949-016-152069	Sequence 152069, A
1157	196.6	15.2	247299	3	US-09-949-016-17590	Sequence 17590, A	1230	196.2	15.2	601	3	US-09-949-016-152069	Sequence 152069, A
cl1158	196.6	15.2	264358	3	US-09-949-016-15725	Sequence 15725, A	1231	196.2	15.2	601	3	US-09-949-016-152142	Sequence 152142, A
cl1159	196.6	15.2	294836	3	US-09-949-016-15974	Sequence 15974, A	1232	196.2	15.2	601	3	US-09-949-016-152288	Sequence 152288, A
1160	196.6	15.2	319608	3	US-09-539-333D-1	Sequence 1, Appl1	1233	196.2	15.2	601	3	US-09-949-016-159374	Sequence 159374, A
cl1161	196.6	15.2	363032	3	US-09-949-016-12415	Sequence 12415, A	1234	196.2	15.2	601	3	US-09-949-016-159447	Sequence 159447, A
cl1162	196.6	15.2	363032	3	US-09-949-016-15754	Sequence 15754, A	1235	196.2	15.2	601	3	US-09-949-016-159520	Sequence 159520, A
cl1163	196.4	15.2	601	3	US-09-949-016-22105	Sequence 22105, A	1236	196.2	15.2	601	3	US-09-949-016-159593	Sequence 159593, A
cl1164	196.4	15.2	601	3	US-09-949-016-22106	Sequence 22106, A	cl1237	196.2	15.2	601	3	US-09-949-002-6961	Sequence 6961, Ap
cl1165	196.4	15.2	601	3	US-09-949-016-28290	Sequence 28290, A	cl1238	196.2	15.2	11570	5	US-09-936-271C-13	Sequence 13, Appl
cl1166	196.4	15.2	601	3	US-09-949-016-33335	Sequence 33335, A	1239	196.2	15.2	11982	3	US-09-949-016-17084	Sequence 17084, A
cl1167	196.4	15.2	601	3	US-09-949-016-69964	Sequence 69964, A	1240	196.2	15.2	15402	3	US-09-949-016-12868	Sequence 12868, A
cl1168	196.4	15.2	601	3	US-09-949-016-109466	Sequence 109466, A	1241	196.2	15.2	17842	3	US-09-949-016-13826	Sequence 13826, A
1169	196.4	15.2	601	3	US-09-949-016-139175	Sequence 139175, A	1242	196.2	15.2	22686	3	US-09-949-016-12979	Sequence 12979, A
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cl1171	196.4	15.2	601	3	US-09-949-016-154106	Sequence 154106, A	cl1244	196.2	15.2	25438	3	US-09-949-016-17161	Sequence 17161, A
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cl1173	196.4	15.2	601	3	US-09-949-016-182675	Sequence 182675, A	1246	196.2	15.2	44608	3	US-09-949-016-15604	Sequence 15604, A
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c1313	196	15.1	80357	3	US-09-949-016-12735	Sequence 12735, A	1386	195.8	15.1	5018	3	US-09-949-016-12315	Sequence 12315, A
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Qy 901 CTCCTCCAGAAGAGTAATTCCTTCATCTAAAGCCACGACAAATGAGTGAAAATGTGCAGTG 960
Db 901 CTCCTCCAGAAGAGTAATTCCTTCATCTAAAGCCACGACAAATGAGTGAAAATGTGCAGTG 960
Qy 961 GCTCAGCCCTGTAATCCAGCACTTTTGGAAAGCGCGCGCGGGATCAGAGGTCAGGA 1020
Db 961 GCTCAGCCCTGTAATCCAGCACTTTTGGAAAGCGCGCGCGGGATCAGAGGTCAGGA 1020
Qy 1021 GTTCTAGACAGTGTGGCAATATGGTGAACCCCATCTCTACTAAATACAAAATTAG 1080
Db 1021 GTTCTAGACAGTGTGGCAATATGGTGAACCCCATCTCTACTAAATACAAAATTAG 1080
Qy 1081 CTGGGCATGTGGCATGTGCTGCAGTTCAGTCTGCTTGGGAGACAGGAGAATCACTTGA 1140
Db 1081 CTGGGCATGTGGCATGTGCTGCAGTTCAGTCTGCTTGGGAGACAGGAGAATCACTTGA 1140
Qy 1141 ACCGGAGCGGAGGTGTCAGTGAGTCAAGCTCAGCCACTGAGTCCAGCCTGGGTAA 1200
Db 1141 ACCGGAGCGGAGGTGTCAGTGAGTCAAGCTCAGCCACTGAGTCCAGCCTGGGTAA 1200
Qy 1201 CAGAGCAAGATTCCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
Db 1201 CAGAGCAAGATTCCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
Qy 1261 TGTAGAAATCTTCAATAAATAATAGCTTGATATTC 1295
Db 1261 TGTAGAAATCTTCAATAAATAATAGCTTGATATTC 1295

RESULT 2

US-09-907-794A-63
; Sequence 63, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63

; LENGTH: 1295									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-907-794A-63									
Query Match 100.0%; Score 1295; DB 3; Length 1295;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CCCAGAGTTC	CAAGGGCCCGCGCTCCTCGCTCCGCTCCGCGCGGACCCCTCGACCTCCT	60					
Db	1	CCCAGAGTTC	CAAGGGCCCGCGCTCCTCGCTCCGCTCCGCGCGGACCCCTCGACCTCCT	60					
Qy	61	CAGAGCAGCC	CGGCTGCGCCCGCGGGAAGATGGCGAGGAGCGCCACCCGCTCCCTCCT	120					
Db	61	CAGAGCAGCC	CGGCTGCGCCCGCGGGAAGATGGCGAGGAGCGCCACCCGCTCCCTCCT	120					
Qy	121	GCTGCTGCT	CGCTACCTGTGGTGGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	180					
Db	121	GCTGCTGCT	CGCTACCTGTGGTGGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	180					
Qy	181	CCCAAGACCA	CAAGTAGTACAGCAGTAGTACCAAGAGCTATTTTAGCCTGCA	240					
Db	181	CCCAAGACCA	CAAGTAGTACAGCAGTAGTACCAAGAGCTATTTTAGCCTGCA	240					
Qy	241	AACCCCAAG	AAGACTGTTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTC	300					
Db	241	AACCCCAAG	AAGACTGTTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTC	300					
Qy	301	CTTTGTCTA	CTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATGA	360					
Db	301	CTTTGTCTA	CTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATGA	360					
Qy	361	TTTCAATAT	CCGGATCAAAATGTGACAGAAAGTATCGGGGAAATATCGTTGGAAT	420					
Db	361	TTTCAATAT	CCGGATCAAAATGTGACAGAAAGTATCGGGGAAATATCGTTGGAAT	420					
Qy	421	TAGTGCCCA	CTCTGAGCAAGGCAAACTCGAAGAGGATACAGTCACTCTGGAAGTATT	480					
Db	421	TAGTGCCCA	CTCTGAGCAAGGCAAACTCGAAGAGGATACAGTCACTCTGGAAGTATT	480					
Qy	481	AGTGGCTCA	GAGCAGTCCATCATGTGAAGTACCTCTCTGCTCTGAGTGGAACTGTGGT	540					
Db	481	AGTGGCTCA	GAGCAGTCCATCATGTGAAGTACCTCTCTGCTCTGAGTGGAACTGTGGT	540					
Qy	541	AGAGCTAG	ATGTCAGCAAGGAATCCAGCTCCCTGAATACACATGTTTAAAGGA	600					
Db	541	AGAGCTAG	ATGTCAGCAAGGAATCCAGCTCCCTGAATACACATGTTTAAAGGA	600					
Qy	601	TGGCATCC	GTGTTGCTAGAAATCCAGACTTGGCTCCCAAGCACCAACAGCTCATAC	660					
Db	601	TGGCATCC	GTGTTGCTAGAAATCCAGACTTGGCTCCCAAGCACCAACAGCTCATAC	660					
Qy	661	AATGAATA	CAAAAACTGGAACTCTGCAATTTAATCTGTTTCCAACTGGACACTGGAGA	720					
Db	661	AATGAATA	CAAAAACTGGAACTCTGCAATTTAATCTGTTTCCAACTGGACACTGGAGA	720					
Qy	721	ATATTCCT	GTGAAGCCCGCAATTCCTGTGGATATCGCAGAGTGTCTGGGAAACGAATGCA	780					
Db	721	ATATTCCT	GTGAAGCCCGCAATTCCTGTGGATATCGCAGAGTGTCTGGGAAACGAATGCA	780					
Qy	781	AGTAGATG	ATCTCAACATAGTGGCATCATAGCAGCCGTAGTGTGGGCTTTAGTGAT	840					
Db	781	AGTAGATG	ATCTCAACATAGTGGCATCATAGCAGCCGTAGTGTGGGCTTTAGTGAT	840					
Qy	841	TTCCGTTT	GTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAC	900					
Db	841	TTCCGTTT	GTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAC	900					
Qy	901	CTCCTTCA	GAGAGTAAATCTTCACTAAAGCCACCAATGAGTGAAAATGTGCAGTG	960					
Db	901	CTCCTTCA	GAGAGTAAATCTTCACTAAAGCCACCAATGAGTGAAAATGTGCAGTG	960					

RESULT 3

US-09-905-125A-63

; Sequence 63, Application US/09905125A

; Patent No. 6664376

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,125A

; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090


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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-125A-63

Query Match      100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAAGATTCAAGGGCCCCGGCTCTCTCGCTCTCTCGCGCGGGACCCCTCGACTCT 60
Db 1 CCCAAGATTCAAGGGCCCCGGCTCTCTCGCTCTCTCGCGCGGGACCCCTCGACTCT 60

Qy 61 CAGAGACGGCTGCGCGCGCGGAGAGTGGGAGGAGCGCCACCGCTCTCTCT 120
Db 61 CAGAGACGGCTGCGCGCGCGGAGAGTGGGAGGAGCGCGCCACCGCTCTCTCT 120

Qy 121 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

Qy 181 CCCAAAAGACAAAGTAGTCAAGAGTAGTCAAGAGAGTCAAGAGAGTCAAGAGAGT 240
Db 181 CCCAAAAGACAAAGTAGTCAAGAGTAGTCAAGAGAGTCAAGAGAGTCAAGAGAGT 240

Qy 241 AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGGAGAGAACTGGGTGGAGTGTCTC 300
Db 241 AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGGAGAGAACTGGGTGGAGTGTCTC 300

Qy 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATA 360
Db 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATA 360

Qy 361 TTTCAATATCCGATCAAAAATGTGACAAAGTAGTACGGGGAATATCGTTGTGAAGT 420
Db 361 TTTCAATATCCGATCAAAAATGTGACAAAGTAGTACGGGGAATATCGTTGTGAAGT 420

Qy 421 TAGTGCCCATCTGAGCAAGGCGCAAACTGGAGAGGATACAGTCACTCTGGAATATT 480
Db 421 TAGTGCCCATCTGAGCAAGGCGCAAACTGGAGAGGATACAGTCACTCTGGAATATT 480

Qy 481 AGTGGCTCCAGAGTTCATCATGTGAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 540
Db 481 AGTGGCTCCAGAGTTCATCATGTGAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 540

Qy 541 AGAGCTACGATGTCAAGCAAAAGAGGAAATCCAGCTCTCTGAAATACATGTTTAAAGGA 600
Db 541 AGAGCTACGATGTCAAGCAAAAGAGGAAATCCAGCTCTCTGAAATACATGTTTAAAGGA 600

Qy 601 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATACAC 660
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RESULT 4

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US-09-902-775A-63
; Sequence 63, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
```



```

; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-902-775A-63

Query Match      100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCCAGAGTTCAGAGGCCCGCCCTCTCGCTCCCTCGCGCGCGGACCCCTCGACCTCCT 60
Db      1  CCCAGAGTTCAGAGGCCCGCCCTCTCGCTCCCTCGCGCGCGGACCCCTCGACCTCCT 60

Qy      61  CAGAGCAGCCGCTGCGCGCCCGGAGAGTGGCGAGGAGCGCCACCGCCCTCCTCCT 120
Db      61  CAGAGCAGCCGCTGCGCGCCCGGAGAGTGGCGAGGAGCGCCACCGCCCTCCTCCT 120

Qy      121  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db      121  GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

Qy      181  CCCAAAGACCAACAGTAGTACAGCAGTAGTACAGCAGTAGTACAGCAGTAGTACAG 240
Db      181  CCCAAAGACCAACAGTAGTACAGCAGTAGTACAGCAGTAGTACAGCAGTAGTACAG 240

Qy      241  AACCCCAAGAGACTGTTTCTCTCAGATTAGGTGGAAGAACTGGGTGCGAGTGTCTC 300

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% Sequence 63, Application US/09906700
% Patent No. 6723535
% GENERAL INFORMATION:
% APPLICANT: Genentech, Inc.
% APPLICANT: Ashkenazi, Avi
% APPLICANT: Botstein, David
% APPLICANT: Desnoyers, Luc
% APPLICANT: Eaton, Dan L.
% APPLICANT: Ferrara, Napoleone
% APPLICANT: Filvaroff, Ellen
% APPLICANT: Fong, Sherman
% APPLICANT: Gao, Wei-Qiang
% APPLICANT: Garber, Hanspeter
% APPLICANT: Gerritsen, Mary E.
% APPLICANT: Goddard, A.
% APPLICANT: Godowski, Paul J.
% APPLICANT: Grimaldi, Christopher J.
% APPLICANT: Hillan, Kenneth, J.
% APPLICANT: Kijavini, Ivar J.
% APPLICANT: Mather, Jennie P.
% APPLICANT: Pan, James
% APPLICANT: Paoni, Nicholas F.
% APPLICANT: Roy, Margaret Ann
% APPLICANT: Stewart, Timothy A.
% APPLICANT: Tumas, Daniel
% APPLICANT: Williams, P. Mickey
% APPLICANT: Wood, William, I.
% TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
% FILE REFERENCE: 10466-14
% CURRENT APPLICATION NUMBER: US/09/906,700
% CURRENT FILING DATE: 2000-09-18
% PRIOR APPLICATION NUMBER: PCT/US00/04414
% PRIOR FILING DATE: 2000-02-22
% PRIOR APPLICATION NUMBER: US 60/143,048
% PRIOR FILING DATE: 1999-07-07
% PRIOR APPLICATION NUMBER: US 60/145,698
% PRIOR FILING DATE: 1999-07-26
% PRIOR APPLICATION NUMBER: US 60/146,222
% PRIOR FILING DATE: 1999-07-28
% PRIOR APPLICATION NUMBER: PCT/US99/20594
% PRIOR FILING DATE: 1999-09-08
% PRIOR APPLICATION NUMBER: PCT/US99/20944
% PRIOR FILING DATE: 1999-09-13
% PRIOR APPLICATION NUMBER: PCT/US99/21090
% PRIOR FILING DATE: 1999-09-15
% PRIOR APPLICATION NUMBER: PCT/US99/21547
% PRIOR FILING DATE: 1999-09-15
% PRIOR APPLICATION NUMBER: PCT/US99/23089
% PRIOR FILING DATE: 1999-10-05
% PRIOR APPLICATION NUMBER: PCT/US99/28214
% PRIOR FILING DATE: 1999-11-29
% PRIOR APPLICATION NUMBER: PCT/US99/28313
% PRIOR FILING DATE: 1999-11-30
% PRIOR APPLICATION NUMBER: PCT/US99/28564
% PRIOR FILING DATE: 1999-12-02
% PRIOR APPLICATION NUMBER: PCT/US99/28565
% PRIOR FILING DATE: 1999-12-02
% PRIOR APPLICATION NUMBER: PCT/US99/30095
% PRIOR FILING DATE: 1999-12-16
% PRIOR APPLICATION NUMBER: PCT/US99/30911
% PRIOR FILING DATE: 1999-12-20
% PRIOR APPLICATION NUMBER: PCT/US99/30999
% PRIOR FILING DATE: 1999-12-20
% PRIOR APPLICATION NUMBER: PCT/US00/00219
% PRIOR FILING DATE: 2000-01-05
% NUMBER OF SEQ ID NOS: 423
% SEQ ID NO 63
% LENGTH: 1295
% TYPE: DNA
% ORGANISM: Homo sapiens
% US-09-906-700-63
```

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Query Match      100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGAGTTCAAGGGCCCCCGGCTCTCTGCGCGCGGACCCCTCGACCTCCT 60
DB 1 CCAGAGTTCAAGGGCCCCCGGCTCTCTGCGCGCGGACCCCTCGACCTCCT 60
QY 61 CAGAGCAGCCGCTGCGCGCGGGAAGATGCGAGGAGCGCCACCGCTCTCCT 120
DB 61 CAGAGCAGCCGCTGCGCGCGGGAAGATGCGAGGAGCGCCACCGCTCTCCT 120
QY 121 GCTGCTGCTGCGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 GCTGCTGCTGCGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 CCAAAAGACCAACAGTAGTCACAGCAGTACAGAGGAGGCTATTTTAGCC 240
DB 181 CCAAAAGACCAACAGTAGTCACAGCAGTACAGAGGAGGCTATTTTAGCC 240
QY 241 AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGGAGAAACTGGGTCGAG 300
DB 241 AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGGAGAAACTGGGTCGAG 300
QY 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCT 360
DB 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCT 360
QY 361 TTTCAATATCCGGATCAAAAATGTGCAAGAGTGTATGCGGGGAAATATCG 420
DB 361 TTTCAATATCCGGATCAAAAATGTGCAAGAGTGTATGCGGGGAAATATCG 420
QY 421 TAGTGCCCATCTGAGCAAGGCGCAAAACCTGGAAGAGGATACAGTCAC 480
DB 421 TAGTGCCCATCTGAGCAAGGCGCAAAACCTGGAAGAGGATACAGTCAC 480
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DB 481 AGTGGCTCAGCAGTTCCATCATGTGAAGTACCTCTTCTGCTGAGTGGAA 540
QY 541 AGAGCTACGATGTCAAGCAAAAGAGGAAATCCAGCTCTCTGATACACAT 600
DB 541 AGAGCTACGATGTCAAGCAAAAGAGGAAATCCAGCTCTCTGATACACAT 600
QY 601 TGGCATCCGTTTGTCTAGAAAATCCAGACTTGGCTCCCAAGCACCACAG 660
DB 601 TGGCATCCGTTTGTCTAGAAAATCCAGACTTGGCTCCCAAGCACCACAG 660
QY 661 AATGAATACAAAACCTGGAACTCTGCAATTTAATACTGTTTCCAACTGG 720
DB 661 AATGAATACAAAACCTGGAACTCTGCAATTTAATACTGTTTCCAACTGG 720
QY 721 ATATTCTGTGAAGCCCGCAATTTCTGTTGGATATCGCAGTGTCTTGGGAA 780
DB 721 ATATTCTGTGAAGCCCGCAATTTCTGTTGGATATCGCAGTGTCTTGGGAA 780
QY 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTGTGGCCCT 840
DB 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTGTGGCCCT 840
QY 841 TTCCGTTTGTGGCCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTT 900
DB 841 TTCCGTTTGTGGCCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTT 900
QY 901 CTCTCTTCCAGAGAGTAAATTTCTTCAATCTAAAGCAGCAATAGTGAAG 960
DB 901 CTCTCTTCCAGAGAGTAAATTTCTTCAATCTAAAGCAGCAATAGTGAAG 960
QY 961 GCTCAGCGCTGTAATCCAGCACTTTTGGAAAGCCCGCGGCGGATCAGAG 1020
DB 961 GCTCAGCGCTGTAATCCAGCACTTTTGGAAAGCCCGCGGCGGATCAGAG 1020
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Db 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA 360
Qy 361 TTTCAATATCCGATCAAAATGTGACAAGAGTATGCGGGGAAATATCTTCTGGAAGT 420
Db 361 TTTCAATATCCGATCAAAATGTGACAAGAGTATGCGGGGAAATATCTTCTGGAAGT 420
Qy 421 TAGTGCCCATCTGAGCAAGGCCAAAACCTTGAAAGAGATACAGTCACTCTGGAAGTATT 480
Db 421 TAGTGCCCATCTGAGCAAGGCCAAAACCTTGAAAGAGATACAGTCACTCTGGAAGTATT 480
Qy 481 AGTGGCTCCAGCAGTCCATCATCTGAGTATGAGTACCTCTTCTGCTGAGTGAACCTGGT 540
Db 481 AGTGGCTCCAGCAGTCCATCATCTGAGTATGAGTACCTCTTCTGCTGAGTGAACCTGGT 540
Qy 541 AGAGCTACGATGTCAAGCAAAAGGAATCCAGACTTGGCTCCCAAGCACCAGCTCATAC 600
Db 541 AGAGCTACGATGTCAAGCAAAAGGAATCCAGACTTGGCTCCCAAGCACCAGCTCATAC 600
Qy 601 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGCACCAGCTCATAC 660
Db 601 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGCACCAGCTCATAC 660
Qy 661 AATGAATACAAAATCGAACTCTGCAATTTAATACTGTTTCCAACTGGACACTGGAGA 720
Db 661 AATGAATACAAAATCGAACTCTGCAATTTAATACTGTTTCCAACTGGACACTGGAGA 720
Qy 721 ATATTCTGTGAAGCCGCAATCTGTTGGATATCGCAGGTGCTCTGGAACCAATGCA 780
Db 721 ATATTCTGTGAAGCCGCAATCTGTTGGATATCGCAGGTGCTCTGGAACCAATGCA 780
Qy 781 AGTAGATGATCTCAACATAGTGGCATCATAGCAGCGTAGTGTGCGCTTAGTGAT 840
Db 781 AGTAGATGATCTCAACATAGTGGCATCATAGCAGCGTAGTGTGCGCTTAGTGAT 840
Qy 841 TTCGGTTTGTGGCTTGTGATGCTATGCTCAGAGAAAGGCTACTTTTCAAAAGAAC 900
Db 841 TTCGGTTTGTGGCTTGTGATGCTATGCTCAGAGAAAGGCTACTTTTCAAAAGAAC 900
Qy 901 CTCTTCCAGAAAGTAACTCTTCAAGCCAGCAGCATGATGAAATGTCAGTG 960
Db 901 CTCTTCCAGAAAGTAACTCTTCAAGCCAGCAGCATGATGAAATGTCAGTG 960
Qy 961 GCTCACGCTGTAAATCCAGCAGCTTTTGAAGCCGCGCGCGGATCACGAGTCAAG 1020
Db 961 GCTCACGCTGTAAATCCAGCAGCTTTTGAAGCCGCGCGCGGATCACGAGTCAAG 1020
Qy 1021 GTTCTAGACAGTCTGGCCAAATATGGTGAACCCCATCTCTAATAAATCAAAAATTAG 1080
Db 1021 GTTCTAGACAGTCTGGCCAAATATGGTGAACCCCATCTCTAATAAATCAAAAATTAG 1080
Qy 1081 CTGGGCGATGGTGGCATGTGCTCAGTTCAGCTGCTTGGGAGACAGGAGTCACTTGA 1140
Db 1081 CTGGGCGATGGTGGCATGTGCTCAGTTCAGCTGCTTGGGAGACAGGAGTCACTTGA 1140
Qy 1141 ACCCGGAGGGGAGGTTGAGTGCAGTGCAGTCAAGCTGAGTCAAGTCCAGCTGGGTAA 1200
Db 1141 ACCCGGAGGGGAGGTTGAGTGCAGTGCAGTCAAGCTGAGTCCAGCTGGGTAA 1200
Qy 1201 CAGAGCAAGATTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
Db 1201 CAGAGCAAGATTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
Qy 1261 TGTAGAATCTTACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1295
Db 1261 TGTAGAATCTTACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1295

RESULT 8
US-909-064-63
; Sequence 63, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-064-63

Query Match 100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGATTCAAGGGCCCCGGGCTCTGCGCTCTGCGCCGCGGACCCCTCGACCTCCT 60
Db 1 CCAGAAAGTTCAAGGGCCCCGGGCTCTGCGCTCTGCGCCGCGGACCCCTCGACCTCCT 60
QY 61 CAGAGCAGCGGCTGCGCGCCCCGGGAAGATGGCGAGGAGAGCGCCACCGCCCTCTCTCCT 120
Db 61 CAGAGCAGCGGCTGCGCGCCCCGGGAAGATGGCGAGGAGAGCGCCACCGCCCTCTCTCCT 120
QY 121 GCTGCTGCTGCGCTACCTGCTGCTGCGCCCTGCGGCTATCATAAAGCCCTATGGGTTTTCTGC 180
Db 121 GCTGCTGCTGCGCTACCTGCTGCTGCGCCCTGCGGCTATCATAAAGCCCTATGGGTTTTCTGC 180
QY 181 CCCAAAAGACAAAGTAGTACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA 240
Db 181 CCCAAAAGACAAAGTAGTACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA 240
QY 241 AACCCCAAAGAACTGTTTTCTCCAGATTAGAGTGGAAAGAACTGGGTCGGAGTGCTC 300
Db 241 AACCCCAAAGAACTGTTTTCTCCAGATTAGAGTGGAAAGAACTGGGTCGGAGTGCTC 300
QY 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTTAAAAATCGAGCTGAGATGAGA 360
Db 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTTAAAAATCGAGCTGAGATGAGA 360
QY 361 TTTCATATCCGGATCAAAAATGTGACAAAGTAGATGCGGGGAAATATCGTTGTGAAGT 420
Db 361 TTTCATATCCGGATCAAAAATGTGACAAAGTAGATGCGGGGAAATATCGTTGTGAAGT 420
QY 421 TAGTGCCCATCTGAGCAAGCCAAACCTGGAAGAGATACAGTCACTCTGGAAGTATT 480
Db 421 TAGTGCCCATCTGAGCAAGCCAAACCTGGAAGAGATACAGTCACTCTGGAAGTATT 480
QY 481 AGTGGCTCCAGCAGTCCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 540
Db 481 AGTGGCTCCAGCAGTCCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 540
QY 541 AGAGCTACGATGTCAAGCAAAAGAGGAAATCCAGCTCTCGAATACACATGTTTAAAGGA 600
Db 541 AGAGCTACGATGTCAAGCAAAAGAGGAAATCCAGCTCTCGAATACACATGTTTAAAGGA 600
QY 601 TGGCATCCGTTTGTAGAAATCCAGACTTGGCTCCAAAGCACCACCAAGCTCATAC 660
Db 601 TGGCATCCGTTTGTAGAAATCCAGACTTGGCTCCAAAGCACCACCAAGCTCATAC 660
QY 661 AATGAATACAAAACCTGGAATCTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGA 720
Db 661 AATGAATACAAAACCTGGAATCTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGA 720
QY 721 ATATTCCTGTGAAGCCCGCAATTTCTGTGTGATATCGCAGGTGCTCGGGAACGAATGCA 780
Db 721 ATATTCCTGTGAAGCCCGCAATTTCTGTGTGATATCGCAGGTGCTCGGGAACGAATGCA 780
QY 781 AGTAGATGATCTCAACATAGTGGCATCATAGCAGCGGTAGTGTGCGCCCTTAGTAT 840
Db 781 AGTAGATGATCTCAACATAGTGGCATCATAGCAGCGGTAGTGTGCGCCCTTAGTAT 840
QY 841 TTCGTTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAAC 900
Db 841 TTCGTTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAAC 900
QY 901 CTCCTCCAGAGAGTAAATTTCTTCATCTAAAGCAGCAATGAGTGAATAATGTGCAGTG 960
Db 901 CTCCTCCAGAGAGTAAATTTCTTCATCTAAAGCAGCAATGAGTGAATAATGTGCAGTG 960
QY 961 GCTCAGCCCTGAATCCAGCACTTTTGGAGGCGCGGGCGGGATCAGAGGTCAGGA 1020
Db 961 GCTCAGCCCTGAATCCAGCACTTTTGGAGGCGCGGGCGGGATCAGAGGTCAGGA 1020
QY 1021 GTTCTAGACCAAGTCTGCGCCAAATATGGTGAACCCCATCTCTACTAAAAATACAAAATTAG 1080
Db 1021 GTTCTAGACCAAGTCTGCGCCAAATATGGTGAACCCCATCTCTACTAAAAATACAAAATTAG 1080

QY 1081 CTGGGCATGTCGCATGTGCTCCAGTTCCTGGAGACAGGAGAAATCACTTGA 1140
Db 1081 CTGGGCATGTCGCATGTGCTCCAGTTCCTGGAGACAGGAGAAATCACTTGA 1140
QY 1141 ACCCGGAGCGCGAGGTTGCTGAGCTGAGATCAGCCACCTGCAGTCCAGCCTGGGTAA 1200
Db 1141 ACCCGGAGCGCGAGGTTGCTGAGCTGAGATCAGCCACCTGCAGTCCAGCCTGGGTAA 1200
QY 1201 CAGAGCAAGATTCCATCTCAAAAAATAAAATAAAATAAAATACTGGTTTTTACC 1260
Db 1201 CAGAGCAAGATTCCATCTCAAAAAATAAAATAAAATAAAATACTGGTTTTTACC 1260
QY 1261 TGTAGAATCTTTACATAAATAATAGCTTGATATTC 1295
Db 1261 TGTAGAATCTTTACATAAATAATAGCTTGATATTC 1295

RESULT 9
US-09-905-381A-63
; Sequence 63, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313

/ CURRENT APPLICATION NUMBER: US/09/906,618									
/ CURRENT FILING DATE: 2001-07-16									
/ PRIOR APPLICATION NUMBER: PCT/US00/04414									
/ PRIOR FILING DATE: 2000-02-22									
/ PRIOR APPLICATION NUMBER: US 60/143,048									
/ PRIOR FILING DATE: 1999-07-07									
/ PRIOR APPLICATION NUMBER: US 60/145,698									
/ PRIOR FILING DATE: 1999-07-26									
/ PRIOR APPLICATION NUMBER: US 60/146,222									
/ PRIOR FILING DATE: 1999-07-28									
/ PRIOR APPLICATION NUMBER: PCT/US99/20594									
/ PRIOR FILING DATE: 1999-09-08									
/ PRIOR APPLICATION NUMBER: PCT/US99/20944									
/ PRIOR FILING DATE: 1999-09-13									
/ PRIOR APPLICATION NUMBER: PCT/US99/21090									
/ PRIOR FILING DATE: 1999-09-15									
/ PRIOR APPLICATION NUMBER: PCT/US99/21547									
/ PRIOR FILING DATE: 1999-09-15									
/ PRIOR APPLICATION NUMBER: PCT/US99/23089									
/ PRIOR FILING DATE: 1999-10-05									
/ PRIOR APPLICATION NUMBER: PCT/US99/28214									
/ PRIOR FILING DATE: 1999-11-29									
/ PRIOR APPLICATION NUMBER: PCT/US99/28313									
/ PRIOR FILING DATE: 1999-11-30									
/ PRIOR APPLICATION NUMBER: PCT/US99/28564									
/ PRIOR FILING DATE: 1999-12-02									
/ PRIOR APPLICATION NUMBER: PCT/US99/28565									
/ PRIOR FILING DATE: 1999-12-02									
/ PRIOR APPLICATION NUMBER: PCT/US99/30095									
/ PRIOR FILING DATE: 1999-12-16									
/ PRIOR APPLICATION NUMBER: PCT/US99/30911									
/ PRIOR FILING DATE: 1999-12-20									
/ PRIOR APPLICATION NUMBER: PCT/US99/30999									
/ PRIOR FILING DATE: 1999-12-20									
/ PRIOR APPLICATION NUMBER: PCT/US00/00219									
/ PRIOR FILING DATE: 2000-01-05									
/ NUMBER OF SEQ ID NOS: 423									
/ SEQ ID NO 63									
/ LENGTH: 1295									
/ TYPE: DNA									
/ ORGANISM: Homo sapiens									
/ US-09-906-618-63									
Query Match 100.0%; Score 1295; DB 3; Length 1295;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CCGAGAAGTTCAAGGGCCCCCGGCTCTCTCGGCTCTCTCGCGCGGGACCCCTCGACCTCT	60						
Db	1	CCGAGAAGTTCAAGGGCCCCCGGCTCTCTCGGCTCTCTCGCGCGGGACCCCTCGACCTCT	60						
Qy	61	CAGAGCAGCGGCTCGCGCCCCCGGAGNATGCGGAGGAGGAGCCGCCACCGCTCTCTCT	120						
Db	61	CAGAGCAGCGGCTCGCGCCCCCGGAGNATGCGGAGGAGGAGCCGCCACCGCTCTCTCT	120						
Qy	121	GCTGCTGCTCGCTACTCGTGTGCTCGGCTATCATAGGCTATGAGGCTATGTTTCTGCG	180						
Db	121	GCTGCTGCTCGCTACTCGTGTGCTCGGCTATCATAGGCTATGAGGCTATGTTTCTGCG	180						
Qy	181	CCCAAAAGACCACCAAGTAGTCACAGCAGTAGAGTACCAGAGGCTATTTTAGCCTGCAA	240						
Db	181	CCCAAAAGACCACCAAGTAGTCACAGCAGTAGAGTACCAGAGGCTATTTTAGCCTGCAA	240						
Qy	241	AACCCCAAGAAGACTGTTTCTCCAGATTAGAGTGGAGAAACTGGGTCGGAGTGTCTC	300						
Db	241	AACCCCAAGAAGACTGTTTCTCCAGATTAGAGTGGAGAAACTGGGTCGGAGTGTCTC	300						
Qy	301	CTTTGTCTACTCAACAGACTCTTTCAGAGTATTTTAAATCGAGCTGAGATGATAGA	360						
Db	301	CTTTGTCTACTCAACAGACTCTTTCAGAGTATTTTAAATCGAGCTGAGATGATAGA	360						
Qy	361	TTTTCATATCCGGATCAAAAATGTGACAAGAGTAGTCGGGGAAAATATCGTTGTGAAGT	420						
RESULT 11									
US-09-953-499-8									
; Sequence 8, Application US/09953499									
; Patent No. 6838554									
; GENERAL INFORMATION:									
; APPLICANT: Genentech, Inc.									
; APPLICANT: Ashkenazi, Avi J.									
; APPLICANT: Fong, Sherman									
; APPLICANT: Goddard, Audrey									
; APPLICANT: Gurney, Austin L.									

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 63
LENGTH: 1295
TYPE: DNA
ORGANISM: Homo sapiens
US-09-906-646-63

Query Match 100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCGAGAGTTCAAGGGCCCGGCTCTCGCTCCGCGCGGGACCCCTCGACCTCCT	60
DB	1	CCGAGAGTTCAAGGGCCCGGCTCTCGCTCCGCGCGGGACCCCTCGACCTCCT	60
QY	61	CAGAGCAGCGGCTGCGCGCCCGGGAAGATGGCGAGGAGCGCCACCGCTCCT	120
DB	61	CAGAGCAGCGGCTGCGCGCCCGGGAAGATGGCGAGGAGCGCCACCGCTCCT	120
QY	121	GCTGCTGCTGGCTACTGCTGGTGGCTATCAAGGCTATAGGGTTTCTGTC	180
DB	121	GCTGCTGCTGGCTACTGCTGGTGGCTATCAAGGCTATAGGGTTTCTGTC	180
QY	181	CCCAAGAGCCAAAGTAGTACAGCAGTAGAGTACCAAGAGCTATTTTACCGTGC	240
DB	181	CCCAAGAGCCAAAGTAGTACAGCAGTAGAGTACCAAGAGCTATTTTACCGTGC	240
QY	241	AACCCCAAGAGAGCTGTTTCTCCAGATTAGAGTGGAGAACTGGGTGGAGTGTCTC	300
DB	241	AACCCCAAGAGAGCTGTTTCTCCAGATTAGAGTGGAGAACTGGGTGGAGTGTCTC	300
QY	301	CTTTGTCTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATA	360

RESULT 13
US-09-904-462-63
; Sequence 63, Application US/09904462
; Patent No. 687807
; GENERAL INFORMATION:

DB	301	CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATA	360
QY	361	TTTCAATATCCGATCAAAATATGTGAAGAAGTGTGCGGGAAATATCGTTGTGAAGT	420
DB	361	TTTCAATATCCGATCAAAATATGTGAAGAAGTGTGCGGGAAATATCGTTGTGAAGT	420
QY	421	TAGTGGCCCATCTGAGCAAGGCGCAAACTCTGGAAGAGGATACAGTCACTCTCGAAGTATT	480
DB	421	TAGTGGCCCATCTGAGCAAGGCGCAAACTCTGGAAGAGGATACAGTCACTCTCGAAGTATT	480
QY	481	AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT	540
DB	481	AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT	540
QY	541	AGAGCTACGATGTCAAGACAAAGAGGGAATCCAGCTCTCTGAATACACATGCTTTAAGGA	600
DB	541	AGAGCTACGATGTCAAGACAAAGAGGGAATCCAGCTCTCTGAATACACATGCTTTAAGGA	600
QY	601	TGGCATCCGTTTGTAGAAATCCAGACTTGGCTCCCAAGACCACCAAGCTCATACAC	660
DB	601	TGGCATCCGTTTGTAGAAATCCAGACTTGGCTCCCAAGACCACCAAGCTCATACAC	660
QY	661	AATGAATACAAAACTGGAACTCTGCAATTTAATACTGTTTCCAAACTGGACACTGAGA	720
DB	661	AATGAATACAAAACTGGAACTCTGCAATTTAATACTGTTTCCAAACTGGACACTGAGA	720
QY	721	ATATTCTCTGAAGCCCGCAATTTCTTGGATATGCGAGGTGCTCGGGAAGCAATGCA	780
DB	721	ATATTCTCTGAAGCCCGCAATTTCTTGGATATGCGAGGTGCTCGGGAAGCAATGCA	780
QY	781	AGTAGATGATCTCAACATAGTGGCATCATAGCCCGTAGTAGTGTGCGCCTTAGTGAT	840
DB	781	AGTAGATGATCTCAACATAGTGGCATCATAGCCCGTAGTAGTGTGCGCCTTAGTGAT	840
QY	841	TTCCGTTTCTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAC	900
DB	841	TTCCGTTTCTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAC	900
QY	901	CTCCTTCCAGAGAGTAATTTCTTCATCTAAAGCCACGACAAATGAGTGAAATGTGAGTG	960
DB	901	CTCCTTCCAGAGAGTAATTTCTTCATCTAAAGCCACGACAAATGAGTGAAATGTGAGTG	960
QY	961	GCTCAGCCTGTATCCAGACTTTTGGAGCCCGCGGGCGGATCAGAGTCAGGA	1020
DB	961	GCTCAGCCTGTATCCAGACTTTTGGAGCCCGCGGGCGGATCAGAGTCAGGA	1020
QY	1021	GTTCAGACAGTCTGGCCCAATATGTTGAAACCCCATCTCTACTAAAAATACAAAAATTAG	1080
DB	1021	GTTCAGACAGTCTGGCCCAATATGTTGAAACCCCATCTCTACTAAAAATACAAAAATTAG	1080
QY	1081	CTGGGCATGTGGCATGTGCTGCAATTCAGCTGCTGGGAGACAGGAGAACTCATTGA	1140
DB	1081	CTGGGCATGTGGCATGTGCTGCAATTCAGCTGCTGGGAGACAGGAGAACTCATTGA	1140
QY	1141	ACCCGGAGCGGAGGTTGAGTGTGAGTACGACCACTGCGAGTCCAGCTCGGGTAA	1200
DB	1141	ACCCGGAGCGGAGGTTGAGTGTGAGTACGACCACTGCGAGTCCAGCTCGGGTAA	1200
QY	1201	CAGAGCAAGATTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1260
DB	1201	CAGAGCAAGATTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1260
QY	1261	TGTAGAAATCTTACAAATAATATAGCTTGATATTC	1295
DB	1261	TGTAGAAATCTTACAAATAATATAGCTTGATATTC	1295

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deanoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,462
PRIORITY FILING DATE: 2001-07-13
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PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
PRIORITY FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 63
LENGTH: 1295
TYPE: DNA
ORGANISM: Homo Sapien
US-09-904-462-63

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RESULT IS
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; Sequence 63, Application US/09906722A

; Patent No. 6946262

: GENERAL INFORMATION:
 : APPLICANT: Genentech, Inc.
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 : APPLICANT: Ferrara, Napoleone
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Gerritsen, Mary E.
 : APPLICANT: Goddard, A.
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, Christopher J.
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth, J.
 : APPLICANT: Kijavits, Ivam J.
 : APPLICANT: Mather, Jeanie P.
 : APPLICANT: Pan, James
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Steward, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Wood, William, I.

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Listing first 1500 summaries

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c 662	208	16.1	21850	11	US-10-330-773-474	Sequence 474, App	735	206	15.9	47941	8	US-10-741-601-5736	Sequence 5736, App
c 663	207.8	16.0	10256	3	US-09-764-847-1182	Sequence 1182, App	736	206	15.9	47941	9	US-10-741-600-17880	Sequence 17880, App
c 664	207.8	16.0	10256	6	US-10-092-154-1182	Sequence 1182, App	737	206	15.9	59554	8	US-10-052-482-202	Sequence 202, App
c 665	207.8	16.0	155515	15	US-11-112-908-42	Sequence 42, App	738	206	15.9	108111	9	US-10-719-993-6843	Sequence 6843, App
c 666	207.8	16.0	155497	15	US-11-112-908-61	Sequence 61, App	739	206	15.9	150482	10	US-10-981-277-33	Sequence 33, App
c 667	207.8	16.0	159660	15	US-11-112-908-43	Sequence 43, App	740	206	15.9	175023	15	US-11-121-086-18	Sequence 18, App
c 668	207.8	16.0	177623	15	US-11-112-908-41	Sequence 41, App	741	206	15.9	176096	10	US-10-981-277-34	Sequence 34, App
c 669	207.4	16.0	611	6	US-10-027-632-290952	Sequence 290952, App	742	205.8	15.9	521	12	US-10-301-480-315271	Sequence 315271, App
c 670	207.4	16.0	611	7	US-10-027-632-290952	Sequence 549632, App	743	205.8	15.9	521	12	US-10-301-480-928680	Sequence 928680, App
c 671	207.4	16.0	998	12	US-10-301-480-546360	Sequence 546360, App	744	205.8	15.9	524	4	US-09-925-065A-231861	Sequence 231861, App
c 672	207.4	16.0	998	12	US-10-301-480-590378	Sequence 590378, App	745	205.8	15.9	524	5	US-09-925-065A-231861	Sequence 231861, App
c 673	207.4	16.0	998	12	US-10-301-480-1159769	Sequence 1159769, App	746	205.8	15.9	680	4	US-09-925-065A-80242	Sequence 80242, A
c 674	207.4	16.0	998	12	US-10-301-480-1203787	Sequence 1203787, App	747	205.8	15.9	680	5	US-09-925-065A-80242	Sequence 80242, A
c 675	207.2	16.0	582	4	US-09-925-065A-18077	Sequence 18077, App	748	205.8	15.9	680	12	US-10-301-480-181481	Sequence 181481, App
c 676	207.2	16.0	582	5	US-09-925-065A-18077	Sequence 18077, App	749	205.8	15.9	680	12	US-10-301-480-794890	Sequence 794890, App
c 677	207.2	16.0	582	12	US-10-301-480-119314	Sequence 119314, App	750	205.8	15.9	1428	4	US-09-925-065A-710168	Sequence 710168, App
c 678	207.2	16.0	582	12	US-10-301-480-732723	Sequence 732723, App	751	205.8	15.9	1428	5	US-09-925-065A-710168	Sequence 710168, App
c 679	207	16.0	680	4	US-09-925-065A-80243	Sequence 80243, A	752	205.8	15.9	49979	8	US-10-741-601-5746	Sequence 5746, App
c 680	207	16.0	680	5	US-09-925-065A-80243	Sequence 80243, A	753	205.8	15.9	49979	9	US-10-741-600-17905	Sequence 17905, App
c 681	207	16.0	680	12	US-10-301-480-181482	Sequence 181482, App	754	205.8	15.9	49979	10	US-10-995-561-13443	Sequence 13443, A
c 682	207	16.0	680	12	US-10-301-480-794891	Sequence 794891, App	755	205.6	15.9	631	12	US-10-301-480-43809	Sequence 43809, A

756	205.6	15.9	631	12	US-10-301-480-663218	Sequence 663218,	829	204.6	15.8	997	7	US-10-027-632-121846	Sequence 121846,
c 757	205.6	15.9	658	6	US-10-027-632-193407	Sequence 193407,	c 830	204.6	15.8	1390	4	US-09-925-065A-88036	Sequence 88036, A
c 758	205.6	15.9	658	7	US-10-027-632-193407	Sequence 193407,	c 831	204.6	15.8	1390	5	US-09-925-065A-88036	Sequence 88036, A
759	205.6	15.9	960	12	US-10-301-480-574800	Sequence 574800,	c 832	204.6	15.8	1390	12	US-10-301-480-189277	Sequence 189277,
760	205.6	15.9	960	12	US-10-301-480-1188209	Sequence 1188209,	c 833	204.6	15.8	1390	12	US-10-301-480-802686	Sequence 802686,
761	205.6	15.9	964	12	US-10-301-480-574801	Sequence 574801,	c 834	204.6	15.8	1485	4	US-09-925-065A-700656	Sequence 700656,
762	205.6	15.9	964	12	US-10-301-480-1188210	Sequence 1188210,	c 835	204.6	15.8	1485	4	US-09-925-065A-700656	Sequence 700656,
c 763	205.6	15.9	4741	7	US-10-352-762-4	Sequence 4,	c 836	204.6	15.8	43103	9	US-10-741-600-17772	Sequence 17772, A
c 764	205.6	15.9	16622	9	US-10-741-600-17704	Sequence 17704, A	c 837	204.6	15.8	46878	10	US-10-995-561-13276	Sequence 13276, A
c 765	205.6	15.9	39599	9	US-10-741-600-17949	Sequence 17949, A	c 838	204.6	15.8	46878	10	US-10-995-561-13276	Sequence 13276, A
c 766	205.6	15.9	200628	15	US-11-121-086-62	Sequence 62, Appl	c 839	204.6	15.8	106707	9	US-10-694-685-8	Sequence 8, Appl
c 767	205.6	15.9	418550	7	US-10-232-738-1463	Sequence 1463, Ap	c 840	204.6	15.8	202814	9	US-10-719-993-6812	Sequence 6812, Ap
c 768	205.6	15.9	680	4	US-09-925-065A-80244	Sequence 80244, A	c 841	204.6	15.8	687411	11	US-10-330-773-26	Sequence 13286, A
c 769	205.4	15.9	680	5	US-09-925-065A-80244	Sequence 80244, A	c 842	204.6	15.8	1125000	10	US-10-995-561-13286	Sequence 520123,
770	205.4	15.9	680	12	US-10-301-480-181483	Sequence 181483,	c 843	204.4	15.8	516	4	US-09-925-065A-520123	Sequence 520123,
771	205.4	15.9	680	12	US-10-301-480-181483	Sequence 181483,	c 844	204.4	15.8	516	4	US-09-925-065A-520123	Sequence 520123,
772	205.4	15.9	989	12	US-10-301-480-794892	Sequence 794892,	c 845	204.4	15.8	582	4	US-09-925-065A-761309	Sequence 761309,
773	205.4	15.9	989	12	US-10-301-480-602363	Sequence 602363,	c 846	204.4	15.8	582	4	US-09-925-065A-761309	Sequence 761309,
c 774	205.4	15.9	32865	6	US-10-087-192-964	Sequence 1215772,	c 847	204.4	15.8	586	4	US-09-925-065A-768648	Sequence 768648,
c 775	205.4	15.9	68123	8	US-10-741-601-5697	Sequence 5697, Ap	c 848	204.4	15.8	586	4	US-09-925-065A-768648	Sequence 768648,
c 776	205.4	15.9	68123	9	US-10-741-600-17774	Sequence 17774, A	c 849	204.4	15.8	605	4	US-09-925-065A-52356	Sequence 52356, A
c 777	205.4	15.9	1790242	9	US-10-719-993-6940	Sequence 6940, Ap	c 850	204.4	15.8	605	4	US-09-925-065A-52356	Sequence 52356, A
778	205.2	15.8	444	9	US-10-674-124A-22050	Sequence 22050, Ap	c 851	204.4	15.8	605	12	US-10-301-480-153594	Sequence 153594,
c 779	205.2	15.8	112132	3	US-09-741-150-3	Sequence 3, Appl	c 852	204.4	15.8	605	12	US-10-301-480-153594	Sequence 153594,
c 780	205.2	15.8	112132	3	US-10-612-012-3	Sequence 3, Appl	c 853	204.4	15.8	820	4	US-09-925-065A-24394	Sequence 24394, A
781	205.2	15.8	116327	9	US-10-719-993-6867	Sequence 6867, Ap	c 854	204.4	15.8	820	4	US-09-925-065A-24394	Sequence 24394, A
782	205.2	15.8	183046	10	US-10-981-277-31	Sequence 31, Appl	c 855	204.4	15.8	820	5	US-09-925-065A-24394	Sequence 24394, A
c 783	205.2	15.8	398287	8	US-10-741-601-5719	Sequence 5719, Ap	c 856	204.4	15.8	820	5	US-09-925-065A-24394	Sequence 24394, A
c 784	205.2	15.8	398287	9	US-10-741-600-17839	Sequence 17839, A	c 857	204.4	15.8	820	12	US-10-301-480-125631	Sequence 125631,
c 785	205.2	15.8	398287	10	US-10-995-561-13396	Sequence 13396, A	c 858	204.4	15.8	820	12	US-10-301-480-125632	Sequence 125632,
c 786	205.2	15.8	602	4	US-09-925-065A-121693	Sequence 121693,	c 859	204.4	15.8	820	12	US-10-301-480-739040	Sequence 739040,
c 787	205.2	15.8	602	5	US-09-925-065A-121693	Sequence 121693,	c 860	204.4	15.8	820	12	US-10-301-480-739041	Sequence 739041,
c 788	205.2	15.8	659	4	US-09-925-065A-666893	Sequence 666893,	c 861	204.4	15.8	894	4	US-09-925-065A-74250	Sequence 74250, A
c 789	205.2	15.8	659	5	US-09-925-065A-666893	Sequence 666893,	c 862	204.4	15.8	894	4	US-09-925-065A-74250	Sequence 74250, A
c 790	205.2	15.8	10283	3	US-09-938-795A-3	Sequence 3, Appl	c 863	204.4	15.8	894	5	US-09-925-065A-74250	Sequence 74250, A
c 791	205.2	15.8	23490	10	US-10-737-082-62	Sequence 62, Appl	c 864	204.4	15.8	894	5	US-09-925-065A-74250	Sequence 74250, A
c 792	205.2	15.8	23490	10	US-10-765-790-62	Sequence 62, Appl	c 865	204.4	15.8	894	5	US-09-925-065A-74250	Sequence 74250, A
793	205.2	15.8	126552	15	US-11-121-086-1	Sequence 1, Appl	c 866	204.4	15.8	894	12	US-10-301-480-175489	Sequence 175489,
c 794	205.2	15.8	169047	15	US-11-121-086-15	Sequence 15, Appl	c 867	204.4	15.8	894	12	US-10-301-480-175489	Sequence 175489,
c 795	205.2	15.8	178877	15	US-11-121-086-17	Sequence 17, Appl	c 868	204.4	15.8	894	12	US-10-301-480-788898	Sequence 788898,
c 796	204.8	15.8	582	4	US-09-925-065A-761310	Sequence 761310,	c 869	204.4	15.8	10500	3	US-09-764-891-8022	Sequence 8022, Ap
c 797	204.8	15.8	582	4	US-09-925-065A-829858	Sequence 829858,	c 870	204.4	15.8	109977	9	US-10-719-993-6870	Sequence 6870, Ap
c 798	204.8	15.8	582	5	US-09-925-065A-761310	Sequence 761310,	c 871	204.4	15.8	159146	15	US-11-121-086-49	Sequence 49, Appl
c 799	204.8	15.8	582	5	US-09-925-065A-829858	Sequence 829858,	c 872	204.4	15.8	159146	15	US-10-893-315-148	Sequence 148, App
c 800	204.8	15.8	586	4	US-09-925-065A-768647	Sequence 768647,	c 873	204.4	15.8	207557	10	US-10-893-315-134	Sequence 134, App
c 801	204.8	15.8	586	4	US-09-925-065A-834164	Sequence 834164,	c 874	204.4	15.8	1691339	6	US-10-067-514-1	Sequence 1, Appl
c 802	204.8	15.8	586	5	US-09-925-065A-768647	Sequence 768647,	c 875	204.4	15.8	1691339	8	US-10-419-723-1	Sequence 1, Appl
c 803	204.8	15.8	586	5	US-09-925-065A-834164	Sequence 834164,	c 876	204.4	15.8	1691139	8	US-10-255-120-1	Sequence 1, Appl
c 804	204.8	15.8	1132	4	US-09-925-065A-28245	Sequence 28245, A	c 877	204.4	15.8	1691140	10	US-10-868-397-1	Sequence 1, Appl
c 805	204.8	15.8	1132	5	US-09-925-065A-28245	Sequence 28245, A	c 878	204.4	15.8	1691140	15	US-11-091-018-1	Sequence 1, Appl
c 806	204.8	15.8	1132	12	US-10-301-480-129482	Sequence 129482,	c 879	204.2	15.8	420	4	US-09-925-065A-286319	Sequence 286319,
c 807	204.8	15.8	1132	12	US-10-301-480-129482	Sequence 129482,	c 880	204.2	15.8	420	4	US-09-925-065A-286319	Sequence 286319,
c 808	204.8	15.8	2066	6	US-10-037-632-97510	Sequence 97510, A	c 881	204.2	15.8	420	5	US-09-925-065A-286319	Sequence 286319,
c 809	204.8	15.8	2066	7	US-10-037-632-97510	Sequence 97510, A	c 882	204.2	15.8	420	5	US-09-925-065A-286319	Sequence 286319,
c 810	204.8	15.8	10040	3	US-09-764-891-8365	Sequence 8365, Ap	c 883	204.2	15.8	582	12	US-10-301-480-674886	Sequence 674886,
c 811	204.8	15.8	34161	6	US-10-087-192-1540	Sequence 1540, Ap	c 884	204.2	15.8	582	12	US-10-301-480-674886	Sequence 674886,
c 812	204.8	15.8	34161	6	US-10-322-281-436	Sequence 436, Ap	c 885	204.2	15.8	592	6	US-10-027-632-113416	Sequence 113416,
c 813	204.8	15.8	92638	8	US-10-450-826-3	Sequence 3, Appl	c 886	204.2	15.8	592	7	US-10-027-632-113416	Sequence 113416,
c 814	204.8	15.8	210204	9	US-10-723-860-1746	Sequence 1746, Ap	c 887	204.2	15.8	608	4	US-09-925-065A-819599	Sequence 819599,
c 815	204.8	15.8	210204	10	US-10-756-149-1685	Sequence 1685, Ap	c 888	204.2	15.8	608	5	US-09-925-065A-819599	Sequence 819599,
c 816	204.6	15.8	614	4	US-09-925-065A-728635	Sequence 728635,	c 889	204.2	15.8	614	12	US-10-301-480-375468	Sequence 375468,
c 817	204.6	15.8	614	4	US-09-925-065A-807925	Sequence 807925,	c 890	204.2	15.8	614	12	US-10-301-480-988877	Sequence 988877,
c 818	204.6	15.8	614	5	US-09-925-065A-807925	Sequence 807925,	c 891	204.2	15.8	620	4	US-09-925-065A-298844	Sequence 298844,
c 819	204.6	15.8	614	5	US-09-925-065A-807925	Sequence 807925,	c 892	204.2	15.8	620	5	US-09-925-065A-298844	Sequence 298844,
c 820	204.6	15.8	617	4	US-09-925-065A-764111	Sequence 764111,	c 893	204.2	15.8	1421	4	US-09-925-065A-667547	Sequence 667547,
c 821	204.6	15.8	617	5	US-09-925-065A-764111	Sequence 764111,	c 894	204.2	15.8	1421	4	US-09-925-065A-667547	Sequence 667547,
c 822	204.6	15.8	625	4	US-09-925-065A-813055	Sequence 813055,	c 895	204.2	15.8	1421	5	US-09-925-065A-667547	Sequence 667547,
c 823	204.6	15.8	625	5	US-09-925-065A-813055	Sequence 813055,	c 896	204.2	15.8	1421	5	US-09-925-065A-667547	Sequence 667547,
c 824	204.6	15.8	978	12	US-10-301-480-544107	Sequence 544107,	c 897	204.2	15.8	1461	4	US-09-925-065A-680305	Sequence 680305,
c 825	204.6	15.8	978	12	US-10-301-480-1157516	Sequence 1157516,	c 898	204.2	15.8	1461	5	US-09-925-065A-680305	Sequence 680305,
c 826	204.6	15.8	997	6	US-10-037-632-121845	Sequence 121845,	c 899	204.2	15.8	2182	4	US-09-925-065A-698956	Sequence 698956,
c 827	204.6	15.8	997	6	US-10-037-632-121846	Sequence 121846,	c 900	204.2	15.8	2182	5	US-09-925-065A-698956	Sequence 698956,
c 828	204.6	15.8	997	7	US-10-027-632-121845	Sequence 121845,	c 901	204.2	15.8	26874	7	US-10-004-113-34	Sequence 34, Appl

1048	203	15.7	1421	12	US-10-301-480-142453	Sequence 142453,	c1121	202.6	15.6	63824	9	US-10-600-009-348	Sequence 348, App
1049	203	15.7	1421	12	US-10-301-480-755862	Sequence 755862,	c1122	202.6	15.6	113589	8	US-10-764-425-9	Sequence 30, Appli
1050	203	15.7	31814	7	US-09-817-182-3	Sequence 3, Appli	c1123	202.6	15.6	158692	15	US-11-121-086-30	Sequence 50, Appli
1051	203	15.7	31814	9	US-10-473-349-3	Sequence 3, Appli	c1124	202.6	15.6	203467	15	US-11-121-086-50	Sequence 50, Appli
1052	203	15.7	42863	7	US-10-017-161-1017	Sequence 1017, Ap	c1125	202.6	15.6	290040	9	US-10-850-591-3	Sequence 3, Appli
1053	203	15.7	42863	7	US-10-232-798-865	Sequence 865, App	c1126	202.6	15.6	290040	9	US-10-850-586-3	Sequence 3, Appli
1054	203	15.7	52242	8	US-10-052-482-172	Sequence 172, App	c1128	202.4	15.6	590	4	US-09-925-065A-70657	Sequence 70657, A
1055	203	15.7	152335	15	US-11-121-086-73	Sequence 73, Appli	c1128	202.4	15.6	590	4	US-09-925-065A-70657	Sequence 70657, A
1056	203	15.7	171427	15	US-11-112-908-60	Sequence 60, Appli	c1129	202.4	15.6	590	12	US-10-301-480-171896	Sequence 171896, A
1057	203	15.7	193084	15	US-11-121-086-82	Sequence 82, Appli	c1130	202.4	15.6	590	12	US-10-301-480-785305	Sequence 785305, A
1058	202.8	15.7	516	4	US-09-925-065A-520122	Sequence 520122,	c1131	202.4	15.6	624	4	US-09-925-065A-786298	Sequence 786298, A
1059	202.8	15.7	516	5	US-09-925-065A-520122	Sequence 520122,	c1132	202.4	15.6	624	5	US-09-925-065A-786298	Sequence 786298, A
1060	202.8	15.7	605	4	US-09-925-065A-52357	Sequence 52357, A	c1133	202.4	15.6	645	4	US-09-925-065A-467691	Sequence 467691, A
1061	202.8	15.7	605	4	US-09-925-065A-52358	Sequence 52358, A	c1134	202.4	15.6	645	5	US-09-925-065A-467691	Sequence 467691, A
1062	202.8	15.7	605	4	US-09-925-065A-52358	Sequence 52358, A	c1135	202.4	15.6	646	6	US-10-027-632-132430	Sequence 132430, A
1063	202.8	15.7	605	5	US-09-925-065A-52357	Sequence 52357, A	c1136	202.4	15.6	646	7	US-10-027-632-132430	Sequence 132430, A
1064	202.8	15.7	605	5	US-09-925-065A-52358	Sequence 52358, A	c1137	202.4	15.6	654	4	US-09-925-065A-878071	Sequence 878071, A
1065	202.8	15.7	605	5	US-09-925-065A-52358	Sequence 52358, A	c1138	202.4	15.6	654	5	US-09-925-065A-878071	Sequence 878071, A
1066	202.8	15.7	605	12	US-10-301-480-153595	Sequence 153595,	c1139	202.4	15.6	675	12	US-10-301-480-41044	Sequence 41044, A
1067	202.8	15.7	605	12	US-10-301-480-153595	Sequence 153595,	c1140	202.4	15.6	675	12	US-10-301-480-654453	Sequence 654453, A
1068	202.8	15.7	605	12	US-10-301-480-153597	Sequence 153597,	c1141	202.4	15.6	682	12	US-10-301-480-455334	Sequence 455334, A
1069	202.8	15.7	605	12	US-10-301-480-767004	Sequence 767004,	c1142	202.4	15.6	682	12	US-10-301-480-1068743	Sequence 1068743, A
1070	202.8	15.7	605	12	US-10-301-480-767005	Sequence 767005,	c1143	202.4	15.6	685	4	US-09-925-065A-386776	Sequence 386776, A
1071	202.8	15.7	605	12	US-10-301-480-767006	Sequence 767006,	c1144	202.4	15.6	685	5	US-09-925-065A-386776	Sequence 386776, A
1072	202.8	15.7	683	10	US-10-915-740A-267	Sequence 267, App	c1145	202.4	15.6	992	12	US-10-301-480-575746	Sequence 575746, A
1073	202.8	15.7	688	4	US-09-925-065A-62542	Sequence 62542, A	c1146	202.4	15.6	992	12	US-10-301-480-575747	Sequence 575747, A
1074	202.8	15.7	688	5	US-09-925-065A-62542	Sequence 62542, A	c1147	202.4	15.6	992	12	US-10-301-480-1189155	Sequence 1189155, A
1075	202.8	15.7	688	12	US-10-301-480-163780	Sequence 163780, A	c1148	202.4	15.6	992	12	US-10-301-480-1189155	Sequence 1189155, A
1076	202.8	15.7	688	12	US-10-301-480-777189	Sequence 777189,	c1149	202.4	15.6	998	12	US-10-301-480-586602	Sequence 586602, A
1077	202.8	15.7	959	12	US-10-301-480-609405	Sequence 609405,	c1150	202.4	15.6	998	12	US-10-301-480-1200011	Sequence 1200011, A
1078	202.8	15.7	959	12	US-10-301-480-1222814	Sequence 1222814,	c1151	202.4	15.6	2157	3	US-09-822-830A-11	Sequence 11, Appli
1079	202.8	15.7	21442	10	US-10-995-561-13469	Sequence 13469, A	c1152	202.4	15.6	2574	12	US-10-301-480-27883	Sequence 27883, A
1080	202.8	15.7	31208	3	US-09-852-067-3	Sequence 3, Appli	c1153	202.4	15.6	2574	12	US-10-301-480-641292	Sequence 641292, A
1081	202.8	15.7	31208	6	US-10-338-691-3	Sequence 3, Appli	c1154	202.4	15.6	3225	4	US-09-925-065A-55808	Sequence 55808, A
1082	202.8	15.7	31208	13	US-11-064-022-3	Sequence 3, Appli	c1155	202.4	15.6	3225	4	US-09-925-065A-55811	Sequence 55811, A
1083	202.8	15.7	33478	8	US-10-322-281-188	Sequence 188, App	c1156	202.4	15.6	3225	5	US-09-925-065A-55808	Sequence 55808, A
1084	202.8	15.7	35770	10	US-10-995-561-13296	Sequence 13296, A	c1157	202.4	15.6	3225	5	US-09-925-065A-55811	Sequence 55811, A
1085	202.8	15.7	64125	6	US-10-322-281-350	Sequence 350, App	c1158	202.4	15.6	3225	6	US-10-027-632-256776	Sequence 256776, A
1086	202.8	15.7	77478	6	US-10-087-192-1378	Sequence 1378, Ap	c1159	202.4	15.6	3225	7	US-10-027-632-256776	Sequence 256776, A
1087	202.8	15.7	83712	10	US-10-995-561-13366	Sequence 13366, A	c1160	202.4	15.6	3225	12	US-10-301-480-91575	Sequence 91575, A
1088	202.8	15.7	86361	10	US-10-995-561-13364	Sequence 13364, A	c1161	202.4	15.6	3225	12	US-10-301-480-157046	Sequence 157046, A
1089	202.8	15.7	109730	9	US-10-741-600-17809	Sequence 17809, A	c1162	202.4	15.6	3225	12	US-10-301-480-157049	Sequence 157049, A
1090	202.8	15.7	113604	6	US-10-227-195A-1	Sequence 1, Appli	c1163	202.4	15.6	3225	12	US-10-301-480-704984	Sequence 704984, A
1091	202.8	15.7	113604	6	US-10-227-195A-2	Sequence 2, Appli	c1164	202.4	15.6	3225	12	US-10-301-480-770455	Sequence 770455, A
1092	202.8	15.7	113604	8	US-10-227-152B-1	Sequence 1, Appli	c1165	202.4	15.6	3225	12	US-10-301-480-770458	Sequence 770458, A
1093	202.8	15.7	113604	8	US-10-227-152B-2	Sequence 2, Appli	c1166	202.4	15.6	7737	3	US-09-764-887-453	Sequence 453, App
1094	202.8	15.7	213300	10	US-10-840-590-7	Sequence 7, Appli	c1167	202.4	15.6	7737	3	US-09-764-847-2001	Sequence 2001, Ap
1095	202.8	15.7	599001	10	US-10-317-869A-4	Sequence 4, Appli	c1168	202.4	15.6	7737	6	US-10-092-154-2001	Sequence 453, App
1096	202.8	15.7	653122	6	US-10-087-192-226	Sequence 226, App	c1169	202.4	15.6	7737	6	US-10-073-961-453	Sequence 8743, Ap
1097	202.6	15.6	392	9	US-10-674-124A-21188	Sequence 21188, A	c1170	202.4	15.6	10198	3	US-09-764-891-8744	Sequence 8744, Ap
1098	202.6	15.6	421	9	US-10-674-124A-311	Sequence 311, App	c1171	202.4	15.6	10198	3	US-09-764-891-8744	Sequence 1558, Ap
1099	202.6	15.6	555	12	US-10-301-480-612598	Sequence 612598,	c1172	202.4	15.6	26332	6	US-10-087-192-1558	Sequence 8149, Ap
1100	202.6	15.6	555	12	US-10-301-480-612598	Sequence 612598,	c1173	202.4	15.6	31474	3	US-09-764-891-8149	Sequence 13, Appli
1101	202.6	15.6	556	4	US-09-925-065A-912560	Sequence 912560,	c1174	202.4	15.6	70000	8	US-10-210-723-13	Sequence 36, Appli
1102	202.6	15.6	556	5	US-09-925-065A-912560	Sequence 912560,	c1175	202.4	15.6	91697	15	US-10-417-375-36	Sequence 44, Appli
1103	202.6	15.6	583	12	US-10-301-480-4412	Sequence 4412, Ap	c1176	202.4	15.6	150437	15	US-11-112-908-44	Sequence 44, Appli
1104	202.6	15.6	583	12	US-10-301-480-617821	Sequence 617821,	c1177	202.4	15.6	150491	15	US-11-112-908-45	Sequence 46, Appli
1105	202.6	15.6	588	4	US-09-925-065A-204287	Sequence 204287,	c1178	202.4	15.6	182314	15	US-11-112-908-45	Sequence 45, Appli
1106	202.6	15.6	588	5	US-09-925-065A-204287	Sequence 204287,	c1179	202.4	15.6	182314	15	US-11-112-908-45	Sequence 45, Appli
1107	202.6	15.6	605	12	US-10-301-480-323857	Sequence 323857,	c1180	202.4	15.6	37952	10	US-10-481-613-71	Sequence 71, Appli
1108	202.6	15.6	605	12	US-10-301-480-937266	Sequence 937266,	c1181	202.4	15.6	1980090	9	US-10-719-993-6815	Sequence 6815, Ap
1109	202.6	15.6	607	12	US-10-301-480-292439	Sequence 292439,	c1182	202.4	15.6	1980090	9	US-10-741-600-17676	Sequence 17676, A
1110	202.6	15.6	607	12	US-10-301-480-292439	Sequence 292439,	c1183	202.2	15.6	482	9	US-10-674-124A-16717	Sequence 16717, A
1111	202.6	15.6	40185	8	US-10-741-601-5687	Sequence 5687, Ap	c1184	202.2	15.6	573	4	US-09-925-065A-833297	Sequence 833297, A
1112	202.6	15.6	40185	9	US-10-741-600-17752	Sequence 17752, A	c1185	202.2	15.6	573	5	US-09-925-065A-833297	Sequence 833297, A
1113	202.6	15.6	42975	9	US-10-741-600-17752	Sequence 17752, A	c1186	202.2	15.6	605	5	US-09-925-065A-890002	Sequence 890002, A
1114	202.6	15.6	43975	9	US-10-741-600-17669	Sequence 17669, A	c1187	202.2	15.6	605	5	US-09-925-065A-890002	Sequence 890002, A
1115	202.6	15.6	43975	10	US-10-995-561-13279	Sequence 13279, A	c1188	202.2	15.6	639	12	US-10-301-480-364138	Sequence 364138, A
1116	202.6	15.6	58922	8	US-10-322-281-526	Sequence 526, App	c1189	202.2	15.6	666	6	US-10-027-632-264517	Sequence 264517, A
1117	202.6	15.6	63045	9	US-10-714-796-76	Sequence 76, Appli	c1190	202.2	15.6	666	7	US-10-027-632-264517	Sequence 264517, A
1118	202.6	15.6	63824	7	US-10-282-174-347	Sequence 347, App	c1191	202.2	15.6	666	12	US-10-301-480-99343	Sequence 99343, A
1119	202.6	15.6	63824	7	US-10-282-174-348	Sequence 348, App	c1192	202.2	15.6	666	12	US-10-301-480-712752	Sequence 712752, A
1120	202.6	15.6	63824	9	US-10-600-009-347	Sequence 347, App	c1193	202.2	15.6	832	12	US-10-301-480-545764	Sequence 545764, A

1194	202.2	15.6	832	12	US-10-301-480-1159173	Sequence 1159173,	cl267	202	15.6	1669	6	US-10-027-632-260804	Sequence 260804,
1195	202.2	15.6	1125	6	US-10-027-632-118242	Sequence 118242,	cl268	202	15.6	1669	7	US-10-027-632-260804	Sequence 260804,
1196	202.2	15.6	1125	7	US-10-027-632-118242	Sequence 118242,	cl268	202	15.6	1669	12	US-10-301-480-25616	Sequence 25616, A
cl197	202.2	15.6	1291	4	US-09-925-065A-52709	Sequence 52709, A	cl269	202	15.6	1669	12	US-10-301-480-709025	Sequence 709025,
cl198	202.2	15.6	1291	4	US-09-925-065A-52710	Sequence 52710, A	cl270	202	15.6	3225	4	US-09-925-065A-55809	Sequence 55809, A
cl199	202.2	15.6	1291	4	US-09-925-065A-52711	Sequence 52711, A	cl271	202	15.6	3225	4	US-09-925-065A-55809	Sequence 55809, A
cl200	202.2	15.6	1291	5	US-09-925-065A-52710	Sequence 52709, A	cl272	202	15.6	3225	5	US-09-925-065A-55809	Sequence 55809, A
cl201	202.2	15.6	1291	5	US-09-925-065A-52710	Sequence 52709, A	cl273	202	15.6	3225	5	US-09-925-065A-55809	Sequence 55809, A
cl202	202.2	15.6	1291	5	US-09-925-065A-52711	Sequence 52710, A	cl274	202	15.6	3225	12	US-10-301-480-157047	Sequence 157047,
cl203	202.2	15.6	1291	12	US-10-301-480-153947	Sequence 153947, A	cl275	202	15.6	3225	12	US-10-301-480-770456	Sequence 770456,
cl204	202.2	15.6	1291	12	US-10-301-480-153948	Sequence 153948, A	cl276	202	15.6	16489	3	US-09-764-868-1483	Sequence 1483, A
cl205	202.2	15.6	1291	12	US-10-301-480-153949	Sequence 153949, A	cl278	202	15.6	30826	7	US-10-074-024-726	Sequence 726, App
cl206	202.2	15.6	1291	12	US-10-301-480-153956	Sequence 153956, A	cl279	202	15.6	31949	3	US-09-764-891-8098	Sequence 8098, App
cl207	202.2	15.6	1291	12	US-10-301-480-153957	Sequence 153957, A	cl280	202	15.6	32186	3	US-09-764-891-8099	Sequence 8099, App
cl208	202.2	15.6	1291	12	US-10-301-480-153958	Sequence 153958, A	cl281	202	15.6	40136	6	US-10-087-192-8088	Sequence 8088, App
cl209	202.2	15.6	1295	4	US-09-925-065A-287245	Sequence 287245, A	cl282	202	15.6	45517	8	US-10-741-601-5753	Sequence 5753, App
cl210	202.2	15.6	1295	5	US-09-925-065A-287245	Sequence 287245, A	cl283	202	15.6	45517	8	US-10-741-601-5753	Sequence 5753, App
cl211	202.2	15.6	1295	4	US-09-925-065A-41844	Sequence 41844, A	cl284	202	15.6	45517	10	US-10-995-561-13455	Sequence 13455, A
cl212	202.2	15.6	1729	5	US-09-925-065A-41844	Sequence 41844, A	cl285	202	15.6	86361	8	US-10-741-601-5702	Sequence 5702, App
cl213	202.2	15.6	1729	12	US-10-301-480-143082	Sequence 143082, A	cl286	202	15.6	86361	9	US-10-741-601-5702	Sequence 5702, App
cl214	202.2	15.6	1729	12	US-10-301-480-1756491	Sequence 1756491, A	cl287	202	15.6	96588	7	US-10-085-117-76	Sequence 17803, A
cl215	202.2	15.6	6257	3	US-09-984-429-381	Sequence 381, App	cl288	202	15.6	96588	7	US-10-085-117-76	Sequence 76, Appl
cl216	202.2	15.6	20991	8	US-10-741-601-5772	Sequence 5772, App	cl289	202	15.6	218336	16	US-11-114-798-57	Sequence 57, Appl
cl217	202.2	15.6	20991	10	US-10-995-561-13488	Sequence 13488, A	cl290	202	15.6	218336	6	US-10-473-939-10	Sequence 10, Appl
cl218	202.2	15.6	24477	9	US-10-741-601-17827	Sequence 17827, A	cl291	202	15.6	226215	6	US-10-087-192-1348	Sequence 1948, App
cl219	202.2	15.6	31657	8	US-10-741-601-5690	Sequence 5690, App	cl292	202	15.6	226215	8	US-10-322-696-58	Sequence 58, Appl
cl220	202.2	15.6	31657	10	US-10-995-561-13334	Sequence 13334, A	cl293	202	15.6	334462	10	US-10-496-011-1	Sequence 1, Appl
cl221	202.2	15.6	33175	8	US-10-741-601-5651	Sequence 5651, App	cl294	201.8	15.6	465	4	US-09-925-065A-947399	Sequence 947399, A
cl222	202.2	15.6	33175	6	US-10-995-561-13270	Sequence 13270, A	cl295	201.8	15.6	465	5	US-09-925-065A-947399	Sequence 947399, A
cl223	202.2	15.6	54016	9	US-10-741-601-17886	Sequence 17886, A	cl296	201.8	15.6	467	4	US-09-925-065A-949560	Sequence 949560, A
cl224	202.2	15.6	73063	11	US-10-330-773-704	Sequence 704, App	cl297	201.8	15.6	467	5	US-09-925-065A-949560	Sequence 949560, A
cl225	202.2	15.6	75007	8	US-10-741-601-5612	Sequence 5612, App	cl298	201.8	15.6	591	6	US-10-027-632-280011	Sequence 280011, A
cl226	202.2	15.6	75007	9	US-10-741-601-17556	Sequence 17556, A	cl299	201.8	15.6	591	6	US-10-027-632-280012	Sequence 280012, A
cl227	202.2	15.6	75007	9	US-10-741-601-17556	Sequence 17556, A	cl300	201.8	15.6	591	7	US-10-027-632-280011	Sequence 280011, A
cl228	202.2	15.6	163350	10	US-10-995-561-13194	Sequence 13194, A	cl301	201.8	15.6	591	7	US-10-027-632-280011	Sequence 280011, A
cl229	202.2	15.6	168174	8	US-10-071-411-63	Sequence 3, Appl	cl302	201.8	15.6	593	4	US-09-925-065A-278768	Sequence 278768, A
cl230	202.2	15.6	168174	9	US-10-914-799-63	Sequence 63, Appl	cl303	201.8	15.6	593	5	US-09-925-065A-278768	Sequence 278768, A
cl231	202.2	15.6	168273	8	US-10-071-411-2	Sequence 2, Appl	cl304	201.8	15.6	601	10	US-10-893-315-382	Sequence 382, App
cl232	202.2	15.6	168273	9	US-10-914-799-2	Sequence 2, Appl	cl305	201.8	15.6	601	10	US-10-893-315-382	Sequence 382, App
cl233	202	15.6	450	12	US-10-301-480-50887	Sequence 50887, A	cl306	201.8	15.6	611	4	US-09-925-065A-821990	Sequence 821990, A
cl234	202	15.6	450	12	US-10-301-480-664296	Sequence 664296, A	cl307	201.8	15.6	611	5	US-09-925-065A-821990	Sequence 821990, A
cl235	202	15.6	555	4	US-09-925-065A-741906	Sequence 741906, A	cl308	201.8	15.6	622	4	US-09-925-065A-729912	Sequence 729912, A
cl236	202	15.6	555	5	US-09-925-065A-741906	Sequence 741906, A	cl309	201.8	15.6	622	5	US-09-925-065A-729912	Sequence 729912, A
cl237	202	15.6	573	4	US-08-925-065A-786528	Sequence 786528, A	cl310	201.8	15.6	633	4	US-09-925-065A-770686	Sequence 770686, A
cl238	202	15.6	573	5	US-08-925-065A-786528	Sequence 786528, A	cl311	201.8	15.6	633	4	US-09-925-065A-770686	Sequence 770686, A
cl239	202	15.6	623	4	US-09-925-065A-8006	Sequence 8006, App	cl312	201.8	15.6	633	5	US-09-925-065A-770686	Sequence 770686, A
cl240	202	15.6	623	5	US-09-925-065A-8006	Sequence 8006, App	cl313	201.8	15.6	639	12	US-10-301-480-364137	Sequence 364137, A
cl241	202	15.6	623	12	US-10-301-480-109243	Sequence 109243, A	cl314	201.8	15.6	639	12	US-10-301-480-364137	Sequence 364137, A
cl242	202	15.6	623	12	US-10-301-480-723652	Sequence 723652, A	cl315	201.8	15.6	639	12	US-10-301-480-364137	Sequence 364137, A
cl243	202	15.6	656	6	US-10-027-632-27832	Sequence 27832, A	cl316	201.8	15.6	878	4	US-09-925-065A-55287	Sequence 55287, A
cl244	202	15.6	656	7	US-10-027-632-27832	Sequence 27832, A	cl317	201.8	15.6	878	5	US-09-925-065A-55287	Sequence 55287, A
cl245	202	15.6	661	6	US-10-027-632-257580	Sequence 257580, A	cl318	201.8	15.6	878	12	US-10-301-480-769934	Sequence 769934, A
cl246	202	15.6	661	7	US-10-027-632-257581	Sequence 257581, A	cl319	201.8	15.6	897	7	US-10-027-632-121729	Sequence 121729, A
cl247	202	15.6	661	7	US-10-027-632-257580	Sequence 257580, A	cl320	201.8	15.6	897	7	US-10-027-632-121729	Sequence 121729, A
cl248	202	15.6	661	7	US-10-027-632-257581	Sequence 257581, A	cl321	201.8	15.6	979	7	US-10-027-632-120531	Sequence 120531, A
cl249	202	15.6	661	7	US-10-027-632-257581	Sequence 257581, A	cl322	201.8	15.6	979	7	US-10-027-632-120531	Sequence 120531, A
cl250	202	15.6	661	12	US-10-301-480-93284	Sequence 93284, A	cl323	201.8	15.6	1367	3	US-09-764-891-9551	Sequence 9551, App
cl251	202	15.6	661	12	US-10-301-480-93285	Sequence 93285, A	cl324	201.8	15.6	16491	3	US-09-764-891-9551	Sequence 5505, App
cl252	202	15.6	661	12	US-10-301-480-705793	Sequence 705793, A	cl325	201.8	15.6	21501	10	US-10-472-533-641	Sequence 641, App
cl253	202	15.6	680	12	US-10-301-480-705794	Sequence 705794, A	cl326	201.8	15.6	21501	10	US-10-472-533-641	Sequence 641, App
cl254	202	15.6	680	12	US-10-301-480-611187	Sequence 611187, A	cl327	201.8	15.6	57095	8	US-10-719-993-7030	Sequence 7030, App
cl255	202	15.6	680	12	US-10-301-480-1224596	Sequence 1224596, A	cl328	201.8	15.6	57095	8	US-10-052-483-82	Sequence 82, Appl
cl256	202	15.6	682	12	US-10-301-480-455335	Sequence 455335, A	cl329	201.8	15.6	106338	8	US-10-322-281-566	Sequence 566, App
cl257	202	15.6	682	12	US-10-301-480-455336	Sequence 455336, A	cl330	201.8	15.6	106338	8	US-10-322-281-566	Sequence 566, App
cl258	202	15.6	682	12	US-10-301-480-1068744	Sequence 1068744, A	cl331	201.8	15.6	108111	9	US-10-719-993-6843	Sequence 6843, App
cl259	202	15.6	682	12	US-10-301-480-1068744	Sequence 1068744, A	cl332	201.8	15.6	108111	9	US-10-719-993-6843	Sequence 6843, App
cl260	202	15.6	685	4	US-09-925-065A-386777	Sequence 386777, A	cl333	201.8	15.6	122673	10	US-10-737-082-33	Sequence 33, Appl
cl261	202	15.6	685	4	US-09-925-065A-386778	Sequence 386778, A	cl334	201.8	15.6	122673	10	US-10-737-082-33	Sequence 33, Appl
cl262	202	15.6	685	5	US-09-925-065A-386777	Sequence 386777, A	cl335	201.8	15.6	200620	10	US-10-765-790-33	Sequence 33, Appl
cl263	202	15.6	685	5	US-09-925-065A-386778	Sequence 386778, A	cl336	201.8	15.6	200620	10	US-10-765-790-33	Sequence 33, Appl
cl264	202	15.6	961	12	US-10-301-480-600485	Sequence 600485, A	cl337	201.8	15.6	238417	10	US-10-461-862-98	Sequence 98, Appl
cl265	202	15.6	961	12	US-10-301-480-1213894	Sequence 1213894, A	cl338	201.6	15.6	468	6	US-10-027-632-195243	Sequence 195243, A
cl266	202	15.6	995	12	US-10-301-480-571572	Sequence 571572, A	cl339	201.6	15.6	468	6	US-10-027-632-195244	Sequence 195244, A
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(without alignments)
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Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	196.2	15.2	394191	6 US-10-506-549-3
6	195.2	15.1	2534	7 US-11-145-307A-58
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8	192.4	14.9	7391	6 US-10-511-937-629
9	190.6	14.7	394191	6 US-10-506-549-3
10	187.4	14.5	138941	6 US-10-489-730-10
11	186	14.4	37426	6 US-10-473-173-32
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c 69	166.2	12.8	1645	6 US-10-513-076-776	Sequence 776, App
c 70	166	12.8	4498	6 US-10-511-937-425	Sequence 425, App
c 71	165.6	12.8	3144	6 US-10-511-937-467	Sequence 467, App
c 72	165	12.7	2101	6 US-10-505-928-756	Sequence 756, App
c 74	164.2	12.7	70665	6 US-10-505-928-596	Sequence 596, App
c 75	164	12.7	4314	6 US-10-511-937-553	Sequence 553, App
c 77	163.2	12.6	3178	6 US-10-505-928-277	Sequence 277, App
c 78	162.8	12.6	5047	6 US-10-505-928-575	Sequence 575, App
c 79	162.2	12.5	1776	6 US-10-505-928-368	Sequence 368, App
c 80	162	12.5	776	1 US-09-949-925-27	Sequence 27, Appl
c 81	161.8	12.5	1145	6 US-10-511-937-377	Sequence 377, App
c 82	161.2	12.4	3248	6 US-10-505-928-222	Sequence 222, App
c 83	161.2	12.4	4540	6 US-10-505-928-750	Sequence 750, App
c 85	160.8	12.4	5250	6 US-10-511-937-2856	Sequence 2856, Ap
c 86	160.4	12.4	5198	6 US-10-505-928-342	Sequence 342, App
c 87	159.2	12.3	2436	6 US-10-505-928-783	Sequence 783, App
c 88	159	12.3	2271	6 US-10-505-928-792	Sequence 792, App
c 89	158.6	12.2	5920	7 US-11-145-307A-185	Sequence 185, App
c 90	158.4	12.2	4156	6 US-10-511-937-453	Sequence 453, App
c 93	156.8	12.1	1177	7 US-11-101-316-129	Sequence 129, App
c 94	156.8	12.1	3350	6 US-10-505-928-637	Sequence 637, App
c 95	156.8	12.1	3350	6 US-10-505-928-641	Sequence 641, App
c 96	156.2	12.1	469	6 US-10-473-173-361	Sequence 361, App
c 98	154	11.9	4365	7 US-11-223-738-1	Sequence 1, Appli
c 99	151.6	11.7	2372	6 US-10-511-937-615	Sequence 615, App
c 101	150.4	11.6	14668	7 US-11-181-115-7	Sequence 7, Appli
c 103	147.2	11.4	363	7 US-11-301-554-878	Sequence 878, App
c 104	146.4	11.3	367	7 US-11-301-554-1143	Sequence 1143, Ap
c 105	146.4	11.3	367	7 US-11-301-554-1626	Sequence 1626, Ap
c 106	146	11.3	1395	7 US-11-101-316-9	Sequence 9, Appli
c 107	145.8	11.3	1837	1 US-09-949-925-72	Sequence 72, Appl
c 108	145.8	11.3	42999	7 US-11-284-877-17	Sequence 17, Appl
c 109	145	11.2	494	6 US-10-488-619-630	Sequence 630, App
c 110	145	11.2	2234	1 US-09-949-925-52	Sequence 52, Appl
c 111	144.2	11.1	420	6 US-10-488-619-713	Sequence 713, App

112	143.2	11.1	2416	6	US-10-501-834-5	Sequence 5, Appl1	201	80.8	6.2	1723	6	US-10-511-937-606	Sequence 606, App
113	143	11.0	6826	6	US-10-505-928-330	Sequence 330, App	C 203	78.8	6.1	550	7	US-11-145-307A-178	Sequence 178, App
C 115	142.2	11.0	364	7	US-11-301-554-867	Sequence 867, App	C 204	78.4	6.1	350	6	US-10-488-613-434	Sequence 434, App
C 116	142.2	11.0	368	7	US-11-301-554-1038	Sequence 1038, App	C 205	77.8	6.0	497	6	US-10-473-173-429	Sequence 429, App
C 117	142.2	11.0	368	7	US-11-301-554-1044	Sequence 1044, Ap	C 206	77.8	6.0	1685	1	US-09-949-925-21	Sequence 21, Appl
C 118	142.2	11.0	368	7	US-11-301-554-1092	Sequence 1092, Ap	C 208	75.2	5.8	1424	6	US-10-511-937-595	Sequence 595, App
C 119	141.2	10.9	6974	6	US-10-505-928-673	Sequence 673, App	C 209	75.2	5.8	1575	6	US-10-511-937-572	Sequence 572, App
C 120	140.6	10.9	368	7	US-11-301-554-1003	Sequence 1003, Ap	C 210	74.2	5.7	399	6	US-10-473-173-485	Sequence 485, App
C 121	140.6	10.9	368	7	US-11-301-554-1584	Sequence 1584, Ap	C 211	74.2	5.7	4534	6	US-10-473-691B-1	Sequence 1, Appli
C 122	140.2	10.8	3697	7	US-11-145-307A-69	Sequence 69, Appl	C 212	73.8	5.7	2010	6	US-10-511-937-612	Sequence 612, App
C 123	139.8	10.8	368	7	US-11-301-554-1164	Sequence 1164, Ap	C 213	72.6	5.6	87	7	US-11-245-444-1	Sequence 1, Appli
C 124	139.6	10.8	3646	6	US-10-511-937-358	Sequence 358, App	C 214	72.2	5.6	3485	7	US-11-145-307A-192	Sequence 192, App
C 125	139.4	10.8	5515	6	US-10-524-021-1	Sequence 1, Appli	C 215	72	5.6	528	7	US-11-301-554-382	Sequence 382, App
C 126	138.8	10.7	675	7	US-11-242-317-4	Sequence 4, Appli	C 216	71.4	5.5	512	7	US-11-301-554-875	Sequence 875, App
C 127	138.4	10.7	630	6	US-10-473-173-166	Sequence 166, App	C 217	71.4	5.5	1361	7	US-11-300-765-1	Sequence 1, Appli
C 128	138.2	10.7	1580	7	US-11-145-307A-16	Sequence 16, Appl	C 218	71.4	5.5	1361	7	US-11-300-765-3	Sequence 3, Appli
C 129	137.8	10.6	4692	6	US-10-511-937-646	Sequence 646, App	C 219	70.8	5.5	400	7	US-11-301-554-281	Sequence 281, App
C 130	137.8	10.6	4908	6	US-10-505-928-226	Sequence 226, App	C 220	70.4	5.4	3408	6	US-10-505-928-184	Sequence 184, App
C 131	136.6	10.5	1192	1	US-09-949-925-66	Sequence 66, Appl	C 221	70.4	5.4	3408	6	US-10-511-937-337	Sequence 337, App
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C 134	134.6	10.4	3301	6	US-10-370-959-10	Sequence 10, Appl	C 223	69.2	5.3	3711	6	US-10-505-928-679	Sequence 679, App
C 135	133.6	10.3	17569	6	US-11-301-554-1804	Sequence 1804, Ap	C 224	68.4	5.3	1885	6	US-10-505-928-141	Sequence 141, App
C 136	133.4	10.3	347	6	US-10-505-928-440	Sequence 440, App	C 226	67	5.2	461	7	US-11-301-554-884	Sequence 884, App
C 137	133.4	10.3	2095	6	US-10-511-937-395	Sequence 395, App	C 227	66.8	5.2	545	6	US-10-473-173-146	Sequence 146, App
C 139	132.2	10.2	5133	6	US-10-511-937-2739	Sequence 2739, Ap	C 228	66.8	5.2	5307	6	US-10-505-928-824	Sequence 824, App
C 141	131.4	10.1	1882	7	US-11-101-316-133	Sequence 133, App	C 229	66.6	5.1	260	7	US-11-301-554-1308	Sequence 1208, Ap
C 142	131	10.1	4896	7	US-11-258-767-61	Sequence 61, Appl	C 230	64.6	5.0	661	7	US-11-301-554-219	Sequence 219, App
C 145	128.8	9.9	807	7	US-11-246-999-22	Sequence 22, Appl	C 231	64	4.9	1538	6	US-10-505-928-336	Sequence 336, App
C 146	127.2	9.8	505	6	US-10-473-173-224	Sequence 224, App	C 232	62.8	4.8	5734	6	US-10-505-928-28	Sequence 28, Appl
C 147	126.2	9.7	3248	6	US-10-505-928-222	Sequence 222, App	C 233	62.2	4.8	403	6	US-10-488-613-441	Sequence 441, App
C 148	125	9.7	6807	6	US-10-511-937-2858	Sequence 2858, Ap	C 234	62.2	4.8	2476	6	US-10-501-834-211	Sequence 211, App
C 149	124.2	9.6	5171	6	US-10-501-834-216	Sequence 216, App	C 237	60.6	4.7	1892	6	US-10-505-928-624	Sequence 624, App
C 150	123.6	9.5	4045	6	US-10-511-937-571	Sequence 571, App	C 238	60.2	4.6	347	7	US-11-222-810-1	Sequence 1, Appli
C 152	121.6	9.4	5747	6	US-10-199-229-1	Sequence 1, Appli	C 239	60.2	4.6	347	7	US-11-222-810-3	Sequence 3, Appli
C 154	119.2	9.2	2243	6	US-10-505-928-732	Sequence 732, App	C 240	60.2	4.6	678	7	US-11-301-554-208	Sequence 208, App
C 155	116.6	9.1	2649	7	US-11-242-505A-46	Sequence 46, Appl	C 241	60.2	4.6	1408	7	US-11-222-810-11	Sequence 11, Appl
C 156	118.2	9.1	2649	7	US-11-242-505A-47	Sequence 47, Appl	C 242	60.2	4.6	1408	7	US-11-223-810-13	Sequence 13, Appl
C 157	117.4	9.1	464	6	US-10-488-619-56	Sequence 56, Appl	C 243	60	4.6	361	7	US-11-301-554-254	Sequence 254, App
C 158	116.6	9.0	2308	6	US-10-511-937-435	Sequence 435, App	C 244	59.8	4.6	452	6	US-10-511-937-2899	Sequence 2899, Ap
C 159	116.2	9.0	308	7	US-11-301-554-1111	Sequence 111, Ap	C 245	59.8	4.6	1773	6	US-10-505-928-135	Sequence 135, App
C 160	116.2	9.0	454	6	US-10-488-619-608	Sequence 608, App	C 246	59.6	4.6	386	7	US-10-505-928-155	Sequence 155, App
C 162	114.6	8.8	416	7	US-11-301-554-971	Sequence 971, App	C 247	59.2	4.6	3223	7	US-11-313-797-3	Sequence 3, Appli
C 163	113.8	8.8	461	6	US-10-488-619-516	Sequence 516, App	C 248	59.2	4.5	5424	6	US-10-505-928-496	Sequence 496, App
C 165	112.2	8.7	551	7	US-11-301-554-1105	Sequence 1105, Ap	C 249	58.6	4.5	2120	6	US-10-511-937-596	Sequence 596, App
C 166	110.6	8.5	535	7	US-10-501-554-992	Sequence 992, App	C 250	58.4	4.5	2295	7	US-11-246-999-15	Sequence 15, Appl
C 167	110.6	8.5	3869	6	US-10-511-937-2853	Sequence 2853, Ap	C 252	57.6	4.4	1849	7	US-11-301-554-170	Sequence 170, App
C 169	110	8.5	2121	7	US-11-101-316-117	Sequence 117, App	C 254	57.6	4.4	1594	6	US-10-505-928-252	Sequence 252, App
C 171	106.8	8.2	417	6	US-10-511-937-624	Sequence 624, App	C 255	57.2	4.4	520	7	US-11-301-554-927	Sequence 927, App
C 172	106.2	8.2	355	7	US-11-301-554-749	Sequence 749, App	C 256	56	4.3	2379	6	US-10-370-959-75	Sequence 75, Appl
C 173	105.4	8.1	975	7	US-11-203-609-1	Sequence 1, Appli	C 257	55.6	4.3	590	7	US-11-301-554-495	Sequence 495, App
C 174	105.2	8.1	412	6	US-10-473-173-202	Sequence 202, App	C 258	55	4.2	1771	6	US-10-511-937-3114	Sequence 3114, Ap
C 175	105.2	8.1	1699	1	US-09-949-925-34	Sequence 34, Appl	C 259	55	4.2	238	7	US-11-301-554-995	Sequence 995, App
C 176	105	8.1	548	6	US-10-473-173-305	Sequence 305, App	C 260	54.8	4.2	604	7	US-11-301-554-258	Sequence 258, App
C 177	104.8	8.1	2917	6	US-10-505-928-384	Sequence 384, App	C 261	54.6	4.2	604	7	US-11-301-554-258	Sequence 258, App
C 178	104.4	8.1	468	6	US-10-511-937-592	Sequence 592, App	C 262	54.2	4.2	557	7	US-11-301-554-196	Sequence 196, App
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C 181	103.6	8.0	1768	6	US-11-101-316-113	Sequence 113, App	C 265	53.2	4.1	1131	6	US-10-511-937-548	Sequence 548, App
C 182	103.2	8.0	5204	6	US-10-524-021-12	Sequence 12, Appl	C 266	52.8	4.1	528	6	US-10-473-173-420	Sequence 420, App
C 183	103	8.0	462	6	US-10-473-173-180	Sequence 180, App	C 267	52.8	4.1	558	7	US-11-301-554-554	Sequence 554, App
C 184	102.6	7.9	1279	1	US-09-949-925-59	Sequence 59, Appl	C 268	52.4	4.0	94	7	US-11-245-444-2	Sequence 2, Appli
C 185	101.4	7.8	331	6	US-10-511-937-583	Sequence 583, App	C 269	52.4	4.0	1076	1	US-09-949-925-25	Sequence 25, Appl
C 186	101	7.8	1216	6	US-10-511-937-490	Sequence 490, App	C 271	52.2	4.0	3597	6	US-10-505-928-651	Sequence 651, App
C 187	100.8	7.8	637	7	US-11-222-810-23	Sequence 23, Appl	C 272	52.2	4.0	3597	6	US-10-511-937-2802	Sequence 2802, Ap
C 188	99.4	7.7	551	6	US-10-473-173-315	Sequence 315, App	C 273	51.6	4.0	943	1	US-09-949-925-39	Sequence 39, Appl
C 190	97.8	7.6	1452	1	US-09-949-925-62	Sequence 62, Appl	C 274	50.8	3.9	444	7	US-11-301-554-1607	Sequence 1607, Ap
C 191	89.4	6.9	341	7	US-11-301-554-756	Sequence 756, App	C 275	50.6	3.9	89	7	US-11-301-554-589	Sequence 589, App
C 192	89.2	6.9	6799	7	US-11-301-554-1883	Sequence 1883, Ap	C 276	50.6	3.9	370	7	US-11-301-554-1117	Sequence 1117, Ap
C 193	86.6	6.7	1750	7	US-11-242-111-3	Sequence 3, Appli	C 278	49.2	3.8	6243	6	US-10-518-039-2	Sequence 2, Appli
C 194	86.6	6.7	3215	6	US-10-505-928-665	Sequence 665, App	C 279	49.2	3.8	6843	6	US-10-518-039-1	Sequence 1, Appli
C 195	86	6.6	779	7	US-11-301-554-187	Sequence 187, App	C 280	49	3.8	534	6	US-10-505-928-2	Sequence 2, Appli
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C 197	85.6	6.6	1074	1	US-09-949-925-28	Sequence 28, Appl	C 282	48.6	3.8	2798	7	US-11-145-307A-179	Sequence 179, App
C 198	84	6.5	1909	6	US-10-511-937-500	Sequence 500, App	C 283	48.6	3.8	3350	6	US-10-505-928-637	Sequence 637, App
C 199	81.8	6.3	1039	1	US-09-949-925-24	Sequence 24, Appl	C 283	48.6	3.8				

c 284	48.6	3.8	3350	6	US-10-505-928-641	Sequence 641, App	c 358	32.4	2.5	520	6	US-10-488-619-2246	Sequence 2246, Ap
285	48.4	3.7	1424	6	US-10-511-937-595	Sequence 595, App	359	32.2	2.5	1062	7	US-11-217-529-81560	Sequence 81560, A
286	48.2	3.7	526	6	US-10-511-937-536	Sequence 536, App	360	31.8	2.5	447	7	US-11-301-554-1610	Sequence 1610, A
c 287	48.2	3.7	3300	6	US-10-370-959-120	Sequence 120, App	361	31.8	2.5	516	6	US-11-217-529-80020	Sequence 80020, A
288	48	3.7	586	7	US-11-145-307A-187	Sequence 187, App	362	31.6	2.4	595	6	US-10-488-619-1034	Sequence 1034, Ap
c 289	48	3.7	2684	6	US-10-509-131-52	Sequence 52, Appl	363	31.4	2.4	5487	6	US-10-473-173-27	Sequence 27, Appl
290	47.8	3.7	320	7	US-11-243-514-10	Sequence 10, Appl	364	31.4	2.4	5487	6	US-10-505-928-120	Sequence 120, App
291	47.8	3.7	1103	7	US-11-283-522-8	Sequence 8, Appli	c 365	31.2	2.4	697	6	US-10-488-619-1108	Sequence 1108, Ap
c 292	47.4	3.7	513	6	US-11-301-554-909	Sequence 909, App	367	31.2	2.4	2661	6	US-10-511-937-562	Sequence 562, App
c 293	47.2	3.6	2661	6	US-10-505-928-848	Sequence 848, App	368	31	2.4	350	6	US-10-488-619-577	Sequence 577, App
c 294	46.8	3.6	391	6	US-10-488-619-963	Sequence 963, App	369	31	2.4	427	7	US-11-301-554-854	Sequence 854, App
c 295	46.8	3.6	4307	6	US-10-511-937-510	Sequence 510, App	370	31	2.4	1047	7	US-11-217-529-81249	Sequence 81249, A
c 296	46.4	3.6	3003	7	US-11-145-307A-38	Sequence 38, Appl	371	30.8	2.4	366	7	US-11-217-529-81128	Sequence 81128, A
c 297	45.2	3.5	481	6	US-11-301-554-583	Sequence 583, App	c 372	30.8	2.4	1412	6	US-10-514-776-1	Sequence 1, Appli
c 298	44.6	3.4	488	7	US-10-473-173-332	Sequence 332, App	373	30.8	2.4	2163	7	US-11-217-529-75785	Sequence 75785, A
c 299	44.4	3.4	2186	7	US-11-238-282-32	Sequence 32, Appl	374	30.8	2.4	3151	6	US-10-511-937-2860	Sequence 2860, Ap
c 300	44.2	3.4	491	7	US-11-301-554-1227	Sequence 1227, Ap	375	30.6	2.4	413	6	US-10-511-937-2923	Sequence 2923, Ap
c 301	44.2	3.4	2188	6	US-10-505-928-816	Sequence 816, App	c 376	30.6	2.4	415	6	US-10-488-619-530	Sequence 530, App
c 302	43.2	3.3	305	7	US-11-222-810-17	Sequence 17, Appl	c 377	30.6	2.4	1377	7	US-11-217-529-80636	Sequence 80636, A
c 303	42.6	3.3	467	6	US-10-488-619-169	Sequence 169, App	c 378	30.6	2.4	1998	6	US-10-370-959-41	Sequence 41, Appl
c 304	42.2	3.3	278	7	US-11-245-514-9	Sequence 9, Appli	379	30.6	2.4	2418	6	US-11-217-529-81958	Sequence 81958, A
c 305	42.2	3.3	372	7	US-11-222-810-14	Sequence 14, Appl	c 380	30.6	2.4	2745	6	US-10-370-959-39	Sequence 39, Appl
c 306	42.2	3.3	416	6	US-11-301-554-469	Sequence 469, App	381	30.6	2.4	6316	6	US-10-541-993-75	Sequence 75, Appl
c 307	41.4	3.2	100	6	US-10-511-935-42	Sequence 42, Appl	382	30.4	2.3	3610	7	US-11-181-115-32	Sequence 32, Appl
c 308	41.4	3.2	748	1	US-09-949-925-31	Sequence 31, Appl	383	30.4	2.3	3708	7	US-11-325-764-1	Sequence 1, Appli
c 310	41.4	3.2	1768	7	US-11-101-316-113	Sequence 113, App	c 384	30.2	2.3	321	6	US-10-473-173-257	Sequence 257, App
c 311	41.2	3.2	1580	7	US-11-145-307A-16	Sequence 16, Appl	c 385	30.2	2.3	331	6	US-10-488-619-579	Sequence 579, App
c 312	41	3.2	690	7	US-11-327-900-7	Sequence 7, Appli	c 386	30.2	2.3	563	6	US-10-488-619-1289	Sequence 1289, Ap
c 313	41	3.2	1650	7	US-11-312-958-39	Sequence 39, Appl	387	30.2	2.3	605	6	US-10-488-619-1468	Sequence 1468, Ap
c 314	40.2	3.1	433	6	US-10-488-619-262	Sequence 262, App	388	30.2	2.3	2537	6	US-10-505-928-149	Sequence 149, App
c 315	39.8	3.1	294	7	US-11-222-810-15	Sequence 15, Appl	c 389	30.2	2.3	5649	7	US-11-217-529-2537	Sequence 2537, Ap
c 316	39.8	3.1	1028	6	US-10-511-937-508	Sequence 508, App	c 390	30	2.3	391	7	US-11-301-554-173	Sequence 173, App
c 317	39.4	3.0	422	6	US-10-488-619-384	Sequence 384, App	c 391	30	2.3	2618	6	US-10-511-937-655	Sequence 655, App
c 318	39.2	3.0	232	7	US-11-301-554-859	Sequence 859, App	c 392	30	2.3	3909	7	US-11-217-529-174364	Sequence 174364, A
c 319	39.2	3.0	312	7	US-11-245-514-11	Sequence 11, Appl	c 393	29.8	2.3	1538	6	US-10-505-928-356	Sequence 356, App
c 320	38.8	3.0	539	6	US-10-488-619-1033	Sequence 1033, Ap	c 394	29.8	2.3	1695	7	US-11-217-529-79012	Sequence 79012, A
c 321	38.6	3.0	8699	7	US-11-156-014A-1	Sequence 1, Appli	c 395	29.6	2.3	337	6	US-10-511-937-530	Sequence 530, App
c 322	38.6	3.0	10143	7	US-11-156-014A-121	Sequence 121, App	c 396	29.6	2.3	1915	7	US-11-145-307A-193	Sequence 193, App
c 323	38.6	3.0	10826	7	US-11-156-014A-87	Sequence 87, Appl	c 397	29.6	2.3	2073	6	US-10-511-937-464	Sequence 464, App
c 324	38.6	3.0	12990	7	US-11-156-014A-110	Sequence 110, App	c 398	29.6	2.3	2163	7	US-11-217-529-3294	Sequence 3294, Ap
c 325	38.6	3.0	13722	7	US-11-156-014A-91	Sequence 91, Appl	c 400	29.4	2.3	333	7	US-11-101-316-147	Sequence 147, App
c 326	38.4	3.0	2876	6	US-10-505-928-468	Sequence 468, App	c 401	29.4	2.3	435	7	US-11-217-529-75781	Sequence 75781, A
c 327	38.2	2.9	1028	6	US-10-511-937-508	Sequence 508, App	c 402	29.4	2.3	781	6	US-10-511-937-396	Sequence 396, App
c 328	38	2.9	704	7	US-11-301-554-206	Sequence 206, App	c 403	29.4	2.3	807	6	US-11-217-529-81784	Sequence 81784, A
c 329	36.8	2.8	568	6	US-10-511-937-451	Sequence 451, App	c 404	29.2	2.3	828	6	US-10-488-619-2165	Sequence 2165, Ap
c 330	36.8	2.8	3048	6	US-10-511-935-45	Sequence 45, Appl	c 405	29.2	2.3	575	6	US-10-488-619-1578	Sequence 1578, Ap
c 331	36.6	2.8	3115	7	US-11-301-554-802	Sequence 802, App	c 406	29.2	2.3	590	6	US-10-488-619-2028	Sequence 2028, Ap
c 332	36.6	2.8	4637	6	US-11-301-554-804	Sequence 804, App	c 407	29.2	2.3	804	7	US-11-217-529-81784	Sequence 81784, A
c 333	36.4	2.8	1521	6	US-10-505-928-400	Sequence 400, App	c 408	29.2	2.3	1134	7	US-11-217-529-79495	Sequence 79495, A
c 334	36.4	2.8	16351	6	US-10-501-834-217	Sequence 217, App	c 409	29.2	2.3	1134	7	US-11-217-529-79495	Sequence 79495, A
c 335	36.2	2.8	349	6	US-10-473-173-230	Sequence 230, App	c 410	29.2	2.3	2042	7	US-11-242-505A-37	Sequence 37, Appl
c 336	36	2.8	2805	7	US-11-145-307A-195	Sequence 195, App	c 411	29.2	2.3	2042	7	US-11-242-505A-38	Sequence 38, Appl
c 337	35.8	2.8	401	6	US-10-488-619-613	Sequence 613, App	c 412	29.2	2.3	5927	6	US-10-505-928-854	Sequence 854, App
c 338	35.8	2.8	445	6	US-10-488-619-612	Sequence 612, App	c 413	29	2.2	282	7	US-11-217-529-79368	Sequence 79368, A
c 339	35.4	2.7	392	6	US-10-488-619-66	Sequence 66, Appl	c 414	29	2.2	1785	7	US-11-217-529-81797	Sequence 81797, A
c 340	35	2.7	350	7	US-11-222-810-18	Sequence 18, Appl	c 415	29	2.2	1824	7	US-11-242-505A-31	Sequence 31, Appl
c 341	34.8	2.7	491	7	US-11-301-554-1155	Sequence 1155, Ap	c 416	29	2.2	1824	7	US-11-242-505A-32	Sequence 32, Appl
c 342	34.6	2.7	41	7	US-11-245-514-25	Sequence 25, Appl	c 417	29	2.2	2280	7	US-11-217-529-1363	Sequence 1363, Ap
c 343	34.6	2.7	41	7	US-11-245-514-26	Sequence 26, Appl	c 418	29	2.2	2658	7	US-11-217-529-249	Sequence 249, App
c 344	34.2	2.6	604	7	US-11-301-554-258	Sequence 258, App	c 419	28.8	2.2	691	6	US-10-511-937-423	Sequence 423, App
c 345	34.2	2.6	277	6	US-10-511-935-4	Sequence 4, Appli	c 420	28.8	2.2	951	7	US-11-217-529-3672	Sequence 3672, Ap
c 346	33.8	2.6	365	7	US-11-301-554-1360	Sequence 1360, Ap	c 421	28.8	2.2	1248	7	US-11-217-529-5949	Sequence 5949, Ap
c 347	33.6	2.6	361	6	US-10-488-619-2566	Sequence 2566, App	c 422	28.8	2.2	1564	6	US-11-217-529-166165	Sequence 166165, A
c 348	33	2.5	363	7	US-11-301-554-1490	Sequence 1490, Ap	c 423	28.8	2.2	1768	6	US-10-505-928-585	Sequence 585, App
c 349	33	2.5	2559	7	US-11-217-529-2747	Sequence 2747, Ap	c 424	28.8	2.2	2942	7	US-11-170-482-17	Sequence 17, Appl
c 350	33	2.5	3303	7	US-11-217-529-166175	Sequence 166175, A	c 425	28.8	2.2	3288	7	US-11-312-797-1	Sequence 1, Appli
c 351	33	2.5	5026	7	US-11-217-529-166180	Sequence 166180, A	c 426	28.8	2.2	4763	6	US-10-505-928-374	Sequence 374, App
c 352	32.8	2.5	592	7	US-11-106-014-31	Sequence 31, Appl	c 427	28.8	2.2	7008	7	US-11-263-326-98	Sequence 98, Appl
c 353	32.8	2.5	721	6	US-10-488-619-1109	Sequence 1109, App	c 428	28.8	2.2	7008	7	US-11-263-326-104	Sequence 104, App
c 354	32.8	2.5	2538	7	US-11-217-529-3979	Sequence 3979, App	c 429	28.8	2.2	9730	6	US-10-501-834-219	Sequence 219, App
c 355	32.6	2.5	6837	7	US-11-217-529-4956	Sequence 4956, Ap	c 430	28.8	2.2	22118	6	US-11-284-877-16	Sequence 16, Appl
c 356	32.4	2.5	318	7	US-11-301-554-444	Sequence 444, App	c 431	28.6	2.2	439	6	US-10-488-619-2863	Sequence 2863, Ap
c 357	32.4	2.5	459	6	US-10-488-619-2245	Sequence 2245, Ap	c 432	28.6	2.2	612	6	US-10-488-619-357	Sequence 357, App
							c 433	28.6	2.2	733	6	US-10-488-619-2864	Sequence 2864, Ap

C 434	28.6	2.2	885	7	US-11-217-529-5467	Sequence 5467, Ap	512	27.4	2.1	3090	7	US-11-217-529-3156	Sequence 3156, Ap
C 435	28.6	2.2	1256	7	US-11-242-111-8	Sequence 8, Appli	513	27.4	2.1	3243	6	US-10-528-032-8	Sequence 8, Appli
C 436	28.6	2.2	1419	7	US-11-217-529-3929	Sequence 3929, Ap	C 514	27.4	2.1	3366	6	US-11-217-529-173839	Sequence 173839,
C 437	28.6	2.2	1665	7	US-11-217-529-4831	Sequence 4831, Ap	515	27.4	2.1	3586	6	US-10-528-032-10	Sequence 10, Appl
C 438	28.6	2.2	2315	6	US-10-511-937-649	Sequence 649, App	516	27.4	2.1	3705	6	US-10-505-928-655	Sequence 655, App
C 439	28.4	2.2	464	6	US-10-488-619-2781	Sequence 2781, Ap	517	27.4	2.1	17593	6	US-10-541-993-42	Sequence 42, Appl
C 440	28.4	2.2	785	6	US-10-946-650-15	Sequence 15, Appl	C 518	27.4	2.1	17756	6	US-10-541-993-47	Sequence 47, Appl
C 441	28.4	2.2	1061	7	US-11-145-307A-12	Sequence 12, Appl	519	27.4	2.1	17877	6	US-10-541-993-37	Sequence 37, Appl
C 442	28.4	2.2	1194	7	US-11-217-529-7834	Sequence 7834, A	C 520	27.4	2.1	22118	7	US-11-284-877-16	Sequence 16, Appl
C 443	28.4	2.2	1581	7	US-11-217-529-5713	Sequence 5713, Ap	C 521	27.2	2.1	252	7	US-11-263-326-159	Sequence 159, App
C 444	28.4	2.2	2422	6	US-10-473-173-53	Sequence 53, Appl	C 522	27.2	2.1	252	7	US-11-217-529-166925	Sequence 166925,
C 445	28.4	2.2	2610	6	US-10-511-937-2914	Sequence 2914, Ap	C 523	27.2	2.1	571	6	US-10-488-619-2686	Sequence 2686, Ap
C 446	28.4	2.2	2749	1	US-09-949-925-29	Sequence 29, Appl	C 524	27.2	2.1	732	6	US-10-488-619-1446	Sequence 1446, Ap
C 447	28.4	2.2	2776	6	US-10-511-937-2822	Sequence 2822, Ap	C 525	27.2	2.1	737	6	US-10-488-619-1819	Sequence 1819, Ap
C 448	28.4	2.2	3375	6	US-10-505-928-629	Sequence 629, App	C 526	27.2	2.1	780	7	US-11-301-554-1866	Sequence 1866, Ap
C 449	28.4	2.2	3844	6	US-10-946-650-32	Sequence 32, Appl	C 527	27.2	2.1	794	7	US-11-301-554-1865	Sequence 1865, Ap
C 450	28.4	2.2	4077	6	US-10-505-928-134	Sequence 134, App	C 528	27.2	2.1	876	6	US-10-488-619-2828	Sequence 2828, Ap
C 451	28.4	2.2	8178	6	US-10-473-173-52	Sequence 52, Appl	C 529	27.2	2.1	1125	7	US-11-217-529-76497	Sequence 76497, A
C 452	28.4	2.2	8331	7	US-11-217-529-166179	Sequence 166179,	C 530	27.2	2.1	1155	7	US-11-217-529-2714	Sequence 2714, Ap
C 453	28.2	2.2	603	7	US-11-217-529-79729	Sequence 79729, A	531	27.2	2.1	1299	7	US-11-134-445-19	Sequence 19, Appl
C 454	28.2	2.2	615	7	US-11-217-529-2766	Sequence 2766, Ap	C 532	27.2	2.1	1309	7	US-11-134-445-29	Sequence 29, Appl
C 455	28.2	2.2	1665	7	US-11-101-316-85	Sequence 85, Appl	C 533	27.2	2.1	1449	7	US-11-217-529-906	Sequence 906, App
C 456	28.2	2.2	1679	7	US-11-251-465-11	Sequence 11, Appl	C 534	27.2	2.1	2298	6	US-10-511-937-633	Sequence 633, App
C 457	28.2	2.2	1816	6	US-10-505-928-850	Sequence 850, App	C 535	27.2	2.1	2895	7	US-11-217-529-77202	Sequence 77202, A
C 458	28.2	2.2	2367	6	US-10-505-928-744	Sequence 744, App	C 536	27.2	2.1	4731	7	US-11-217-529-2762	Sequence 2762, Ap
C 459	28.2	2.2	2367	6	US-10-505-928-360	Sequence 360, App	C 537	27	2.1	423	7	US-11-217-529-5817	Sequence 5817, Ap
C 460	28.2	2.2	4767	6	US-11-145-307A-150	Sequence 150, App	C 538	27	2.1	430	6	US-10-488-619-3006	Sequence 3006, Ap
C 461	28.2	2.2	5849	7	US-11-270-287-1	Sequence 1, Appli	C 539	27	2.1	450	6	US-10-488-619-746	Sequence 746, App
C 462	28.2	2.2	731	6	US-11-264-784-123	Sequence 123, App	C 540	27	2.1	518	6	US-10-488-619-747	Sequence 747, App
C 463	28.2	2.2	10448	7	US-11-190-750-112	Sequence 112, App	C 541	27	2.1	535	6	US-10-488-619-1469	Sequence 1469, Ap
C 464	28.2	2.2	10448	7	US-11-326-265-10	Sequence 129, App	C 542	27	2.1	564	7	US-10-488-619-741	Sequence 741, App
C 465	28.2	2.2	1749	6	US-10-511-937-2884	Sequence 2884, Ap	C 543	27	2.1	567	7	US-11-301-554-1414	Sequence 1414, Ap
C 466	28.2	2.2	2088	6	US-10-505-928-822	Sequence 822, App	C 544	27	2.1	677	6	US-10-488-619-2850	Sequence 2850, Ap
C 467	28.2	2.2	2104	6	US-10-505-928-72	Sequence 72, Appl	C 545	27	2.1	789	7	US-11-301-554-1867	Sequence 1867, Ap
C 468	28.2	2.2	4017	7	US-11-326-265-10	Sequence 1897, Ap	C 546	27	2.1	789	7	US-11-217-529-5206	Sequence 5206, Ap
C 469	28	2.2	4204	6	US-10-505-928-760	Sequence 32, Appl	C 547	27	2.1	817	6	US-10-488-619-2366	Sequence 2366, Ap
C 470	28	2.2	4833	7	US-11-312-958-37	Sequence 37, Appl	C 548	27	2.1	999	7	US-11-217-529-80388	Sequence 80388, A
C 471	28	2.2	4911	7	US-11-217-529-75783	Sequence 75783, A	C 549	27	2.1	1000	7	US-11-233-726-36	Sequence 36, Appl
C 472	28	2.2	8331	7	US-11-217-529-166179	Sequence 166179,	C 550	27	2.1	1458	6	US-10-511-937-598	Sequence 598, App
C 473	28	2.2	884	7	US-11-101-316-135	Sequence 135, App	C 551	27	2.1	1872	7	US-11-217-529-75612	Sequence 75612, A
C 474	28	2.2	1461	7	US-11-217-529-76499	Sequence 76499, A	C 552	27	2.1	1887	7	US-11-217-529-1154	Sequence 1154, App
C 475	28	2.2	1554	7	US-11-217-529-180	Sequence 180, App	C 553	27	2.1	2154	6	US-10-511-937-420	Sequence 420, App
C 476	28	2.2	1806	7	US-11-217-529-2074	Sequence 2074, Ap	C 554	27	2.1	2181	6	US-10-504-120-13	Sequence 13, Appl
C 477	28	2.2	2328	7	US-11-217-529-1805	Sequence 1805, Ap	C 555	27	2.1	2207	7	US-11-075-398-6	Sequence 6, Appli
C 478	28	2.2	2500	6	US-10-505-928-394	Sequence 394, App	C 556	27	2.1	2610	7	US-11-217-529-78823	Sequence 78823, A
C 479	28	2.2	2768	7	US-11-101-316-15	Sequence 15, Appl	C 557	27	2.1	2646	7	US-11-217-529-78638	Sequence 78638, A
C 480	28	2.2	7391	6	US-10-511-937-629	Sequence 629, App	C 558	27	2.1	2952	6	US-10-511-937-654	Sequence 654, App
C 481	27.8	2.1	718	6	US-10-488-619-2466	Sequence 2466, Ap	C 559	27	2.1	2961	6	US-10-511-455-53	Sequence 53, Appl
C 482	27.8	2.1	1096	6	US-10-488-619-3024	Sequence 3024, Ap	C 560	27	2.1	3393	7	US-11-217-529-80432	Sequence 80432, A
C 483	27.6	2.1	1104	7	US-11-217-529-77800	Sequence 77800, A	C 561	27	2.1	3428	6	US-10-511-455-51	Sequence 51, Appl
C 484	27.6	2.1	1242	7	US-11-217-529-80620	Sequence 80620, A	C 562	27	2.1	3743	6	US-10-502-993-1	Sequence 1, Appli
C 485	27.6	2.1	1242	7	US-11-217-529-80741	Sequence 80741, A	C 563	27	2.1	4098	6	US-10-510-508-2	Sequence 2, Appli
C 486	27.6	2.1	1635	7	US-11-301-554-1798	Sequence 1798, Ap	C 564	27	2.1	4600	7	US-10-473-173-80	Sequence 80, Appl
C 487	27.6	2.1	1748	7	US-11-246-999-16	Sequence 16, Appl	C 565	27	2.1	4600	7	US-11-301-554-1797	Sequence 1797, Ap
C 488	27.6	2.1	1837	6	US-10-511-937-382	Sequence 382, App	C 566	27	2.1	5752	6	US-10-473-173-80	Sequence 80, Appl
C 489	27.6	2.1	2126	7	US-11-269-213-3	Sequence 3, Appli	C 567	27	2.1	5752	6	US-11-301-554-1804	Sequence 1804, Ap
C 490	27.6	2.1	2126	7	US-11-311-754-1	Sequence 1, Appli	C 568	26.8	2.1	572	6	US-11-301-554-1804	Sequence 428, App
C 491	27.6	2.1	2745	6	US-10-370-959-39	Sequence 39, Appl	C 569	26.8	2.1	572	6	US-10-488-619-1603	Sequence 1603, Ap
C 492	27.6	2.1	3116	6	US-10-511-937-589	Sequence 589, App	C 570	26.8	2.1	594	7	US-11-270-287-39	Sequence 39, Appl
C 493	27.6	2.1	3851	6	US-10-505-928-730	Sequence 730, App	C 571	26.8	2.1	660	7	US-11-301-554-1761	Sequence 1761, App
C 494	27.6	2.1	5132	6	US-10-505-928-663	Sequence 663, App	C 572	26.8	2.1	666	7	US-11-217-529-1721	Sequence 1721, Ap
C 495	27.6	2.1	5132	6	US-10-505-928-663	Sequence 663, App	C 573	26.8	2.1	785	7	US-11-301-554-1868	Sequence 1868, Ap
C 496	27.6	2.1	246	7	US-11-217-529-5046	Sequence 5046, Ap	C 574	26.8	2.1	835	6	US-10-488-619-1440	Sequence 1440, Ap
C 497	27.6	2.1	591	6	US-10-488-619-1169	Sequence 1169, Ap	C 575	26.8	2.1	983	7	US-11-256-428-68	Sequence 68, Appl
C 498	27.4	2.1	729	7	US-11-217-529-2618	Sequence 2618, Ap	C 576	26.8	2.1	1047	7	US-11-217-529-1204	Sequence 1204, Ap
C 499	27.4	2.1	768	7	US-11-217-529-81743	Sequence 81743, A	C 577	26.8	2.1	2025	7	US-11-217-529-76064	Sequence 76064, A
C 500	27.4	2.1	781	6	US-10-488-619-1651	Sequence 1651, Ap	C 578	26.8	2.1	2026	6	US-10-528-032-9	Sequence 9, Appli
C 501	27.4	2.1	1520	6	US-10-541-993-35	Sequence 35, Appl	C 579	26.8	2.1	2175	7	US-11-217-529-3088	Sequence 3088, Ap
C 502	27.4	2.1	2631	6	US-10-511-937-505	Sequence 505, App	C 580	26.8	2.1	2175	7	US-11-217-529-187	Sequence 187, App
C 503	27.6	2.1	3851	6	US-10-505-928-730	Sequence 730, App	C 581	26.8	2.1	2250	7	US-11-217-529-17360	Sequence 17360, A
C 504	27.6	2.1	5132	6	US-10-505-928-663	Sequence 663, App	C 582	26.8	2.1	2283	7	US-11-217-529-75360	Sequence 75360, A
C 505	27.4	2.1	246	7	US-11-217-529-5046	Sequence 5046, Ap	C 583	26.8	2.1	2628	7	US-11-217-529-251	Sequence 251, App
C 506	27.4	2.1	591	6	US-10-488-619-1169	Sequence 1169, Ap	C 584	26.8	2.1	2841	7	US-11-217-529-77067	Sequence 77067, A
C 507	27.4	2.1	729	7	US-11-217-529-2618	Sequence 2618, Ap	C 585	26.8	2.1	2964	7	US-11-217-529-76841	Sequence 76841, A
C 508	27.4	2.1	768	7	US-11-217-529-81743	Sequence 81743, A	C 586	26.8	2.1	3396	6	US-10-505-928-346	Sequence 346, App
C 509	27.4	2.1	781	6	US-10-488-619-1651	Sequence 1651, Ap							
C 510	27.4	2.1	1520	6	US-10-541-993-35	Sequence 35, Appl							
C 511	27.4	2.1	2631	6	US-10-511-937-505	Sequence 505, App							

587	26.8	2.1	4289	6	US-10-946-650-60	Sequence 60, Appl	668	26.2	2.0	1524	7	US-11-217-529-77900	Sequence 77900, A
C 588	26.8	2.1	4898	6	US-10-505-928-372	Sequence 372, Appl	C 669	26.2	2.0	1604	6	US-10-505-928-180	Sequence 180, App
C 589	26.8	2.1	5849	7	US-11-270-287-1	Sequence 1, Appl1	C 670	26.2	2.0	1824	7	US-11-145-307A-39	Sequence 39, Appl
C 590	26.6	2.1	493	7	US-11-301-554-750	Sequence 750, App	C 671	26.2	2.0	1977	7	US-11-217-529-3395	Sequence 3395, Ap
C 591	26.6	2.1	540	6	US-10-488-619-2626	Sequence 2626, Ap	C 672	26.2	2.0	2019	7	US-11-217-529-79218	Sequence 79218, A
592	26.6	2.1	593	7	US-11-270-287-35	Sequence 35, Appl	673	26.2	2.0	2372	6	US-10-511-937-671	Sequence 615, App
593	26.6	2.1	594	7	US-11-270-287-29	Sequence 29, Appl	674	26.2	2.0	2745	7	US-11-217-529-3143	Sequence 3143, Ap
594	26.6	2.1	594	7	US-11-270-287-30	Sequence 30, Appl	675	26.2	2.0	5137	6	US-10-505-928-802	Sequence 802, App
595	26.6	2.1	594	7	US-11-270-287-33	Sequence 33, Appl	676	26.2	2.0	5220	6	US-10-511-937-2856	Sequence 2856, Ap
596	26.6	2.1	594	7	US-11-270-287-34	Sequence 34, Appl	C 677	26.2	2.0	5307	6	US-10-505-928-824	Sequence 824, App
597	26.6	2.1	594	7	US-11-270-287-37	Sequence 37, Appl	C 678	26.2	2.0	9588	6	US-10-505-928-101	Sequence 101, App
598	26.6	2.1	594	7	US-11-270-287-38	Sequence 38, Appl	C 679	26.2	2.0	13128	7	US-11-118-524-1	Sequence 1, Appl1
599	26.6	2.1	645	7	US-11-217-529-5053	Sequence 5053, Ap	C 680	26	2.0	244	6	US-10-488-619-1090	Sequence 1090, Ap
600	26.6	2.1	696	6	US-10-488-619-2542	Sequence 2542, Ap	C 681	26	2.0	455	6	US-10-509-131-19	Sequence 19, Appl
C 601	26.6	2.1	696	7	US-11-217-529-79746	Sequence 79746, A	C 682	26	2.0	459	7	US-11-217-529-1756	Sequence 1756, Ap
C 602	26.6	2.1	739	6	US-10-488-619-2034	Sequence 2034, Ap	C 683	26	2.0	468	7	US-11-246-999-142	Sequence 142, App
C 604	26.6	2.1	1101	7	US-11-217-529-81532	Sequence 81532, Ap	C 684	26	2.0	527	7	US-11-301-554-67	Sequence 67, Appl
605	26.6	2.1	1152	6	US-10-511-937-402	Sequence 402, App	C 685	26	2.0	711	7	US-11-217-529-78816	Sequence 78816, A
606	26.6	2.1	1263	7	US-11-217-529-80982	Sequence 80982, A	C 686	26	2.0	732	7	US-11-217-529-1895	Sequence 1895, Ap
607	26.6	2.1	1356	7	US-11-217-529-5472	Sequence 5472, Ap	C 687	26	2.0	755	7	US-11-217-529-191046	Sequence 191046, A
609	26.6	2.1	1734	7	US-11-101-316-51	Sequence 51, Appl	C 688	26	2.0	972	7	US-11-217-529-3556	Sequence 3556, Ap
610	26.6	2.1	1854	7	US-11-217-529-1678	Sequence 1678, Ap	C 689	26	2.0	1086	7	US-11-217-529-166166	Sequence 166166, A
C 611	26.6	2.1	1905	7	US-11-217-529-80161	Sequence 80161, A	C 691	26	2.0	1257	7	US-11-101-316-121	Sequence 121, App
612	26.6	2.1	2430	7	US-11-217-529-1342	Sequence 1342, Ap	C 692	26	2.0	1293	7	US-11-217-529-75909	Sequence 75909, A
C 614	26.6	2.1	2457	7	US-11-217-529-1494	Sequence 1494, Ap	C 693	26	2.0	1335	7	US-11-217-529-75936	Sequence 75936, A
C 615	26.6	2.1	2661	6	US-10-511-937-562	Sequence 562, App	C 694	26	2.0	1339	6	US-10-505-928-53	Sequence 53, Appl
C 616	26.6	2.1	3015	7	US-11-217-529-76510	Sequence 76510, A	C 695	26	2.0	1458	7	US-11-217-529-4057	Sequence 4057, Ap
C 617	26.6	2.1	3129	6	US-10-511-937-588	Sequence 588, App	C 696	26	2.0	1676	1	US-09-949-925-43	Sequence 43, Appl
618	26.6	2.1	3183	6	US-10-199-229-3	Sequence 3, Appl1	C 697	26	2.0	1788	7	US-11-315-766-3	Sequence 3, Appl
619	26.6	2.1	3415	6	US-10-511-937-488	Sequence 488, App	C 698	26	2.0	1964	7	US-11-145-307A-26	Sequence 26, Appl
620	26.6	2.1	3945	7	US-11-217-529-82661	Sequence 82661, A	C 699	26	2.0	2025	7	US-11-217-529-81827	Sequence 81827, A
621	26.6	2.1	4712	6	US-10-505-928-164	Sequence 164, App	C 700	26	2.0	2078	7	US-11-217-529-3773	Sequence 3773, A
C 622	26.6	2.1	4712	6	US-10-505-928-164	Sequence 164, App	C 703	26	2.0	2452	7	US-11-242-505A-22	Sequence 22, Appl
C 623	26.4	2.0	105	7	US-11-217-529-80635	Sequence 80635, A	C 704	26	2.0	2729	6	US-10-505-928-830	Sequence 830, App
C 624	26.4	2.0	258	7	US-11-193-682-1	Sequence 1, Appl1	C 705	26	2.0	2736	7	US-11-217-529-3470	Sequence 3470, Ap
C 625	26.4	2.0	427	6	US-10-488-619-386	Sequence 386, App	C 706	26	2.0	3039	7	US-11-217-529-3489	Sequence 3489, Ap
C 626	26.4	2.0	514	6	US-10-488-619-1032	Sequence 1032, Ap	C 707	26	2.0	3054	6	US-10-505-928-492	Sequence 492, App
C 627	26.4	2.0	633	7	US-11-217-529-82572	Sequence 82572, A	C 708	26	2.0	3516	6	US-10-505-928-110	Sequence 110, App
629	26.4	2.0	644	7	US-11-101-316-55	Sequence 55, Appl	C 709	26	2.0	3598	6	US-10-505-928-84	Sequence 84, Appl
630	26.4	2.0	648	7	US-11-217-529-81312	Sequence 81312, A	C 711	26	2.0	4815	7	US-11-075-398-1	Sequence 1, Appl1
631	26.4	2.0	660	6	US-10-488-619-2763	Sequence 2763, Ap	C 712	26	2.0	6184	6	US-10-505-928-14	Sequence 14, Appl
C 632	26.4	2.0	729	7	US-11-217-529-78933	Sequence 78933, A	C 713	26	2.0	6383	6	US-10-511-937-2838	Sequence 2838, Ap
C 633	26.4	2.0	732	6	US-10-488-619-1993	Sequence 1993, Ap	C 714	25.8	2.0	168	7	US-11-217-529-174430	Sequence 174430, A
C 634	26.4	2.0	764	6	US-10-488-619-2530	Sequence 2530, Ap	C 715	25.8	2.0	239	7	US-11-301-554-116	Sequence 116, App
C 635	26.4	2.0	1000	7	US-11-233-726-3	Sequence 3, Appl1	C 716	25.8	2.0	534	7	US-11-217-529-3516	Sequence 3516, Ap
636	26.4	2.0	1170	6	US-10-541-993-76	Sequence 76, Appl	C 717	25.8	2.0	573	7	US-11-217-529-76893	Sequence 76893, A
637	26.4	2.0	1317	7	US-11-217-529-4266	Sequence 4266, Ap	C 718	25.8	2.0	582	7	US-11-217-529-79759	Sequence 79759, A
638	26.4	2.0	1398	7	US-11-217-529-726	Sequence 726, App	C 719	25.8	2.0	600	7	US-11-217-529-1694	Sequence 1694, Ap
639	26.4	2.0	1433	6	US-10-505-928-192	Sequence 192, App	C 720	25.8	2.0	642	7	US-11-217-529-81467	Sequence 81467, A
640	26.4	2.0	1443	7	US-11-249-111-15	Sequence 15, Appl	C 721	25.8	2.0	767	6	US-10-488-619-1375	Sequence 1375, Ap
641	26.4	2.0	1505	7	US-11-217-529-166169	Sequence 166169, A	C 722	25.8	2.0	960	7	US-11-217-529-80888	Sequence 80888, A
642	26.4	2.0	1722	7	US-11-217-529-987	Sequence 987, App	C 723	25.8	2.0	1000	7	US-11-233-726-30	Sequence 30, Appl
C 645	26.4	2.0	2166	7	US-11-217-529-77110	Sequence 77110, A	C 724	25.8	2.0	1221	7	US-11-217-529-3373	Sequence 3373, Ap
C 646	26.4	2.0	2391	7	US-11-217-529-76407	Sequence 76407, A	C 725	25.8	2.0	1254	6	US-10-505-928-29	Sequence 29, Appl
C 647	26.4	2.0	2454	6	US-10-511-937-2817	Sequence 2817, Ap	C 726	25.8	2.0	1290	7	US-11-217-529-191180	Sequence 191180, A
648	26.4	2.0	2643	7	US-11-217-529-77861	Sequence 77861, A	C 727	25.8	2.0	1610	7	US-11-242-505A-4	Sequence 4, Appl1
C 649	26.4	2.0	2652	7	US-11-217-529-1260	Sequence 1260, Ap	C 728	25.8	2.0	1816	6	US-10-528-032-5	Sequence 5, Appl1
C 650	26.4	2.0	2716	7	US-11-246-976-2	Sequence 2, Appl1	C 729	25.8	2.0	1836	6	US-11-217-529-6027	Sequence 6027, App
651	26.4	2.0	2716	7	US-11-246-976-4	Sequence 4, Appl1	C 730	25.8	2.0	1843	6	US-10-511-937-620	Sequence 6207, App
652	26.4	2.0	2904	7	US-11-145-307A-161	Sequence 161, App	C 731	25.8	2.0	1847	6	US-10-528-032-3	Sequence 3, Appl1
653	26.4	2.0	3012	7	US-11-217-529-79922	Sequence 79922, A	C 732	25.8	2.0	2031	7	US-11-217-529-78545	Sequence 78545, A
654	26.4	2.0	3441	7	US-11-217-529-76893	Sequence 76893, A	C 733	25.8	2.0	2310	7	US-11-145-307A-155	Sequence 155, App
655	26.4	2.0	4058	6	US-10-199-229-2	Sequence 2, Appl1	C 734	25.8	2.0	2529	6	US-10-505-928-572	Sequence 572, App
656	26.4	2.0	4071	7	US-11-217-529-1426	Sequence 1426, Ap	C 735	25.8	2.0	2577	7	US-11-217-529-79098	Sequence 79098, A
C 657	26.4	2.0	4633	6	US-10-505-928-600	Sequence 600, App	C 736	25.8	2.0	2591	6	US-10-511-937-603	Sequence 603, App
C 658	26.4	2.0	5524	6	US-10-473-173-51	Sequence 51, Appl	C 737	25.8	2.0	2604	7	US-11-217-529-2700	Sequence 2700, Ap
659	26.4	2.0	5650	6	US-10-505-928-212	Sequence 212, App	C 738	25.8	2.0	2631	7	US-11-217-529-78359	Sequence 78359, A
660	26.4	2.0	13971	6	US-10-501-834-3	Sequence 3, Appl1	C 739	25.8	2.0	2833	7	US-11-145-307A-155	Sequence 155, App
661	26.2	2.0	408	6	US-10-488-619-510	Sequence 510, App	C 741	25.8	2.0	2848	7	US-11-101-316-97	Sequence 97, Appl
C 662	26.2	2.0	543	6	US-10-488-619-2662	Sequence 2662, App	C 742	25.8	2.0	3074	6	US-10-524-021-7	Sequence 7, Appl1
663	26.2	2.0	728	7	US-11-217-529-191120	Sequence 191120, A	C 743	25.8	2.0	3204	6	US-10-199-229-6	Sequence 6, Appl1
C 664	26.2	2.0	987	6	US-10-515-716-7	Sequence 7, Appl1	C 744	25.8	2.0	3541	6	US-10-505-928-113	Sequence 113, App
665	26.2	2.0	1134	7	US-11-217-529-166160	Sequence 166160, A	C 745	25.8	2.0	3743	6	US-10-502-993-1	Sequence 1, Appl1
667	26.2	2.0	1404	7	US-11-217-529-80331	Sequence 80331, A	C 745	25.8	2.0	4553	6	US-10-505-928-95	Sequence 95, Appl

C 746	25.8	2.0	4856	6	US-10-505-928-242	Sequence 242, App	C 822	25.4	2.0	1740	7	US-11-217-529-78441	Sequence 78441, A
C 747	25.8	2.0	5133	6	US-10-511-937-2799	Sequence 2799, App	C 823	25.4	2.0	1804	7	US-11-251-465-7	Sequence 7, Appli
C 748	25.8	2.0	5181	7	US-11-217-529-2050	Sequence 2050, App	C 824	25.4	2.0	1845	7	US-11-311-778-7	Sequence 7, Appli
C 749	25.8	2.0	5994	6	US-10-505-928-701	Sequence 701, App	C 825	25.4	2.0	1904	7	US-11-301-554-1793	Sequence 1793, Ap
C 750	25.8	2.0	6035	6	US-10-511-937-2815	Sequence 2815, App	C 826	25.4	2.0	1929	7	US-11-217-529-1871	Sequence 1871, Ap
C 751	25.8	2.0	6335	6	US-10-505-928-178	Sequence 178, App	C 827	25.4	2.0	1941	7	US-11-217-529-190926	Sequence 190926,
C 752	25.8	2.0	6429	7	US-11-217-529-4027	Sequence 4027, App	C 828	25.4	2.0	2180	6	US-10-505-928-771	Sequence 771, Appl
C 753	25.8	2.0	2394	7	US-11-217-529-166824	Sequence 166824, App	C 829	25.4	2.0	2251	6	US-10-946-650-77	Sequence 77, Appl
C 754	25.6	2.0	571	6	US-10-488-619-2288	Sequence 2288, App	C 830	25.4	2.0	2307	7	US-11-217-529-738	Sequence 738, Ap
C 755	25.6	2.0	576	6	US-10-488-619-1065	Sequence 1065, App	C 831	25.4	2.0	2394	7	US-11-217-529-81691	Sequence 81691, A
C 756	25.6	2.0	592	7	US-11-106-014-31	Sequence 31, Appl	C 832	25.4	2.0	2484	7	US-11-217-529-77735	Sequence 77735, A
C 757	25.6	2.0	717	7	US-11-301-554-212	Sequence 212, App	C 833	25.4	2.0	2508	7	US-11-217-529-191162	Sequence 191162,
C 758	25.6	2.0	1086	7	US-11-217-529-79462	Sequence 79462, A	C 834	25.4	2.0	2523	7	US-11-217-529-75363	Sequence 75363, A
C 759	25.6	2.0	1152	6	US-10-511-937-402	Sequence 402, App	C 835	25.4	2.0	2700	6	US-10-511-937-410	Sequence 410, App
C 760	25.6	2.0	1227	7	US-11-217-529-5446	Sequence 5446, App	C 836	25.4	2.0	2716	7	US-11-246-976-2	Sequence 2, Appli
C 761	25.6	2.0	1354	7	US-11-145-307A-6	Sequence 6, Appli	C 837	25.4	2.0	2716	7	US-11-246-976-2	Sequence 4, Appli
C 762	25.6	2.0	1407	7	US-11-217-529-81186	Sequence 81186, A	C 838	25.4	2.0	3056	6	US-10-511-937-461	Sequence 461, App
C 763	25.6	2.0	1484	6	US-10-511-937-339	Sequence 339, App	C 839	25.4	2.0	3257	6	US-10-505-928-562	Sequence 562, App
C 764	25.6	2.0	1725	7	US-11-217-529-191011	Sequence 191011, App	C 840	25.4	2.0	3257	6	US-10-505-928-562	Sequence 23, Appl
C 765	25.6	2.0	1784	7	US-11-312-958-27	Sequence 27, Appl	C 841	25.4	2.0	3531	7	US-11-311-778-23	Sequence 4976, Ap
C 766	25.6	2.0	1848	6	US-10-519-335-5	Sequence 5, Appli	C 842	25.4	2.0	4257	7	US-11-217-529-4376	Sequence 398, App
C 767	25.6	2.0	1878	6	US-10-519-335-3	Sequence 3, Appli	C 843	25.4	2.0	4414	6	US-10-505-928-398	Sequence 2891, Ap
C 768	25.6	2.0	1913	7	US-11-312-958-41	Sequence 41, Appl	C 844	25.4	2.0	4482	7	US-11-217-529-2891	Sequence 854, App
C 769	25.6	2.0	1932	6	US-10-519-335-1	Sequence 1, Appli	C 845	25.4	2.0	5927	6	US-10-505-928-854	Sequence 854, App
C 770	25.6	2.0	1935	7	US-11-217-529-2838	Sequence 2838, App	C 846	25.4	2.0	6335	6	US-10-505-928-178	Sequence 178, App
C 771	25.6	2.0	2022	7	US-11-217-529-7628	Sequence 7628, App	C 847	25.4	2.0	7032	6	US-10-505-928-832	Sequence 832, App
C 772	25.6	2.0	2025	7	US-11-342-505A-23	Sequence 23, Appl	C 848	25.4	2.0	14756	6	US-10-505-928-570	Sequence 570, App
C 773	25.6	2.0	2205	7	US-11-217-529-77601	Sequence 77601, A	C 849	25.4	2.0	15304	6	US-10-505-928-828	Sequence 828, App
C 774	25.6	2.0	2277	7	US-11-302-678-16	Sequence 16, Appl	C 850	25.2	1.9	283	6	US-10-473-173-458	Sequence 458, App
C 775	25.6	2.0	2325	7	US-11-217-529-1012	Sequence 1012, App	C 851	25.2	1.9	431	6	US-10-488-619-2705	Sequence 2705, Ap
C 776	25.6	2.0	2331	7	US-11-217-529-5632	Sequence 5632, App	C 852	25.2	1.9	705	7	US-11-217-529-4680	Sequence 4680, Ap
C 777	25.6	2.0	2376	7	US-11-217-529-78788	Sequence 78788, App	C 853	25.2	1.9	729	7	US-11-217-529-5921	Sequence 5921, Ap
C 778	25.6	2.0	2409	7	US-11-217-529-82843	Sequence 82843, A	C 854	25.2	1.9	762	6	US-10-541-993-72	Sequence 29, Appl
C 779	25.6	2.0	2414	6	US-10-511-937-389	Sequence 389, App	C 855	25.2	1.9	762	6	US-10-541-993-72	Sequence 72, Appl
C 780	25.6	2.0	2426	6	US-10-505-928-27	Sequence 27, Appl	C 856	25.2	1.9	861	7	US-11-217-529-78736	Sequence 78736, A
C 781	25.6	2.0	2619	7	US-11-302-678-18	Sequence 18, Appl	C 857	25.2	1.9	1122	7	US-11-217-529-3376	Sequence 3376, Ap
C 782	25.6	2.0	2815	6	US-10-505-928-526	Sequence 526, App	C 858	25.2	1.9	1269	7	US-11-217-529-3899	Sequence 3899, Ap
C 783	25.6	2.0	2827	7	US-11-217-529-76927	Sequence 76927, App	C 859	25.2	1.9	1290	7	US-11-217-529-3899	Sequence 3899, Ap
C 786	25.6	2.0	3120	7	US-11-217-529-4779	Sequence 4779, App	C 860	25.2	1.9	1329	7	US-11-217-529-79611	Sequence 79611, A
C 787	25.6	2.0	3216	7	US-11-217-529-77601	Sequence 77601, A	C 861	25.2	1.9	1332	7	US-11-217-529-81182	Sequence 81182, A
C 788	25.6	2.0	3232	7	US-11-302-678-16	Sequence 16, Appl	C 862	25.2	1.9	1425	6	US-10-511-937-416	Sequence 7, Appli
C 789	25.6	2.0	3243	7	US-11-217-529-76988	Sequence 76988, A	C 863	25.2	1.9	1455	7	US-11-217-529-257	Sequence 416, App
C 790	25.6	2.0	3297	7	US-11-217-529-78860	Sequence 78860, A	C 864	25.2	1.9	1455	7	US-11-217-529-4434	Sequence 257, App
C 791	25.6	2.0	3573	7	US-11-217-529-79161	Sequence 79161, A	C 865	25.2	1.9	1560	7	US-11-217-529-4485	Sequence 4434, Ap
C 792	25.6	2.0	3969	6	US-10-982-908-15	Sequence 15, Appl	C 866	25.2	1.9	1596	6	US-10-505-928-478	Sequence 4485, Ap
C 793	25.6	2.0	4059	7	US-11-106-014-47	Sequence 47, Appl	C 867	25.2	1.9	1620	7	US-11-217-529-1408	Sequence 478, App
C 794	25.6	2.0	4767	6	US-10-505-928-360	Sequence 360, App	C 868	25.2	1.9	1728	7	US-11-217-529-77037	Sequence 1408, Ap
C 795	25.6	2.0	4767	7	US-11-145-307A-150	Sequence 150, App	C 869	25.2	1.9	1752	7	US-11-217-529-2287	Sequence 2287, A
C 796	25.6	2.0	4898	6	US-10-505-928-372	Sequence 372, App	C 870	25.2	1.9	1770	7	US-11-217-529-2290	Sequence 2287, Ap
C 797	25.6	2.0	5676	7	US-11-131-901-5	Sequence 5, Appli	C 871	25.2	1.9	2103	7	US-11-301-554-1898	Sequence 2290, Ap
C 798	25.6	2.0	6505	6	US-10-505-928-721	Sequence 721, App	C 872	25.2	1.9	2118	7	US-11-217-529-78040	Sequence 1898, Ap
C 799	25.6	2.0	11564	6	US-10-505-928-105	Sequence 105, App	C 873	25.2	1.9	2233	7	US-11-217-529-78291	Sequence 78040, A
C 800	25.4	2.0	393	7	US-11-217-529-3977	Sequence 3977, App	C 874	25.2	1.9	2233	7	US-11-217-529-78291	Sequence 78291, A
C 801	25.4	2.0	407	7	US-11-301-554-1268	Sequence 1268, App	C 875	25.2	1.9	2310	7	US-11-217-529-4722	Sequence 4722, Ap
C 802	25.4	2.0	452	6	US-10-488-619-830	Sequence 830, App	C 876	25.2	1.9	2412	6	US-10-511-937-2878	Sequence 2878, Ap
C 803	25.4	2.0	459	7	US-11-217-529-77593	Sequence 77593, A	C 877	25.2	1.9	2473	6	US-10-505-928-264	Sequence 2878, Ap
C 804	25.4	2.0	474	7	US-11-217-529-76743	Sequence 76743, App	C 878	25.2	1.9	2473	6	US-10-505-928-264	Sequence 264, App
C 805	25.4	2.0	489	6	US-10-473-173-287	Sequence 287, App	C 879	25.2	1.9	2654	6	US-10-511-937-489	Sequence 489, App
C 806	25.4	2.0	600	7	US-11-217-529-166167	Sequence 166167, App	C 880	25.2	1.9	2654	6	US-10-505-928-352	Sequence 352, App
C 807	25.4	2.0	600	7	US-11-217-529-166167	Sequence 166167, App	C 881	25.2	1.9	3084	6	US-10-511-937-448	Sequence 448, App
C 808	25.4	2.0	636	6	US-10-488-619-1813	Sequence 1813, App	C 882	25.2	1.9	3183	6	US-10-199-229-3	Sequence 3, Appli
C 809	25.4	2.0	790	6	US-10-510-162-3	Sequence 3, Appli	C 883	25.2	1.9	3354	6	US-10-505-928-362	Sequence 362, Appl
C 810	25.4	2.0	816	7	US-11-217-529-78542	Sequence 78542, A	C 884	25.2	1.9	3657	7	US-11-217-529-191048	Sequence 345, App
C 811	25.4	2.0	909	7	US-11-217-529-78608	Sequence 78608, A	C 885	25.2	1.9	3657	7	US-11-217-529-191048	Sequence 191048,
C 812	25.4	2.0	916	6	US-10-511-937-2921	Sequence 2921, App	C 886	25.2	1.9	3662	6	US-10-505-928-844	Sequence 844, App
C 813	25.4	2.0	942	7	US-11-145-307A-172	Sequence 172, App	C 887	25.2	1.9	4329	7	US-11-217-529-1487	Sequence 1487, Ap
C 814	25.4	2.0	1008	7	US-11-217-529-79011	Sequence 79011, A	C 888	25.2	1.9	4428	6	US-10-511-937-2823	Sequence 2823, Ap
C 815	25.4	2.0	1035	7	US-11-217-529-59312	Sequence 59312, App	C 889	25.2	1.9	5028	7	US-11-217-529-5947	Sequence 5947, Ap
C 816	25.4	2.0	1124	6	US-10-511-937-465	Sequence 465, App	C 890	25.2	1.9	5703	7	US-11-312-958-63	Sequence 63, Appl
C 817	25.4	2.0	1251	7	US-11-217-529-174115	Sequence 174115, App	C 891	25.2	1.9	6184	6	US-10-505-928-14	Sequence 14, Appl
C 818	25.4	2.0	1452	7	US-11-217-529-75640	Sequence 75640, A	C 892	25.2	1.9	6317	6	US-10-511-937-387	Sequence 387, App
C 819	25.4	2.0	1611	7	US-11-217-529-81129	Sequence 81129, A	C 893	25.2	1.9	17118	6	US-10-541-993-48	Sequence 48, Appl
C 820	25.4	2.0	1686	7	US-11-217-529-78427	Sequence 78427, A	C 894	25.2	1.9	17756	6	US-10-541-993-51	Sequence 51, Appl
C 821	25.4	2.0	1695	7	US-11-217-529-1887	Sequence 1887, App	C 895	25.2	1.9	18333	6	US-10-541-993-51	Sequence 51, Appl
							C 896	25.2	1.9	18617	6	US-10-541-993-50	Sequence 50, Appl
										250	7	US-11-301-554-1264	Sequence 1264, Ap

c 898	25	1.9	252	7	US-11-301-554-1423	Sequence 1423, Ap	973	24.8	1.9	877	7	US-11-238-282-22	Sequence 22, Appl
c 899	25	1.9	352	6	US-10-488-619-213	Sequence 213, App	974	24.8	1.9	957	7	US-11-024-544A-112	Sequence 112, App
c 900	25	1.9	371	7	US-11-301-554-1355	Sequence 1355, Ap	975	24.8	1.9	957	7	US-11-024-545-40	Sequence 40, Appl
c 901	25	1.9	371	7	US-11-301-554-1539	Sequence 1539, Ap	976	24.8	1.9	957	7	US-11-185-301-28	Sequence 28, Appl
c 902	25	1.9	438	6	US-10-473-173-468	Sequence 468, App	977	24.8	1.9	957	7	US-11-190-750-95	Sequence 95, Appl
c 903	25	1.9	495	7	US-11-217-529-173725	Sequence 173725, Ap	978	24.8	1.9	957	7	US-11-251-466-14	Sequence 14, Appl
c 904	25	1.9	540	6	US-10-488-619-1015	Sequence 1015, Ap	979	24.8	1.9	957	7	US-11-254-173-28	Sequence 28, Appl
c 905	25	1.9	541	6	US-10-488-619-2277	Sequence 2277, Ap	980	24.8	1.9	957	7	US-11-264-784-19	Sequence 19, Appl
c 906	25	1.9	556	6	US-10-488-619-2316	Sequence 2316, Ap	981	24.8	1.9	971	1	US-09-949-925-63	Sequence 63, Appl
c 907	25	1.9	571	6	US-10-488-619-2657	Sequence 2657, Ap	982	24.8	1.9	999	6	US-10-525-126-92	Sequence 92, Appl
c 908	25	1.9	595	7	US-11-270-287-36	Sequence 36, Appl	984	24.8	1.9	1026	7	US-11-217-529-1112	Sequence 1112, Ap
c 909	25	1.9	600	7	US-11-217-529-166177	Sequence 166177, Ap	985	24.8	1.9	1050	7	US-11-217-529-2194	Sequence 2194, Ap
c 910	25	1.9	603	6	US-10-488-619-1286	Sequence 1286, Ap	986	24.8	1.9	1149	7	US-11-217-529-34	Sequence 34, Appl
c 911	25	1.9	603	7	US-11-301-554-1062	Sequence 1062, Ap	987	24.8	1.9	1155	7	US-11-217-529-2714	Sequence 2714, Ap
c 912	25	1.9	621	7	US-11-301-554-676	Sequence 676, App	988	24.8	1.9	1233	7	US-11-217-529-2893	Sequence 2893, Ap
c 913	25	1.9	672	7	US-11-217-529-4009	Sequence 4009, Ap	989	24.8	1.9	1239	7	US-11-217-529-81143	Sequence 81143, A
c 914	25	1.9	717	7	US-11-217-529-4041	Sequence 4041, Ap	c 991	24.8	1.9	1344	7	US-11-246-999-24	Sequence 24, Appl
c 915	25	1.9	730	6	US-10-488-619-1921	Sequence 1921, Ap	992	24.8	1.9	1542	6	US-10-511-937-514	Sequence 514, App
c 916	25	1.9	738	7	US-11-217-529-76729	Sequence 76729, A	994	24.8	1.9	1689	7	US-11-217-529-78901	Sequence 78901, A
c 917	25	1.9	762	7	US-11-259-950-1	Sequence 1, Appl	995	24.8	1.9	1767	7	US-11-217-529-76039	Sequence 76039, A
c 918	25	1.9	1014	7	US-11-217-529-3336	Sequence 3336, Ap	c 996	24.8	1.9	1779	7	US-11-217-529-1993	Sequence 1993, Ap
c 919	25	1.9	1194	7	US-11-217-529-2971	Sequence 2971, Ap	997	24.8	1.9	1894	7	US-11-190-075-1	Sequence 1, Appl
c 920	25	1.9	1260	7	US-11-259-950-7	Sequence 7, Appl	998	24.8	1.9	1935	7	US-11-217-529-76932	Sequence 76932, A
c 921	25	1.9	1275	7	US-11-259-950-77	Sequence 77, Appl	999	24.8	1.9	1965	7	US-11-217-529-1789	Sequence 1789, Ap
c 922	25	1.9	1278	7	US-11-217-529-75548	Sequence 75548, A	c1000	24.8	1.9	2025	6	US-10-511-937-414	Sequence 414, App
c 923	25	1.9	1282	7	US-11-259-950-9	Sequence 9, Appl	c1001	24.8	1.9	2152	7	US-11-245-628-7	Sequence 7, Appl
c 924	25	1.9	1356	7	US-11-217-529-3008	Sequence 3008, Ap	1002	24.8	1.9	2556	7	US-11-217-529-80665	Sequence 80665, A
c 925	25	1.9	1455	7	US-11-217-529-81009	Sequence 81009, A	c1003	24.8	1.9	2627	6	US-10-505-928-240	Sequence 240, App
c 926	25	1.9	1524	7	US-11-217-529-6166	Sequence 6166, Ap	c1004	24.8	1.9	2712	7	US-11-217-529-82177	Sequence 82177, A
c 927	25	1.9	1526	7	US-11-301-554-1931	Sequence 1931, A	1005	24.8	1.9	2805	6	US-10-505-928-536	Sequence 536, App
c 928	25	1.9	1611	7	US-11-217-529-3860	Sequence 3860, Ap	1006	24.8	1.9	2916	6	US-10-505-928-675	Sequence 675, App
c 929	25	1.9	1653	6	US-10-505-928-587	Sequence 587, App	c1007	24.8	1.9	3054	6	US-10-505-928-492	Sequence 492, App
c 930	25	1.9	1719	7	US-11-217-529-79365	Sequence 79365, A	1008	24.8	1.9	3336	7	US-11-217-529-80440	Sequence 80440, A
c 931	25	1.9	1804	7	US-11-251-465-7	Sequence 7, Appl	1009	24.8	1.9	3366	7	US-11-217-529-3330	Sequence 3330, Ap
c 932	25	1.9	1836	7	US-11-301-554-1933	Sequence 1933, Ap	c1010	24.8	1.9	3378	7	US-11-452-276-151	Sequence 151, App
c 933	25	1.9	1841	7	US-11-145-307A-163	Sequence 163, App	1011	24.8	1.9	3450	7	US-11-217-529-78684	Sequence 78684, A
c 934	25	1.9	1849	6	US-10-511-937-360	Sequence 360, App	1012	24.8	1.9	3655	6	US-10-511-937-346	Sequence 346, App
c 935	25	1.9	1923	7	US-11-145-307A-52	Sequence 52, Appl	1013	24.8	1.9	4157	7	US-11-145-307A-176	Sequence 176, App
c 936	25	1.9	1962	7	US-11-183-218-65	Sequence 65, Appl	1014	24.8	1.9	4215	7	US-11-217-529-79183	Sequence 79183, A
c 937	25	1.9	1971	7	US-11-217-529-76164	Sequence 76164, A	1015	24.8	1.9	4740	6	US-10-511-937-380	Sequence 380, App
c 938	25	1.9	2156	6	US-10-522-043-6	Sequence 6, Appl	c1016	24.8	1.9	4833	7	US-11-452-276-21	Sequence 21, Appl
c 939	25	1.9	2291	7	US-11-242-505A-43	Sequence 43, Appl	1017	24.8	1.9	6540	7	US-11-254-173-60	Sequence 60, Appl
c 940	25	1.9	2291	7	US-11-242-505A-44	Sequence 44, Appl	1018	24.8	1.9	6540	7	US-11-264-784-135	Sequence 135, App
c 941	25	1.9	2295	7	US-11-217-529-2907	Sequence 2907, Ap	c1019	24.8	1.9	7381	6	US-10-505-928-200	Sequence 200, App
c 942	25	1.9	2296	6	US-10-473-173-24	Sequence 24, Appl	c1020	24.8	1.9	10838	7	US-11-024-544A-138	Sequence 138, App
c 943	25	1.9	2334	7	US-11-217-529-810	Sequence 810, App	c1021	24.8	1.9	10838	7	US-11-024-545-57	Sequence 57, Appl
c 944	25	1.9	2784	7	US-11-217-529-456	Sequence 456, App	c1022	24.8	1.9	10838	7	US-11-251-466-31	Sequence 31, Appl
c 945	25	1.9	3006	7	US-11-217-529-4215	Sequence 4215, Ap	c1023	24.8	1.9	10838	7	US-11-264-784-130	Sequence 130, App
c 946	25	1.9	3213	7	US-11-217-529-2671	Sequence 2671, Ap	1024	24.8	1.9	12649	7	US-11-024-544A-110	Sequence 110, App
c 947	25	1.9	3303	7	US-11-217-529-166175	Sequence 166175, A	1025	24.8	1.9	12649	7	US-11-024-545-38	Sequence 38, Appl
c 948	25	1.9	3303	7	US-11-217-529-78086	Sequence 78086, A	1026	24.8	1.9	12649	7	US-11-185-301-27	Sequence 27, Appl
c 949	25	1.9	3346	6	US-10-473-173-124	Sequence 124, App	1027	24.8	1.9	12649	7	US-11-190-750-93	Sequence 93, Appl
c 950	25	1.9	3501	7	US-11-217-529-4446	Sequence 4446, Ap	1028	24.8	1.9	12649	7	US-11-251-466-12	Sequence 12, Appl
c 951	25	1.9	3653	6	US-10-504-120-16	Sequence 16, Appl	1029	24.8	1.9	12649	7	US-11-254-173-26	Sequence 26, Appl
c 952	25	1.9	3747	7	US-11-217-529-78696	Sequence 78696, A	1030	24.8	1.9	12649	7	US-11-264-784-114	Sequence 114, App
c 953	25	1.9	3881	6	US-10-505-928-602	Sequence 602, App	1031	24.8	1.9	12663	7	US-11-254-173-49	Sequence 49, Appl
c 954	25	1.9	3900	6	US-10-488-619-3023	Sequence 3023, Ap	1032	24.8	1.9	12663	7	US-11-264-784-132	Sequence 132, App
c 955	25	1.9	5026	7	US-11-217-529-166180	Sequence 166180, Ap	1033	24.8	1.9	13321	7	US-11-264-784-136	Sequence 136, App
c 956	25	1.9	5601	6	US-10-511-937-2798	Sequence 2798, Ap	c1034	24.8	1.9	14864	7	US-11-254-173-58	Sequence 58, Appl
c 957	25	1.9	5645	6	US-10-505-928-392	Sequence 392, App	c1035	24.8	1.9	14864	7	US-11-264-784-134	Sequence 134, App
c 958	25	1.9	6152	6	US-10-528-659-6	Sequence 6, Appl	1036	24.8	1.9	15456	7	US-11-324-284-22	Sequence 22, Appl
c 959	25	1.9	6218	6	US-10-505-928-460	Sequence 460, App	1037	24.8	1.9	15456	7	US-11-324-284-23	Sequence 23, Appl
c 960	25	1.9	6828	6	US-10-505-928-691	Sequence 691, App	1038	24.6	1.9	333	7	US-11-217-529-166733	Sequence 166733, A
c 961	25	1.9	8372	7	US-11-301-554-1893	Sequence 1893, Ap	c1039	24.6	1.9	402	7	US-11-301-554-571	Sequence 571, App
c 962	25	1.9	228	7	US-11-217-529-78378	Sequence 78378, A	c1040	24.6	1.9	402	7	US-11-301-554-579	Sequence 579, App
c 963	24.8	1.9	366	7	US-11-217-529-80664	Sequence 80664, A	c1041	24.6	1.9	435	7	US-11-301-554-1649	Sequence 1649, App
c 964	24.8	1.9	402	7	US-11-217-529-75995	Sequence 75995, A	1042	24.6	1.9	440	6	US-10-488-619-1304	Sequence 1304, Ap
c 965	24.8	1.9	471	7	US-11-217-529-174475	Sequence 174475, A	1043	24.6	1.9	449	6	US-10-488-619-46	Sequence 46, Appl
c 966	24.8	1.9	474	7	US-11-217-529-80222	Sequence 80222, A	c1044	24.6	1.9	503	6	US-10-488-619-2198	Sequence 2198, Ap
c 967	24.8	1.9	547	6	US-10-488-619-2225	Sequence 2225, Ap	c1045	24.6	1.9	546	7	US-11-217-529-79919	Sequence 79919, A
c 968	24.8	1.9	597	7	US-11-217-529-77932	Sequence 77932, A	1046	24.6	1.9	582	7	US-11-217-529-1812	Sequence 1812, Ap
c 969	24.8	1.9	604	6	US-10-488-619-2226	Sequence 2226, Ap	1047	24.6	1.9	600	7	US-11-217-529-5850	Sequence 5850, Ap
c 970	24.8	1.9	762	7	US-11-217-529-80718	Sequence 80718, A	1048	24.6	1.9	604	6	US-10-488-619-2226	Sequence 2226, Ap

c1049	24.6	1.9	605	6	US-10-488-619-1416	Sequence 1416, Ap	c1124	24.6	1.9	16954	6	US-10-541-993-43	Sequence 43, Appl
c1050	24.6	1.9	631	6	US-10-473-173-483	Sequence 483, App	c1125	24.6	1.9	16954	6	US-10-541-993-44	Sequence 44, Appl
c1051	24.6	1.9	697	6	US-10-488-619-1955	Sequence 1755, Ap	c1126	24.6	1.9	17238	6	US-10-541-993-38	Sequence 38, Appl
c1052	24.6	1.9	716	6	US-10-488-619-1755	Sequence 1755, Ap	c1127	24.6	1.9	17238	6	US-10-541-993-39	Sequence 39, Appl
c1053	24.6	1.9	744	6	US-11-217-190943	Sequence 190943, Ap	c1128	24.6	1.9	17593	6	US-10-541-993-42	Sequence 42, Appl
c1054	24.6	1.9	824	6	US-10-488-619-1933	Sequence 1933, Ap	c1129	24.6	1.9	17593	6	US-10-541-993-37	Sequence 37, Appl
c1055	24.6	1.9	843	6	US-11-217-4598	Sequence 4598, Ap	c1130	24.6	1.9	18449	6	US-10-541-993-40	Sequence 40, Appl
c1056	24.6	1.9	861	6	US-10-505-928-534	Sequence 534, App	c1131	24.6	1.9	18449	6	US-10-541-993-41	Sequence 41, Appl
c1057	24.6	1.9	861	7	US-11-217-529-81505	Sequence 81505, A	c1132	24.6	1.9	18449	6	US-10-541-993-49	Sequence 49, Appl
c1058	24.6	1.9	1003	7	US-11-226-605-21	Sequence 21, Appl	c1133	24.6	1.9	19491	6	US-10-541-993-45	Sequence 45, Appl
c1059	24.6	1.9	1013	7	US-11-233-726-21	Sequence 21, Appl	c1134	24.6	1.9	21300	6	US-10-541-993-46	Sequence 46, Appl
c1060	24.6	1.9	1083	7	US-11-217-529-4517	Sequence 4517, Ap	c1135	24.4	1.9	261	7	US-11-217-529-81715	Sequence 81715, A
c1061	24.6	1.9	1095	7	US-11-226-605-45	Sequence 45, Appl	c1136	24.4	1.9	283	6	US-10-488-619-981	Sequence 981, App
c1062	24.6	1.9	1095	7	US-11-217-529-7515	Sequence 7515, A	c1137	24.4	1.9	306	7	US-11-217-529-76992	Sequence 76992, A
c1063	24.6	1.9	1194	7	US-11-217-529-2097	Sequence 2097, Ap	c1138	24.4	1.9	307	7	US-11-301-554-84	Sequence 84, App
c1064	24.6	1.9	1194	7	US-11-217-529-3408	Sequence 3408, Ap	c1139	24.4	1.9	435	6	US-10-488-619-270	Sequence 270, App
c1065	24.6	1.9	1203	7	US-11-217-529-2839	Sequence 2839, Ap	c1140	24.4	1.9	467	6	US-10-488-619-952	Sequence 952, App
c1066	24.6	1.9	1363	1	US-09-949-925-50	Sequence 50, Appl	c1141	24.4	1.9	522	7	US-11-259-950-11	Sequence 11, Appl
c1067	24.6	1.9	1392	7	US-11-217-529-166163	Sequence 166163, Ap	c1142	24.4	1.9	522	7	US-11-259-950-13	Sequence 13, Appl
c1068	24.6	1.9	1432	7	US-11-327-900-3	Sequence 3, Appl	c1143	24.4	1.9	525	6	US-10-488-619-15	Sequence 15, Appl
c1069	24.6	1.9	1446	7	US-11-217-529-82770	Sequence 82770, A	c1144	24.4	1.9	539	6	US-10-488-619-497	Sequence 497, App
c1070	24.6	1.9	1450	7	US-11-145-307A-168	Sequence 168, Appl	c1145	24.4	1.9	539	6	US-11-145-307A-152	Sequence 152, App
c1071	24.6	1.9	1454	7	US-11-292-215-2	Sequence 2, Appl	c1146	24.4	1.9	562	6	US-10-488-619-2011	Sequence 2011, Ap
c1072	24.6	1.9	1494	6	US-10-511-937-339	Sequence 339, App	c1147	24.4	1.9	600	7	US-11-217-529-166167	Sequence 166167, Ap
c1073	24.6	1.9	1486	6	US-10-505-928-483	Sequence 483, App	c1148	24.4	1.9	600	7	US-11-217-529-166177	Sequence 166177, Ap
c1075	24.6	1.9	1554	7	US-11-217-529-75545	Sequence 75545, A	c1149	24.4	1.9	619	7	US-11-259-950-5	Sequence 5, Appl
c1076	24.6	1.9	1674	7	US-11-217-529-76477	Sequence 76477, A	c1150	24.4	1.9	654	7	US-11-259-950-3	Sequence 3, Appl
c1077	24.6	1.9	1740	7	US-11-217-529-78999	Sequence 78999, A	c1151	24.4	1.9	728	6	US-10-488-619-1172	Sequence 1172, Ap
c1078	24.6	1.9	1881	7	US-11-217-529-173225	Sequence 173225, Ap	c1152	24.4	1.9	735	7	US-11-217-529-3878	Sequence 3878, Ap
c1079	24.6	1.9	1970	7	US-11-106-014-25	Sequence 25, Appl	c1153	24.4	1.9	765	7	US-11-217-529-82489	Sequence 82489, A
c1080	24.6	1.9	2070	7	US-11-217-529-6049	Sequence 6049, Ap	c1154	24.4	1.9	821	7	US-11-217-529-190991	Sequence 190991, Ap
c1081	24.6	1.9	2119	7	US-11-024-544A-1	Sequence 1, Appl	c1155	24.4	1.9	837	7	US-11-217-529-77522	Sequence 77522, A
c1082	24.6	1.9	2119	7	US-11-024-545-3	Sequence 3, Appl	c1156	24.4	1.9	846	7	US-11-217-529-1366	Sequence 1366, Ap
c1083	24.6	1.9	2119	7	US-11-190-750-43	Sequence 43, Appl	c1157	24.4	1.9	919	7	US-11-233-726-14	Sequence 14, Appl
c1084	24.6	1.9	2119	7	US-11-164-784-89	Sequence 89, Appl	c1158	24.4	1.9	945	7	US-11-301-554-1861	Sequence 1861, Ap
c1085	24.6	1.9	2236	6	US-10-511-937-516	Sequence 516, App	c1159	24.4	1.9	990	7	US-11-217-529-6009	Sequence 6009, Ap
c1086	24.6	1.9	2372	6	US-11-101-316-5	Sequence 5, Appl	c1160	24.4	1.9	1003	7	US-11-226-605-52	Sequence 52, Appl
c1087	24.6	1.9	2476	7	US-11-217-529-166168	Sequence 166168, Ap	c1161	24.4	1.9	1006	6	US-10-525-126-108	Sequence 108, App
c1088	24.6	1.9	2586	7	US-11-101-316-7	Sequence 7, Appl	c1162	24.4	1.9	1064	7	US-11-242-111-6	Sequence 6, Appl
c1089	24.6	1.9	2700	7	US-11-217-529-79652	Sequence 79652, A	c1163	24.4	1.9	1080	7	US-11-217-529-81180	Sequence 81180, A
c1090	24.6	1.9	2775	6	US-11-217-529-79238	Sequence 79238, A	c1164	24.4	1.9	1095	1	US-09-949-925-23	Sequence 23, Appl
c1091	24.6	1.9	2781	6	US-10-370-959-12	Sequence 12, Appl	c1165	24.4	1.9	1155	7	US-11-217-529-82615	Sequence 82615, A
c1092	24.6	1.9	2788	6	US-10-505-928-378	Sequence 378, App	c1166	24.4	1.9	1212	6	US-10-473-173-97	Sequence 97, Appl
c1093	24.6	1.9	2876	6	US-10-505-928-468	Sequence 468, App	c1167	24.4	1.9	1260	7	US-11-302-678-45	Sequence 45, Appl
c1094	24.6	1.9	2916	7	US-11-217-529-76000	Sequence 76000, A	c1168	24.4	1.9	1379	6	US-10-511-937-506	Sequence 506, App
c1095	24.6	1.9	3115	6	US-10-505-928-645	Sequence 645, App	c1169	24.4	1.9	1467	7	US-11-217-529-5430	Sequence 5430, Ap
c1096	24.6	1.9	3174	6	US-10-511-937-626	Sequence 626, App	c1170	24.4	1.9	1505	7	US-11-217-529-166169	Sequence 166169, Ap
c1097	24.6	1.9	3174	6	US-11-217-529-427	Sequence 427, App	c1171	24.4	1.9	1539	7	US-11-217-529-79579	Sequence 79579, A
c1098	24.6	1.9	3301	6	US-10-370-959-10	Sequence 10, Appl	c1172	24.4	1.9	1539	7	US-11-217-529-75619	Sequence 75619, A
c1100	24.6	1.9	3362	6	US-10-511-937-2874	Sequence 2874, Ap	c1173	24.4	1.9	1632	7	US-11-217-529-80623	Sequence 80623, A
c1101	24.6	1.9	3411	6	US-10-504-120-2	Sequence 2, Appl	c1174	24.4	1.9	1674	7	US-11-217-529-5430	Sequence 5430, Ap
c1102	24.6	1.9	3637	6	US-10-370-959-1	Sequence 1, Appl	c1175	24.4	1.9	1674	7	US-11-217-529-5430	Sequence 5430, Ap
c1103	24.6	1.9	3637	6	US-10-370-959-1	Sequence 49, Appl	c1176	24.4	1.9	1917	7	US-11-217-529-2256	Sequence 2256, Ap
c1104	24.6	1.9	3780	6	US-10-511-937-2811	Sequence 2811, Ap	c1177	24.4	1.9	1973	6	US-10-505-928-462	Sequence 462, App
c1105	24.6	1.9	3813	6	US-11-217-529-81012	Sequence 81012, A	c1178	24.4	1.9	2013	7	US-11-217-529-77807	Sequence 77807, A
c1106	24.6	1.9	4181	6	US-10-505-928-480	Sequence 480, App	c1179	24.4	1.9	2081	6	US-10-505-928-764	Sequence 764, Appl
c1107	24.6	1.9	4260	7	US-11-217-529-2191	Sequence 2191, Ap	c1180	24.4	1.9	2103	7	US-11-252-080-1	Sequence 1, Appl
c1108	24.6	1.9	4407	6	US-10-505-928-506	Sequence 506, App	c1181	24.4	1.9	2147	6	US-10-505-928-820	Sequence 820, App
c1109	24.6	1.9	4465	6	US-10-505-928-528	Sequence 528, App	c1182	24.4	1.9	2230	6	US-10-511-937-354	Sequence 354, App
c1110	24.6	1.9	4465	6	US-10-511-937-460	Sequence 460, App	c1183	24.4	1.9	2265	7	US-11-217-529-75454	Sequence 75454, A
c1111	24.6	1.9	5449	6	US-10-505-928-800	Sequence 800, App	c1184	24.4	1.9	2295	7	US-11-217-529-77305	Sequence 77305, A
c1112	24.6	1.9	5637	7	US-11-217-529-1074	Sequence 1074, Ap	c1185	24.4	1.9	2304	7	US-11-251-465-1	Sequence 1, Appl
c1113	24.6	1.9	5940	7	US-11-217-529-82606	Sequence 82606, A	c1186	24.4	1.9	2304	7	US-11-217-529-76341	Sequence 76341, A
c1114	24.6	1.9	6629	6	US-10-946-650-49	Sequence 49, Appl	c1187	24.4	1.9	2461	6	US-10-514-738-34	Sequence 34, Appl
c1115	24.6	1.9	6837	7	US-11-217-529-4956	Sequence 4956, Ap	c1188	24.4	1.9	2484	7	US-11-145-307A-65	Sequence 65, Appl
c1116	24.6	1.9	11300	6	US-10-946-650-62	Sequence 62, Appl	c1189	24.4	1.9	2711	7	US-11-145-307A-189	Sequence 189, App
c1117	24.6	1.9	12225	6	US-10-501-834-1	Sequence 1, Appl	c1190	24.4	1.9	2772	7	US-11-302-678-43	Sequence 43, Appl
c1118	24.6	1.9	12290	6	US-10-946-650-59	Sequence 59, Appl	c1191	24.4	1.9	2841	7	US-11-217-529-1287	Sequence 1287, Ap
c1119	24.6	1.9	12509	6	US-10-946-650-63	Sequence 63, Appl	c1193	24.4	1.9	2846	7	US-11-101-316-37	Sequence 37, Appl
c1120	24.6	1.9	13383	6	US-10-946-650-61	Sequence 61, Appl	c1195	24.4	1.9	2889	7	US-11-217-529-111	Sequence 111, App
c1121	24.6	1.9	15739	6	US-10-541-993-3	Sequence 3, Appl	c1196	24.4	1.9	2943	7	US-11-242-505A-34	Sequence 34, Appl
c1122	24.6	1.9	16103	6	US-10-541-993-62	Sequence 62, Appl	c1197	24.4	1.9	2943	7	US-11-242-505A-35	Sequence 35, Appl
c1123	24.6	1.9	16245	6	US-10-541-993-36	Sequence 36, Appl	c1199	24.4	1.9	3021	7	US-11-181-115-9	Sequence 9, Appl
										3498	6	US-10-511-937-2854	Sequence 2854, Ap

c1200	24.4	1.9	3666	7	US-11-217-529-2206	Sequence 2206, Ap	1274	24.2	1.9	2530	7	US-11-066-633-1	Sequence 1, Appli
c1201	24.4	1.9	3909	7	US-11-217-529-174364	Sequence 174364, Ap	1275	24.2	1.9	2565	7	US-11-315-766-19	Sequence 19, Appl
1202	24.4	1.9	4235	7	US-11-301-554-317	Sequence 317, App	c1276	24.2	1.9	2572	7	US-11-312-958-15	Sequence 15, Appl
c1203	24.4	1.9	4560	7	US-11-170-482-11	Sequence 11, Appl	1277	24.2	1.9	2609	7	US-11-246-999-11	Sequence 11, Appl
1204	24.4	1.9	5132	6	US-10-505-928-663	Sequence 663, App	1278	24.2	1.9	2681	7	US-11-145-307A-194	Sequence 194, App
c1205	24.4	1.9	6105	7	US-11-217-529-1399	Sequence 1399, Ap	1279	24.2	1.9	2700	7	US-11-315-766-23	Sequence 23, Appl
c1206	24.4	1.9	6805	6	US-10-520-210-29	Sequence 29, Appl	1280	24.2	1.9	2749	1	US-09-949-925-29	Sequence 29, Appl
c1207	24.4	1.9	7032	6	US-10-505-928-832	Sequence 832, App	c1281	24.2	1.9	2776	6	US-10-511-937-2822	Sequence 2822, Ap
c1208	24.4	1.9	7330	6	US-10-520-210-31	Sequence 31, Appl	1282	24.2	1.9	2802	7	US-11-145-307A-197	Sequence 197, App
1209	24.4	1.9	7603	6	US-10-511-937-2852	Sequence 2852, Ap	1283	24.2	1.9	2846	6	US-10-505-928-444	Sequence 444, App
c1210	24.4	1.9	7603	6	US-10-511-937-2852	Sequence 2852, Ap	1284	24.2	1.9	2988	7	US-11-217-529-1106	Sequence 1106, Ap
c1211	24.4	1.9	13295	7	US-11-264-784-125	Sequence 125, App	c1285	24.2	1.9	2994	7	US-11-217-529-82666	Sequence 82666, A
c1212	24.4	1.9	15543	7	US-11-264-784-124	Sequence 124, App	c1286	24.2	1.9	3003	7	US-11-145-307A-38	Sequence 38, Appl
1213	24.2	1.9	347	6	US-10-488-619-878	Sequence 878, App	1287	24.2	1.9	3129	6	US-10-511-937-588	Sequence 588, App
c1214	24.2	1.9	390	7	US-11-217-529-2943	Sequence 2943, Ap	1288	24.2	1.9	3225	7	US-11-217-529-79745	Sequence 79745, A
c1215	24.2	1.9	423	7	US-11-217-529-3995	Sequence 3995, Ap	c1289	24.2	1.9	3270	7	US-11-217-529-2390	Sequence 2390, Ap
c1216	24.2	1.9	441	7	US-11-217-529-80586	Sequence 80586, A	c1290	24.2	1.9	3415	6	US-10-511-937-488	Sequence 488, App
c1217	24.2	1.9	482	6	US-10-488-619-2881	Sequence 2881, Ap	c1291	24.2	1.9	3675	7	US-11-217-529-79669	Sequence 79669, A
1218	24.2	1.9	509	6	US-10-488-619-1281	Sequence 1281, Ap	c1292	24.2	1.9	3935	7	US-11-254-173-9	Sequence 9, Appli
1219	24.2	1.9	519	7	US-11-301-554-78	Sequence 78, Appl	c1293	24.2	1.9	3935	7	US-11-264-784-100	Sequence 100, App
c1220	24.2	1.9	537	7	US-11-301-554-637	Sequence 637, App	c1294	24.2	1.9	3982	6	US-10-505-928-350	Sequence 350, App
c1221	24.2	1.9	573	7	US-11-217-529-173476	Sequence 173476, A	1295	24.2	1.9	4086	7	US-11-301-554-1801	Sequence 1801, Ap
1222	24.2	1.9	606	7	US-11-217-529-1748	Sequence 1748, Ap	c1296	24.2	1.9	4093	7	US-11-315-766-35	Sequence 35, Appl
c1223	24.2	1.9	606	7	US-11-217-529-82353	Sequence 82353, A	1297	24.2	1.9	4284	7	US-11-217-529-75774	Sequence 75774, A
1224	24.2	1.9	672	7	US-11-217-529-79872	Sequence 79872, A	1298	24.2	1.9	4624	7	US-11-223-945-44	Sequence 44, Appl
1225	24.2	1.9	690	6	US-10-488-619-2915	Sequence 2915, Ap	c1299	24.2	1.9	4712	6	US-10-505-928-164	Sequence 164, App
1226	24.2	1.9	729	7	US-11-217-529-6078	Sequence 6078, Ap	c1300	24.2	1.9	5262	7	US-11-217-529-786	Sequence 786, App
1227	24.2	1.9	777	7	US-11-217-529-5146	Sequence 5146, Ap	1301	24.2	1.9	5983	6	US-10-520-210-30	Sequence 30, Appl
c1228	24.2	1.9	876	6	US-10-473-173-48	Sequence 48, Appl	1302	24.2	1.9	6504	7	US-11-217-529-76393	Sequence 76393, A
1229	24.2	1.9	891	7	US-11-217-529-173957	Sequence 173957, A	1303	24.2	1.9	7017	6	US-10-505-928-452	Sequence 452, App
c1230	24.2	1.9	906	7	US-11-217-529-4183	Sequence 4183, Ap	c1304	24.2	1.9	8370	7	US-11-217-529-77	Sequence 77, Appl
1231	24.2	1.9	914	7	US-11-075-398-14	Sequence 14, Appl	c1305	24	1.9	191	6	US-10-861-934-50	Sequence 50, Appl
1232	24.2	1.9	945	7	US-11-217-529-82750	Sequence 82750, A	c1306	24	1.9	213	6	US-10-488-619-450	Sequence 450, App
c1233	24.2	1.9	966	7	US-11-254-173-21	Sequence 21, Appl	c1307	24	1.9	411	7	US-11-217-529-173579	Sequence 173579, A
c1234	24.2	1.9	966	7	US-11-264-784-103	Sequence 103, App	c1308	24	1.9	428	7	US-11-301-554-1244	Sequence 1244, Ap
1235	24.2	1.9	995	7	US-11-233-726-22	Sequence 22, Appl	1309	24	1.9	432	7	US-11-217-529-79720	Sequence 5, Appli
c1236	24.2	1.9	1000	7	US-11-233-726-4	Sequence 4, Appli	1310	24	1.9	449	7	US-11-252-080-5	Sequence 5, Appli
1237	24.2	1.9	1074	7	US-11-302-678-39	Sequence 39, Appl	c1311	24	1.9	534	7	US-11-301-554-1310	Sequence 1310, Ap
1238	24.2	1.9	1159	7	US-11-302-678-37	Sequence 37, Appl	c1312	24	1.9	544	6	US-10-473-173-263	Sequence 263, App
c1239	24.2	1.9	1215	7	US-11-217-529-191062	Sequence 191062, A	c1313	24	1.9	548	6	US-10-488-619-1694	Sequence 1694, Ap
1240	24.2	1.9	1254	7	US-11-217-529-406	Sequence 406, App	c1314	24	1.9	558	6	US-10-488-619-1612	Sequence 1616, App
c1241	24.2	1.9	1266	7	US-11-217-529-798	Sequence 798, App	c1315	24	1.9	580	6	US-10-488-619-1712	Sequence 1712, Ap
1242	24.2	1.9	1302	7	US-11-217-529-287	Sequence 287, App	c1316	24	1.9	584	6	US-10-511-937-371	Sequence 371, App
c1243	24.2	1.9	1326	7	US-11-217-529-280	Sequence 280, App	1317	24	1.9	595	6	US-10-488-619-2043	Sequence 2043, Ap
c1244	24.2	1.9	1333	7	US-11-217-529-2417	Sequence 2417, Ap	c1318	24	1.9	591	7	US-11-217-529-79822	Sequence 79822, A
1245	24.2	1.9	1389	7	US-11-217-529-78881	Sequence 78881, A	c1319	24	1.9	600	7	US-11-217-529-166176	Sequence 166176, A
1246	24.2	1.9	1392	7	US-11-217-529-2799	Sequence 2799, Ap	c1320	24	1.9	618	7	US-11-217-529-79699	Sequence 79699, A
c1247	24.2	1.9	1431	7	US-11-217-529-79572	Sequence 79572, A	c1321	24	1.9	680	6	US-10-488-619-2925	Sequence 2925, Ap
1248	24.2	1.9	1511	6	US-10-505-928-90	Sequence 90, Appl	1322	24	1.9	708	7	US-11-217-529-76663	Sequence 76663, A
c1249	24.2	1.9	1563	7	US-11-270-287-40	Sequence 40, Appl	c1323	24	1.9	738	7	US-11-217-529-81285	Sequence 81285, A
c1250	24.2	1.9	1563	7	US-11-270-287-41	Sequence 41, Appl	1325	24	1.9	765	6	US-10-488-619-2151	Sequence 2151, Ap
1251	24.2	1.9	1572	7	US-11-217-529-77950	Sequence 77950, A	c1326	24	1.9	777	7	US-11-217-529-173451	Sequence 173451, A
c1252	24.2	1.9	1635	7	US-11-217-529-2352	Sequence 2352, Ap	1327	24	1.9	812	6	US-10-510-162-1	Sequence 1, Appli
c1253	24.2	1.9	1641	7	US-11-217-529-76449	Sequence 76449, A	c1328	24	1.9	834	6	US-10-861-934-15	Sequence 15, Appl
1255	24.2	1.9	1677	7	US-11-217-529-79982	Sequence 79982, A	1329	24	1.9	834	7	US-11-217-529-79821	Sequence 79821, A
c1256	24.2	1.9	1698	7	US-11-217-529-79882	Sequence 79882, A	1330	24	1.9	849	7	US-11-217-529-81090	Sequence 81090, A
1257	24.2	1.9	1773	7	US-11-217-529-78093	Sequence 78093, A	c1331	24	1.9	883	6	US-10-488-619-2070	Sequence 2070, Ap
c1258	24.2	1.9	1778	7	US-11-251-465-16	Sequence 16, Appl	1332	24	1.9	906	7	US-11-217-529-78257	Sequence 78257, A
1259	24.2	1.9	1887	7	US-11-217-529-4927	Sequence 4927, Ap	c1333	24	1.9	925	6	US-10-861-934-46	Sequence 46, Appl
c1260	24.2	1.9	1956	7	US-11-217-529-2243	Sequence 2243, Ap	1334	24	1.9	1002	7	US-11-217-529-82611	Sequence 82611, A
1261	24.2	1.9	1977	7	US-11-217-529-2600	Sequence 2600, Ap	c1335	24	1.9	1003	7	US-11-217-529-3175	Sequence 56, Appl
c1262	24.2	1.9	2000	7	US-11-312-958-43	Sequence 43, Appl	c1336	24	1.9	1011	7	US-11-217-529-174322	Sequence 174322, A
1263	24.2	1.9	2004	7	US-11-217-529-3839	Sequence 3839, Ap	c1337	24	1.9	1036	7	US-11-217-529-98	Sequence 98, Appl
c1264	24.2	1.9	2022	7	US-11-217-529-77628	Sequence 77628, A	c1338	24	1.9	1032	7	US-11-217-529-79997	Sequence 79997, A
c1265	24.2	1.9	2094	6	US-10-473-173-34	Sequence 34, Appl	c1339	24	1.9	1035	7	US-11-217-529-166174	Sequence 166174, A
1266	24.2	1.9	2298	6	US-10-505-928-354	Sequence 354, App	1340	24	1.9	1059	7	US-11-217-529-3175	Sequence 3175, Ap
1267	24.2	1.9	2298	6	US-10-511-937-434	Sequence 434, App	1342	24	1.9	1161	6	US-10-014-320-1	Sequence 1, Appli
c1268	24.2	1.9	2304	6	US-10-505-928-196	Sequence 196, App	c1343	24	1.9	1212	7	US-11-217-529-174520	Sequence 174520, A
1269	24.2	1.9	2376	7	US-11-217-529-793	Sequence 793, App	1344	24	1.9	1236	7	US-11-217-529-81192	Sequence 81192, A
1270	24.2	1.9	2433	7	US-11-217-529-77906	Sequence 77906, A	c1345	24	1.9	1278	6	US-10-370-959-9	Sequence 9, Appl
1271	24.2	1.9	2448	7	US-11-217-529-1195	Sequence 1195, A	c1346	24	1.9	1281	7	US-11-217-529-78226	Sequence 78226, A
1272	24.2	1.9	2514	7	US-11-217-529-2574	Sequence 2574, Ap	c1347	24	1.9	1299	7	US-11-134-445-19	Sequence 19, Appl
1273	24.2	1.9	2529	7	US-11-217-529-77336	Sequence 77336, A	c1348	24	1.9	1309	7	US-11-134-445-29	Sequence 29, Appl

c1349	24	1.9	1334	6	US-10-370-959-7	Sequence 7, Appl1	1424	23.8	1.8	474	7	US-11-301-554-174	Sequence 174, App
1350	24	1.9	1362	7	US-11-217-529-75523	Sequence 75523, A	1425	23.8	1.8	493	7	US-11-301-554-750	Sequence 750, App
1351	24	1.9	1410	7	US-11-217-529-82049	Sequence 82049, A	1426	23.8	1.8	508	6	US-10-488-619-1321	Sequence 1321, Ap
c1352	24	1.9	1413	7	US-11-217-529-81039	Sequence 81039, A	1427	23.8	1.8	515	6	US-10-488-619-2367	Sequence 2367, Ap
1353	24	1.9	1500	7	US-11-217-529-79129	Sequence 79129, A	1428	23.8	1.8	517	6	US-10-509-131-17	Sequence 17, Appl
1354	24	1.9	1536	6	US-10-513-255-1	Sequence 1, Appl1	1429	23.8	1.8	522	6	US-10-488-619-1549	Sequence 1549, Ap
c1355	24	1.9	1623	6	US-10-861-934-25	Sequence 25, Appl	1430	23.8	1.8	528	7	US-11-301-554-64	Sequence 64, Appl
1356	24	1.9	1647	7	US-11-217-529-3824	Sequence 3824, Ap	c1431	23.8	1.8	537	7	US-11-217-529-82362	Sequence 82362, A
1357	24	1.9	1650	7	US-11-217-529-2286	Sequence 2286, Ap	1432	23.8	1.8	544	6	US-10-559-415-5	Sequence 5, Appl1
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(without alignments)
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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AL544740	AL544740	813	1	AL544740	48.1	622.8	25
CF127652	UI-HF-BT0	753	5	CF127652	47.6	616	26
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AK013914	Mus muscu	1167	6	AK013914	46.5	602.2	32
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BU730372	UI-E-C11-	727	3	BU730372	46.3	600.2	34
AK078128	Mus muscu	1195	6	AK078128	46.3	599	35
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DA293800	DA293800	814	4	DA293800	45.0	582.8	39
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EX920450	EX920450	715	4	EX920450	44.8	579.8	41
AK153636	Mus muscu	1290	6	AK153636	44.5	576.6	42
DB235140	DB235140	572	9	DB235140	44.2	572	43
CB994990	AGENCOURT	847	4	CB994990	44.1	570.6	44
DA190737	DA190737	602	9	DA190737	43.9	569	45
CG482835	CG482835	755	9	CG482835	43.8	567.4	46
DA224223	DA224223	629	2	DA224223	43.7	566.2	47
CG482835	CG482835	586	9	CG482835	43.6	565	48
CD109386	AGENCOURT	775	4	CD109386	43.5	563.4	49
DA860407	DA860407	564	9	DA860407	43.2	558.8	50
CK004092	AGENCOURT	623	5	CK004092	43.0	557.2	51
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DA805880	DA805880	557	9	DA805880	42.4	549	56
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DA864069	DA864069	603	9	DA864069	41.9	542.4	60
DA841803	DA841803	549	9	DA841803	41.7	540.4	61
DA802337	DA802337	553	9	DA802337	41.7	540.4	62
DB212449	DB212449	556	9	DB212449	41.4	536	63
CB125035	K-EST0173	602	4	CB125035	41.2	534	64
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DA840703	DA840703	559	9	DA840703	38.4	496.8	78
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CR747485	CR747485	494	8	CR747485	38.1	494	80
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AA725566	AA725566	566	9	AA725566	37.7	488.4	83
AA725566	AA725566	712	1	AA725566	36.8	477.4	84
DB279571	DB279571	516	9	DB279571	36.8	476.8	85
BX332036	BX332036	843	4	BX332036	36.7	476.4	86
DA797212	DA797212	563	9	DA797212	36.1	467.4	87
EX343701	EX343701	915	4	EX343701	36.0	466.4	88
CX218247	CX218247	839	8	CX218247	34.8	450.4	89
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101	426.2	32.9	923	4	BY12952	BY12952	BY12952	174	311	24.0	534	9	DA231316	DA231316	DA231316 DA231316
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104	421.8	32.6	522	4	BX353447	BX353447	BX353447	177	305.2	23.6	404	7	BF150380	BF150380	7199d03.x
105	420.2	32.4	512	1	AI421450	AI421450	t15b10.x	178	305.2	23.6	404	7	BF056970	BF056970	7k12h01.x
106	420.2	32.4	731	3	BQ210314	BQ210314	UI-R-DY1-	179	305.2	23.6	415	1	AI652914	AI652914	w4Q003.x
107	419.4	32.4	520	4	BY1392127	BY1392127	BY1392127	180	305	23.6	527	9	DB070238	DB070238	DB070238 DB070238
108	419.4	32.4	564	3	BM956133	BM956133	EST0522 H	181	298.4	23.0	628	12	CG589793	CG589793	OST4242455
109	418.8	32.3	592	1	AM018574	AM018574	AM018574	182	294.4	22.7	520	9	DA757224	DA757224	DA757224 DA757224
110	416.6	32.2	594	8	CO658359	CO658359	DG34-2f23	183	293	22.6	502	12	CG602718	CG602718	OST376379
111	414.4	32.0	800	3	BU748393	BU748393	CH3#019 G	184	291.4	22.5	582	3	BP229524	BP229524	BP229524 BP229524
112	414	32.0	593	1	AM017760	AM017760	AM017760	185	288.4	22.3	291	3	BM955592	BM955592	EST0521 H
113	410.2	31.7	556	9	CX593621	CX593621	CT020005B	186	287	22.2	349	8	CO761891	CO761891	brain_EST
114	408	31.5	549	9	DB276398	DB276398	DB276398	187	287	22.2	349	7	BF221504	BF221504	7k13h01.x
115	406.8	31.4	440	3	BQ375392	BQ375392	CM1-TN013	188	286.8	22.1	355	7	BF091146	BF091146	PM2-TN002
116	400.6	30.9	599	3	BP437892	BP437892	BP427892	189	286.8	22.1	741	4	BY710270	BY710270	BY710270 BY710270
117	399.4	30.8	534	9	CN394857	CN394857	L1B3934-0	190	285.6	22.1	526	1	AI853724	AI853724	MI-M-BHO-
118	398.8	30.8	876	1	AL553676	AL553676	AL553676	191	284.4	22.0	583	3	BP320097	BP320097	BP320097 BP320097
119	389.6	30.1	668	7	BB627619	BB627619	BB627619	192	281.2	21.7	510	3	BQ211610	BQ211610	UI-R-DY1-
120	389.2	30.1	679	8	CO715331	CO715331	DG14-249m	193	280.2	21.6	577	2	BM538432	BM538432	ha95e10.g
121	389.2	30.1	850	9	CK870550	CK870550	HESCA 46	194	278.2	21.5	671	7	BB642937	BB642937	BB642937 BB642937
122	386.4	29.8	444	2	BF845761	BF845761	CM0-EN004	195	278.2	21.5	741	4	BY710270	BY710270	BY710270
123	386	29.8	797	3	BU852962	BU852962	AGENCOURT	196	278.2	21.5	1094	6	AK010826	AK010826	Mus muscu
124	385.4	29.8	510	6	CR612856	CR612856	full-len9	197	278.2	21.5	1999	6	AK045095	AK045095	Mus muscu
125	385.2	29.7	485	1	AA912674	AA912674	O130B01.8	198	273.4	21.1	470	7	BF189965	BF189965	235761 MA
126	384.4	29.7	592	8	CV558990	CV558990	UI-M-HZ0-	199	270.2	21.1	470	8	AI154320	AI154320	u031d06.f
127	383.6	29.6	675	8	CO039152	CO039152	UI-M-AL1-	200	270.6	20.9	480	8	CR468808	CR468808	CR468808
128	382.6	29.5	428	7	AW022646	AW022646	dF41G07.Y	201	270.4	20.9	328	9	DN391113	DN391113	L1B3924-0
129	382.6	29.5	478	7	AW022835	AW022835	dF44G07.Y	202	269.8	20.8	403	1	AI3112805	AI3112805	QD74b05.x
130	382.4	29.5	800	5	CD172203	CD172203	AGENCOURT	203	269.2	20.8	674	7	BB046911	BB046911	BB046911
131	381	29.4	468	9	DB278689	DB278689	DB278689	204	266	20.5	738	3	BQ207505	BQ207505	UI-R-DY1-
132	380.2	29.4	489	2	BI491748	BI491748	dF14G03.w	205	265.4	20.5	534	9	DA810910	DA810910	DA810910
133	379	29.3	386	7	AW020783	AW020783	dF14G03.Y	206	265.2	20.5	534	9	DA125245	DA125245	DA125245
134	379	29.3	430	2	BF846982	BF846982	CM0-EN004	207	265.2	20.5	534	11	AO441827	AO441827	HS 5106 B
135	378.6	29.2	665	7	BB627936	BB627936	BB627936	208	264.2	20.4	308	7	AW593293	AW593293	hg12e12.x
136	377.8	29.2	644	7	BB622205	BB622205	BB622205	209	264.2	20.4	466	12	CG607524	CG607524	OST286494
137	376	29.0	614	7	BB613061	BB613061	BB613061	210	262.8	20.3	858	3	BU470108	BU470108	60335843
138	375	29.0	838	5	CK599264	CK599264	AGENCOURT	211	261.6	20.2	507	1	AJ507041	AJ507041	AJ507041
139	372.8	28.8	537	9	DB071270	DB071270	DB071270	212	260	20.1	565	9	DA233331	DA233331	DA233331
140	370.2	28.6	481	1	AI952846	AI952846	wG48h04.x	213	259.8	20.1	427	2	BF709908	BF709908	MI-P-AY1-
141	370	28.6	716	10	DR769501	DR769501	ILLUMIGEN	214	259	20.0	556	9	DB065689	DB065689	DB065689
142	368	28.4	825	4	CB573834	CB573834	AGENCOURT	215	258.4	20.0	555	9	DB133113	DB133113	DB133113
143	361	27.9	692	2	BG720249	BG720249	602692309	216	257	19.8	828	2	BI157375	BI157375	602923864
144	357.6	27.6	394	7	AW393829	AW393829	QV0-TT000	217	253.6	19.6	535	9	DA220037	DA220037	DA220037
145	357.6	27.6	599	10	DV873456	DV873456	LB02521.C	218	252.2	19.5	356	1	AI017553	AI017553	ou35d03.x
146	356.8	27.6	765	4	BX453733	BX453733	BX453733	219	252	19.5	508	9	DB263521	DB263521	DB263521
147	355.2	27.4	457	1	AI123727	AI123727	ou21s07.x	220	245.2	18.9	596	3	BP770982	BP770982	BP770982
148	354.2	27.4	405	7	AW393887	AW393887	QV0-TT000	221	243.4	18.8	602	9	DA127769	DA127769	DA127769
149	354	27.3	600	4	CA528989	CA528989	8092-83 M	222	242.6	18.7	843	3	BU750528	BU750528	CH3#034_A
150	352	27.2	579	4	CA873574	CA873574	K0926B10-	223	242.2	18.7	343	7	AW474261	AW474261	xg99f07.x
151	350.2	27.0	411	9	DN345547	DN345547	L1B3551-0	224	242.2	18.7	345	7	AW474261	AW474261	xg23c07.x
152	349.6	27.0	666	2	BI817130	BI817130	UNW16C09	225	242.2	18.7	346	1	AI366088	AI366088	ao87b09.x
153	349.2	27.0	449	7	BE218057	BE218057	hv34g11.x	226	242	18.7	557	8	CO592416	CO592416	DG2-62C19
154	347.6	26.8	916	5	CF407265	CF407265	CH3#047.D	227	241.2	18.6	832	9	CX884829	CX884829	JGT_CAL2
155	345.2	26.7	460	9	DA857077	DA857077	DA857077	228	236.6	18.3	546	12	CG645278	CG645278	OST389673
156	344.2	26.6	493	1	AI199779	AI199779	q160h03.x	229	236.2	18.2	532	9	DB336126	DB336126	DB336126 DB336126
157	342.6	26.5	972	3	BM804795	BM804795	AGENCOURT	230	235.4	18.2	311	4	CB137090	CB137090	K-EST0189
158	342.4	26.4	707	4	CB521570	CB521570	UI-M-GHO-	231	235	18.1	618	12	CG588364	CG588364	OST239173
159	338.2	26.1	794	4	CB318894	CB318894	AGENCOURT	232	234	18.1	343	12	CG496542	CG496542	OST36638
160	336	25.9	575	9	DN434658	DN434658	L1B4217-1	233	233.2	18.0	519	1	AI418268	AI418268	tg31b05.x
161	330.8	25.5	953	3	BU503587	BU503587	AGENCOURT	234	232.6	18.0	380	12	CG535813	CG535813	OST123088
162	328	25.3	700	1	AJ942995	AJ942995	AJ942995	235	231	17.8	377	12	CG498385	CG498385	OST99661
163	327	25.3	364	2	BF848293	BF848293	CM0-EN004	236	230.4	17.8	355	1	AI052637	AI052637	os18a04.x
164	326	25.2	639	9	DA139294	DA139294	DA139294	237	230.4	17.8	424	12	CG500225	CG500225	OST42979
165	325.8	25.2	609	2	BI732178	BI732178	603352794	238	229.8	17.7	422	12	CG497261	CG497261	OST37749

239	229.8	17.7	449	12	CG512231	CG512231	OST65057	312	207	16.0	813	10	DR761522	DR761522	HESC4_129
240	229.8	17.7	503	12	CG492599	OST30532		c 313	207	16.0	908	4	BX411321	BX411321	BX411321
241	229.2	17.7	330	12	CG495419	OST34804		314	207	16.0	916	8	CK164329	CK164329	CK164329
242	229	17.7	541	12	CG570152	OST198791		315	206.8	16.0	504	11	BH001309	BH001309	BH001309
243	229	17.7	555	9	DR281775	DR281775		316	206.6	16.0	310	3	BU537772	AGENCOURT	BU537772
244	228.8	17.7	408	12	CG605104	OST281411		c 317	206.4	15.9	735	4	BX389850	BX389850	BX389850
245	226.2	17.5	802	9	CK888495	JGI_CRAM2		318	206.2	15.9	340	4	BX645111	DRF2p781M	BX645111
246	226.4	17.6	502	4	BY477702	BY477702		319	206.2	15.9	636	8	CK333099	170004551	CK333099
c 247	226.4	17.5	732	9	DR107648	JHU144B05		c 320	206	15.9	986	2	BG169377	602320936	BG169377
248	225.8	17.4	435	12	CG506984	OST56760		c 321	205.8	15.9	470	7	AW327624	dq01e02.y	AW327624
249	225.8	17.4	445	12	CG551037	OST157738		c 322	205.8	15.9	782	7	AV755677	AV755677	AV755677
250	225.8	17.4	482	12	CG539560	OST130739		323	205.8	15.9	807	3	BU935557	AGENCOURT	BU935557
251	225.6	17.4	339	12	CG514649	OST68527		324	205.8	15.9	969	4	BX420927	BX420927	BX420927
252	225.2	17.4	445	12	CG568316	OST195236		c 325	205.6	15.9	340	2	BG943853	ax42h02.x	BG943853
253	225.2	17.4	513	12	CG625693	OST332417		c 326	205.6	15.9	411	12	CG598103	OST262197	CG598103
254	224.8	17.4	454	12	CG523774	OST96556		327	205.6	15.9	435	4	CB114258	K-EST0157	CB114258
255	224.2	17.3	437	12	CG541713	OST135238		328	205.6	15.9	492	7	AV758790	AV758790	AV758790
256	223	17.2	469	12	CG517537	OST78071		329	205.6	15.9	551	9	DB269889	DB269889	DB269889
c 257	219.8	17.0	492	8	CO594463	CG2-96d21		330	205.6	15.9	604	7	AV763388	AV763388	AV763388
c 258	218.8	16.9	545	7	AW082343	AW082343	xb65g01.x	331	205.6	15.9	654	8	CK333100	170004245	CK333100
259	217.6	16.8	403	12	CG572210	OST202508		c 332	205.6	15.9	1820	6	HSMB08590	Homo sapi	BX648442
c 260	217.6	16.8	509	11	AO810242	HS_5023_B		c 333	205.4	15.9	316	1	AI783911	tr30c12.x	AI783911
261	217.4	16.8	347	12	CG514469	OST68282		c 334	205.4	15.9	412	12	CG585601	OST233132	CG585601
262	217.4	16.8	957	2	B4335143	602507157		335	205.4	15.9	602	5	CK430039	oj44c10.y	CK430039
263	216	16.7	428	12	CG658984	OST436033		336	205.4	15.9	638	5	CK232048	ILLUMIGEN	CK232048
264	215.8	16.7	422	12	CG504458	OST25558		337	205.2	15.8	403	1	AV710482	AV710482	AV710482
265	215.6	16.6	339	12	CG598159	OST262313		c 338	205.2	15.8	714	13	CZ459896	CZ459896	CZ459896
266	215.4	16.6	445	12	CG616790	OST309395		c 339	205	15.8	496	9	CK783302	CK783302	CK783302
267	215.2	16.6	457	12	CG655131			340	205	15.8	681	14	AG091568	AG091568	AG091568
268	215.2	16.6	468	12	CG635842	OST425078		341	204.8	15.8	451	12	CG950844	CG950844	CG950844
269	215.2	16.6	786	4	BX283014	BX283014		c 342	204.8	15.8	587	11	B48415	B48415	B48415
270	215.2	16.6	786	8	CR738526	CR738526		c 343	204.8	15.8	976	2	B1463787	B1463787	B1463787
271	214.8	16.6	399	4	BY514942	BY514942		c 344	204.6	15.8	393	4	CA436084	CA436084	CA436084
272	214.6	16.6	533	12	CG662003	OST444083		c 345	204.6	15.8	402	2	BF767878	BF767878	BF767878
273	214.2	16.5	408	12	CG648347	OST401540		c 346	204.6	15.8	564	9	DA955389	DA955389	DA955389
274	214.2	16.5	495	12	CG640726	OST374100		347	204.6	15.8	582	11	B89843	B89843	B89843
275	214	16.5	489	12	CG625930	OST333211		c 348	204.6	15.8	660	14	AG178223	AG178223	AG178223
276	214	16.5	772	9	DN392017	LI83934-0		c 349	204.6	15.8	698	14	AG178127	AG178127	AG178127
277	212.4	16.4	839	14	DU979221	fy01_fp00		c 350	204.6	15.8	2175	6	BC051878	BC051878	BC051878
c 278	212.4	16.4	932	3	BQ716029	AGENCOURT		c 351	204.4	15.8	352	2	BG942327	BG942327	BG942327
279	212.2	16.4	922	12	CG496904	OST73225		352	204.4	15.8	558	4	BX494334	BX494334	BX494334
280	212	16.4	423	7	AV763538	AV763538		353	204.2	15.8	531	9	DB198439	DB198439	DB198439
281	211.6	16.3	332	12	CG661287	CG661287	OST442208	c 354	204.2	15.8	623	11	AQ634211	AQ634211	AQ634211
282	211.6	16.3	1018	3	BQ049850	AGENCOURT		c 355	204	15.8	446	11	AQ005107	AQ005107	AQ005107
283	211.4	16.3	364	12	CG659115	OST436465		c 356	204	15.8	495	9	DB124037	DB124037	DB124037
c 284	211.4	16.3	492	1	AL753488	cr11d02.x		c 357	203.8	15.7	519	9	DA083484	DA083484	DA083484
c 285	211.4	16.3	701	3	BU685646	UI-CF-DUI		c 358	203.8	15.7	558	9	DB144261	DB144261	DB144261
286	211	16.3	454	12	CG507182	OST57042		c 359	203.6	15.7	571	9	DA108811	DA108811	DA108811
287	210.8	16.3	348	10	DM467041	HHAGB0083		c 360	203.6	15.7	452	4	C06046	C06046	C06046
288	210.8	16.3	757	2	BG540416	BG540416	602568728	361	203.6	15.7	840	13	CZ460116	CZ460116	CZ460116
c 289	210.8	16.3	773	6	BC034441	Homo sapi		c 362	203.6	15.7	3971	6	HSMB03975	HSMB03975	HSMB03975
c 290	210.4	16.2	765	4	BX110390	BX110390		c 363	203.4	15.7	318	3	BU536666	BU536666	BU536666
291	210.2	16.2	561	9	DA856475	DA856475		c 364	203.4	15.7	645	8	CR752070	CR752070	CR752070
c 292	210	16.2	2478	6	BC037540	Homo sapi		365	203.4	15.7	747	2	B1601304	B1601304	B1601304
293	209.8	16.2	314	3	BU927594	BU927594	AGENCOURT	c 366	203.2	15.7	226	7	AW000593	AW000593	AW000593
c 294	209.8	16.2	522	9	DB310869	DB310869		c 367	203.2	15.7	552	3	BQ614372	BQ614372	BQ614372
c 295	209.4	16.2	775	12	BZ773942	RCV82g06.		c 368	203.2	15.7	642	7	AV759557	AV759557	AV759557
296	209.2	16.2	347	10	DM467225	HHAGB0084		369	203.2	15.7	782	3	BU930243	BU930243	BU930243
297	209.2	16.2	496	12	CG43181	OST381341		370	203.2	15.7	1375	14	DU9799908	DU9799908	DU9799908
c 298	209	16.1	356	12	CG599907	CG599907	OST267964	c 371	203	15.7	387	4	BX485020	BX485020	BX485020
c 299	208.8	16.1	498	8	CO591452	CO591452	DG2-49n6	c 372	203	15.7	643	14	AG169898	AG169898	AG169898
300	208.4	16.1	537	8	CR544001	CR544001		c 373	203	15.7	851	3	CR788530	CR788530	CR788530
c 301	208.4	16.1	838	3	BU570963	AGENCOURT		374	202.8	15.7	751	3	BQ772858	BQ772858	BQ772858
302	208.2	16.1	799	7	AV755512	AV755512		c 375	202.6	15.6	381	1	AI556456	AI556456	AI556456
c 303	207.8	16.0	1598	6	CR611538	full-length		c 376	202.6	15.6	566	9	DA062327	DA062327	DA062327
304	207.6	16.0	470	7	BE653351	UI-M-AL1-		c 377	202.4	15.6	530	9	DA961685	DA961685	DA961685
305	207.6	16.0	600	7	BF678990	602153630		c 378	202.4	15.6	673	9	DA219710	DA219710	DA219710
306	207.4	16.0	423	12	CG595339	OST254712		c 379	202.4	15.6	639	4	BX510123	BX510123	BX510123
c 307	207.4	16.0	592	9	DB230732	DB230732		380	202.4	15.6	672	14	AG142612	AG142612	AG142612
308	207.2	16.0	330	12	CG571674	OST201560		381	202.4	15.6	678	11	AV703259	AV703259	AV703259
309	207.2	16.0	662	14	AG180496	Pan trogl		c 382	202.4	15.6	720	11	AQ0588993	AQ0588993	AQ0588993
310	207	16.0	317	3	BU602934	AGENCOURT		c 383	202.4	15.6	742	4	BX389851	BX389851	BX389851
311	207	16.0	534	12	CG654462	OST422612		384	202.4	15.6	957	4	BX350104	BX350104	BX350104

C 385	202.4	15.6	2731	6	BC013209	RC013209 Homo sapi	C 458	200	15.4	545	9	DB114773	DB114773
C 386	202.2	15.6	497	1	AI620585	AI620585 tU95907.x	C 459	200	15.4	557	9	DA266894	DA266894
C 387	202.2	15.6	568	9	DB344764	DB344764 DB344764	C 460	200	15.4	572	9	DA493555	DA493555
C 388	202.2	15.6	597	11	AQ035555	AQ035555 CIT-HSP-2	C 461	200	15.4	577	9	DA332183	DA332183
C 389	202.2	15.6	665	12	BZ598162	BZ598162 WHAAD32TF	C 462	200	15.4	586	9	DA155616	DA155616
C 390	202.2	15.6	722	13	CZ455870	CZ455870 MCF73811F	C 463	200	15.4	589	9	DA043357	DA043357
C 391	202.2	15.6	2165	6	CR858633	CR858633 Pongo pyg	C 464	200	15.4	607	7	AV761714	AV761714
C 392	202	15.6	586	3	BU737474	BU737474 UI-E-DWI-	C 465	200	15.4	658	5	CD721834	CD721834
C 393	202	15.6	885	13	CZ453204	CZ453204 MCF734n15	C 466	200	15.4	669	14	AG155696	AG155696
C 394	201.8	15.6	564	9	DB325927	DB325927 DB325927	C 467	200	15.4	693	14	AG145808	AG145808
C 395	201.8	15.6	584	1	AV721886	AV721886 AV721886	C 468	199.8	15.4	318	13	BU858322	BU858322
C 396	201.8	15.6	592	3	DB155232	DB155232 UI-H-FLO-	C 469	199.8	15.4	366	7	AV762982	AV762982
C 397	201.8	15.6	682	3	BU630852	BU630852 DB1-H-FLO-	C 470	199.8	15.4	537	11	AZ254548	AZ254548
C 398	201.8	15.6	715	7	BE393367	BE393367 601311041	C 471	199.8	15.4	539	11	AQ544113	AQ544113
C 399	201.8	15.6	750	5	CF453960	CF453960 AGENCOURT	C 472	199.8	15.4	541	8	CN277524	CN277524
C 400	201.6	15.6	590	7	AW979096	AW979096 EST391206	C 473	199.8	15.4	660	3	BU928994	BU928994
C 401	201.6	15.6	704	1	AL1596482	AL1596482 DKF2P761A	C 474	199.8	15.4	695	8	CN277620	CN277620
C 402	201.6	15.6	4470	6	HSM801519	AL136545 Homo sapi	C 475	199.8	15.4	698	12	BZ599606	BZ599606
C 403	201.4	15.6	682	14	AG097896	AG097896 Pan trogl	C 476	199.8	15.4	737	2	BI601300	BI601300
C 404	201.4	15.6	1029	12	BZ610725	BZ610725 WHACK01TF	C 477	199.8	15.4	753	14	AG029376	AG029376
C 405	201.2	15.5	581	9	DA661479	DA661479 DA661479	C 478	199.6	15.4	423	12	CS535702	CS535702
C 406	201.2	15.5	635	4	BX504265	BX504265 DKF2P686E	C 479	199.6	15.4	519	8	CN333096	CN333096
C 407	201.2	15.5	734	2	BG617387	BG617387 602615225	C 480	199.6	15.4	622	7	AV761862	AV761862
C 408	201	15.5	392	11	AQ150925	AQ150925 HS 3109 A	C 481	199.6	15.4	631	4	BA496321	BA496321
C 409	201	15.5	504	11	AQ884300	AQ884300 HS-5504 B	C 482	199.6	15.4	653	11	B70304	B70304
C 410	201	15.5	514	8	CN414996	CN414996 328801351	C 483	199.6	15.4	772	5	CJ434109	CJ434109
C 411	201	15.5	566	11	DA6714827	AQ274827 RPCI-1-21	C 484	199.6	15.4	801	4	CJ229884	CJ229884
C 412	201	15.5	596	11	B95532	B95532 CIT-HSP-216	C 485	199.6	15.4	825	4	BX335093	BX335093
C 413	201	15.5	602	11	AQ16912	AQ16912 RPCI11-96	C 486	199.6	15.4	865	11	AQ739513	AQ739513
C 414	201	15.5	738	4	CA428400	CA428400 UI-H-DFO-	C 487	199.6	15.4	899	1	AU122470	AU122470
C 415	200.8	15.5	396	11	AQ131277	AQ131277 HS 3039 A	C 488	199.6	15.4	4033	6	CR859526	CR859526
C 416	200.8	15.5	429	7	AW576211	AW576211 UI-HF-BNG	C 489	199.4	15.4	391	1	AI358089	AI358089
C 417	200.8	15.5	526	8	CR556387	CR556387 DKF2P459P	C 490	199.4	15.4	469	4	CB217725	CB217725
C 418	200.8	15.5	560	9	DB320019	DB320019 DB320019	C 491	199.4	15.4	526	9	DA289448	DA289448
C 419	200.8	15.5	562	5	CD690288	CD690288 EST6811 h	C 492	199.4	15.4	569	9	DA158644	DA158644
C 420	200.8	15.5	698	14	AG168225	AG168225 Pan trogl	C 493	199.4	15.4	792	5	CD655541	CD655541
C 421	200.8	15.5	709	11	AQ740331	AQ740331 HS 5501 A	C 494	199.4	15.4	792	5	CJ459318	CJ459318
C 422	200.6	15.5	460	1	AA130647	AA130647 zol0505.5	C 495	199.4	15.4	820	5	CD653272	CD653272
C 423	200.6	15.5	620	1	AL042635	AL042635 DKF2P434M	C 496	199.4	15.4	3005	6	BC111052	BC111052
C 424	200.6	15.5	710	5	CD326863	CD326863 FNPAD612	C 497	199.2	15.4	534	9	DA222852	DA222852
C 425	200.6	15.5	711	11	AQ415030	AQ415030 RPCI-11-2	C 498	199.2	15.4	547	9	DA696294	DA696294
C 426	200.6	15.5	818	11	AQ749952	AQ749952 HS 5576 A	C 499	199.2	15.4	575	13	CZ459988	CZ459988
C 427	200.4	15.5	347	10	DM467237	DM467237 HJAGE00B5	C 500	199.2	15.4	622	3	BQ020620	BQ020620
C 428	200.4	15.5	429	11	AQ090219	AQ090219 HS 3009 A	C 501	199.2	15.4	632	4	BX953656	BX953656
C 429	200.4	15.5	460	3	BQ025751	BQ025751 UI-1-BBIP	C 502	199.2	15.4	640	7	BF325535	BF325535
C 430	200.4	15.5	465	11	AQ475002	AQ475002 CITBI-EI-	C 503	199.2	15.4	664	7	BE395137	BE395137
C 431	200.4	15.5	485	9	DA790852	DA790852 DA790852	C 504	199.2	15.4	754	9	CX870603	CX870603
C 432	200.4	15.5	492	9	DA185032	DA185032 DA185032	C 505	199.2	15.4	802	13	CZ448306	CZ448306
C 433	200.4	15.5	492	9	DA792268	DA792268 DA792268	C 506	199.2	15.4	1010	2	BM465334	BM465334
C 434	200.4	15.5	504	11	AQ546477	AQ546477 CITBI-EI-	C 507	199	15.4	313	8	CR753238	CR753238
C 435	200.4	15.5	540	11	AQ483367	AQ483367 RPCI-11-2	C 508	199	15.4	359	1	AI357823	AI357823
C 436	200.4	15.5	555	9	DA330733	DA330733 DA330733	C 509	199	15.4	470	14	AG190706	AG190706
C 437	200.4	15.5	557	9	DA184086	DA184086 DA184086	C 510	199	15.4	498	11	AQ540219	AQ540219
C 438	200.4	15.5	558	9	DA314731	DA314731 DA314731	C 511	199	15.4	564	9	DA281927	DA281927
C 439	200.4	15.5	566	9	DB184937	DB184937 DB184937	C 512	199	15.4	568	9	DA028891	DA028891
C 440	200.4	15.5	571	3	BP239973	BP239973 BP239973	C 513	199	15.4	569	9	DA712607	DA712607
C 441	200.4	15.5	577	9	DA295876	DA295876 DA295876	C 514	199	15.4	572	13	CZ455724	CZ455724
C 442	200.4	15.5	670	14	AG135650	AG135650 Pan trogl	C 515	199	15.4	588	7	AV763417	AV763417
C 443	200.4	15.5	773	2	BI918051	BI918051 603181928	C 516	199	15.4	617	11	AQ545585	AQ545585
C 444	200.4	15.5	817	3	BU853545	BU853545 AGENCOURT	C 517	199	15.4	654	4	BA483784	BA483784
C 445	200.4	15.5	885	3	BQ955197	BQ955197 AGENCOURT	C 518	199	15.4	657	11	AQ624700	AQ624700
C 446	200.2	15.5	412	1	AA454177	AA454177 zx46H07.8	C 519	199	15.4	669	9	DR157225	DR157225
C 447	200.2	15.5	504	11	BE674881	BE674881 7696f11.x	C 520	199	15.4	715	13	CZ451172	CZ451172
C 448	200.2	15.5	521	7	BA4788	BA4788 HS-1060-AI-	C 521	199	15.4	731	8	CN307840	CN307840
C 449	200.2	15.5	534	11	AQ282060	AQ282060 RPCI11-81	C 522	199	15.4	735	5	CF146929	CF146929
C 450	200.2	15.5	615	4	CA437649	CA437649 UI-H-DHO-	C 523	199	15.4	940	13	CZ452766	CZ452766
C 451	200.2	15.5	624	14	AG098912	AG098912 Pan trogl	C 524	198.8	15.4	389	4	BY508025	BY508025
C 452	200.2	15.5	627	4	CA441204	CA441204 UI-H-DFO-	C 525	198.8	15.4	444	11	AQ112326	AQ112326
C 453	200.2	15.5	695	11	AQ387117	AQ387117 RPCI11-15	C 526	198.8	15.4	445	4	CA867048	CA867048
C 454	200.2	15.5	848	14	CR361389	CR361389 Homo sapi	C 527	198.8	15.4	527	9	DA954579	DA954579
C 455	200.2	15.5	1002	3	BQ938400	BQ938400 AGENCOURT	C 528	198.8	15.4	552	9	DA017321	DA017321
C 456	200.2	15.5	1753	6	HSM801060	AL117536 Homo sapi	C 529	198.8	15.4	565	9	DB091799	DB091799
C 457	200	15.4	417	1	AA829065	AA829065 od82c10.8	C 530	198.8	15.4	566	9	DA225478	DA225478

531	198.8	15.4	569	9	DA777850	DA777850	531	197.8	15.3	813	11	AY758725	AY758725 RP43-128n
532	198.8	15.4	575	9	DA233703	DA233703	532	197.8	15.3	831	13	CZ451040	CZ451040 MCF731p16
533	198.8	15.4	602	9	DA109423	DA109423	533	197.8	15.3	933		BO959144	BO959144 AGENCOURT
534	198.8	15.4	638	11	AQ348792	AQ348792	534	197.8	15.3	979	7	BM469390	BM469390 AGENCOURT
535	198.8	15.4	641	11	B64250	B64250	535	197.8	15.3	979	7	AV758903	AV758903 AV758903
536	198.8	15.4	648	3	BM991131	BM991131	536	197.6	15.3	608	9	DA798480	DA798480 DA798480
537	198.8	15.4	673	1	AL696209	AL696209	537	197.6	15.3	504	9	DA798480	DA798480 DA798480
538	198.8	15.4	706	11	B72182	B72182	538	197.6	15.3	508	2	BG944867	BG944867 ax56h08.x
539	198.8	15.4	709	3	BO181930	BO181930	539	197.6	15.3	517	1	AL046409	AL046409 DKF2p434N
540	198.8	15.4	793	3	BU616465	BU616465	540	197.6	15.3	518	2	BG577022	BG577022 602599429
541	198.8	15.4	793	3	BU616465	BU616465	541	197.6	15.3	548	3	BU602613	BU602613 AGENCOURT
542	198.8	15.4	873	3	BQ708185	BQ708185	542	197.6	15.3	549	4	BX493137	BX493137 DKF2p781E
543	198.8	15.4	1181	7	AV763078	AV763078	543	197.6	15.3	552	9	DA369810	DA369810 DA369810
544	198.6	15.3	4741	6	CR933670	CR933670	544	197.6	15.3	566	9	DA108357	DA108357 DA108357
545	198.6	15.3	363	7	AV762979	AV762979	545	197.6	15.3	582	3	BP292705	BP292705 BP292705
546	198.6	15.3	434	2	BF991208	BF991208	546	197.6	15.3	594	9	DA192037	DA192037 DA192037
547	198.6	15.3	441	5	CD693386	CD693386	547	197.6	15.3	594	9	DA192037	DA192037 DA192037
548	198.6	15.3	510	1	AL046746	AL046746	548	197.6	15.3	614	11	AQ055703	AQ055703 CIT-HSP-2
549	198.6	15.3	527	7	AW504686	AW504686	549	197.6	15.3	622	11	AQ055543	AQ055543 RPCI-11-4
550	198.6	15.3	555	9	DA262530	DA262530	550	197.6	15.3	662	14	AG019520	AG019520 Homo sapi
551	198.6	15.3	567	9	DA357821	DA357821	551	197.6	15.3	671	4	BX504272	BX504272 DKF2p686F
552	198.6	15.3	588	9	DA100593	DA100593	552	197.6	15.3	679	8	CN304238	CN304238 170004247
553	198.6	15.3	591	9	DB154223	DB154223	553	197.6	15.3	689	14	AG141493	AG141493 Pan trogl
554	198.6	15.3	610	9	DA529548	DA529548	554	197.6	15.3	708	11	AQ0530231	AQ0530231 RPCI-11-3
555	198.6	15.3	620	4	CA441227	CA441227	555	197.6	15.3	734	3	BU853264	BU853264 AGENCOURT
556	198.6	15.3	791	4	CD104542	CD104542	556	197.6	15.3	1028	3	BM564754	BM564754 AGENCOURT
557	198.6	15.3	868	3	BU933126	BU933126	557	197.6	15.3	1387	3	BO923793	BO923793 AGENCOURT
558	198.4	15.3	1900	6	HSMB03785	HSMB03785	558	197.6	15.3	1775	6	CR613749	CR613749 full1-leng
559	198.4	15.3	409	8	CN411699	CN411699	559	197.4	15.2	5282	6	HSMB01753	HSMB01753 Homo sapi
560	198.4	15.3	473	9	DB016498	DB016498	560	197.4	15.2	316	4	BX479256	BX479256 DKF2p686M
561	198.4	15.3	488	11	AQ042204	AQ042204	561	197.4	15.2	396	4	BX478578	BX478578 DKF2p686C
562	198.4	15.3	560	11	AQ046373	AQ046373	562	197.4	15.2	435	9	DA224227	DA224227 DA224227
563	198.4	15.3	573	9	DB046273	DB046273	563	197.4	15.2	520	11	AQ441751	AQ441751 HS 5067 B
564	198.4	15.3	594	4	BX504370	BX504370	564	197.4	15.2	529	11	AQ420175	AQ420175 RPCI-11-1
565	198.4	15.3	637	4	CA428427	CA428427	565	197.4	15.2	549	9	DA399272	DA399272 DA399272
566	198.2	15.3	359	1	AA904275	AA904275	566	197.4	15.2	558	1	AA402129	AA402129 zu55a08.r
567	198.2	15.3	376	1	A1849051	A1849051	567	197.4	15.2	571	1	AL700533	AL700533 DKF2p686F
568	198.2	15.3	384	11	B91064	B91064	568	197.4	15.2	572	9	DN601915	DN601915 HESG3 73
569	198.2	15.3	465	2	B1324823	B1324823	569	197.4	15.2	585	2	BF941382	BF941382 7d98b09.x
570	198.2	15.3	492	11	AQ020554	AQ020554	570	197.4	15.2	709	14	AG185983	AG185983 Pan trogl
571	198.2	15.3	521	4	CB128427	CB128427	571	197.4	15.2	716	11	AQ375786	AQ375786 RPCI11-14
572	198.2	15.3	544	2	BG739841	BG739841	572	197.4	15.2	732	5	CD357649	CD357649 AGENCOURT
573	198.2	15.3	664	11	AQ343449	AQ343449	573	197.4	15.2	736	2	BG548055	BG548055 602575976
574	198.2	15.3	675	4	BX954661	BX954661	574	197.4	15.2	796	11	AQ750744	AQ750744 HS 5576 B
575	198.2	15.3	691	11	AQ346310	AQ346310	575	197.4	15.2	4697	6	CR859207	CR859207 Pongo pyg
576	198.2	15.3	916	2	BG429122	BG429122	576	197.2	15.2	4697	6	CR859207	CR859207 Pongo pyg
577	198.2	15.3	1863	6	CR599842	CR599842	577	197.2	15.2	6046	6	HSMB08580	HSMB08580 Homo sapi
578	198.2	15.3	453	2	BF725844	BF725844	578	197.2	15.2	420	4	BX482443	BX482443 DKF2p686N
579	198.2	15.3	461	9	DA880294	DA880294	579	197.2	15.2	456	11	AQ474984	AQ474984 CITBI-E1-
580	198.2	15.3	468	1	A1696793	A1696793	580	197.2	15.2	501	9	DA125262	DA125262 DA125262
581	198.2	15.3	500	4	CA771717	CA771717	581	197.2	15.2	526	4	BX493956	BX493956 DKF2p781E
582	198.2	15.3	511	9	DA194480	DA194480	582	197.2	15.2	534	7	AW500029	AW500029 UI-HF-BNO
583	198.2	15.3	574	9	DA250747	DA250747	583	197.2	15.2	591	9	DA303160	DA303160 DA303160
584	198.2	15.3	581	7	BF677892	BF677892	584	197.2	15.2	600	9	DA237284	DA237284 DA237284
585	198.2	15.3	688	14	AG052800	AG052800	585	197.2	15.2	629	11	AQ536231	AQ536231 RPCI-11-3
586	198.2	15.3	688	7	AV726885	AV726885	586	197.2	15.2	638	8	CR769528	CR769528 DKF2p469H
587	198.2	15.3	698	5	CF146894	CF146894	587	197.2	15.2	641	11	AQ357243	AQ357243 CITBI-E1-
588	198.2	15.3	947	3	BQ710747	BQ710747	588	197.2	15.2	644	5	CK002149	CK002149 AGENCOURT
589	197.8	15.3	376	1	AA579179	AA579179	589	197.2	15.2	689	14	AG092556	AG092556 Pan trogl
590	197.8	15.3	415	8	CR752548	CR752548	590	197.2	15.2	742	5	CF127609	CF127609 UI-HF-ET0
591	197.8	15.3	530	11	AQ412791	AQ412791	591	197.2	15.2	815	12	BZ608327	BZ608327 WHACC28TR
592	197.8	15.3	553	11	B51123	B51123	592	197.2	15.2	817	5	CJ447438	CJ447438 CJ447438
593	197.8	15.3	593	9	DB173577	DB173577	593	197.2	15.2	868	7	BF337291	BF337291 602034658
594	197.8	15.3	618	4	BX507346	BX507346	594	197.2	15.2	955	2	BG029224	BG029224 602292436
595	197.8	15.3	628	5	CD366995	CD366995	595	197.2	15.2	354	10	DM466089	DM466089 HHAGE0073
596	197.8	15.3	663	1	AL705955	AL705955	596	197.2	15.2	442	12	CG668943	CG668943 OST463402
597	197.8	15.3	680	3	BQ879409	BQ879409	597	197.2	15.2	480	11	AQ415807	AQ415807 RPCI-11-2
598	197.8	15.3	680	4	CA439454	CA439454	598	197.2	15.2	533	11	AQ082371	AQ082371 RPCI-11-55
599	197.8	15.3	693	11	AQ742077	AQ742077	599	197.2	15.2	553	9	DB129190	DB129190 DB129190
600	197.8	15.3	694	14	AG172896	AG172896	600	197.2	15.2	577	9	DA241923	DA241923 DA241923
601	197.8	15.3	723	2	BG617547	BG617547	601	197.2	15.2	697	12	BZ608759	BZ608759 WHAAT07TF
602	197.8	15.3	777	2	BG193279	BG193279	602	197.2	15.2	734	5	CD238958	CD238958 FNPBIE08
603	197.8	15.3	779	2	BG197390	BG197390	603	196.8	15.2	748	12	BZ610883	BZ610883 WHADJ91TF
										3181	6	CR936826	CR936826 Homo sapi
										318	3	BU589799	BU589799 AGENCOURT

C 677	196.8	15.2	497	11	B56584	B56584 CIT-HSP-200	573	9	DA752064	DA752064
C 678	196.8	15.2	501	7	AW502949	AW502949 UI-HF-BPO	585	11	AQ149696	AQ149696 HS 3178_A
C 679	196.8	15.2	560	11	DA033093	DA033093 DA033093	593	8	CN315167	CN315167 170004180
680	196.8	15.2	564	11	AQ031899	AQ031899 RPT11-11	612	11	AQ395455	AQ395455 CITBI-EI-
681	196.8	15.2	602	7	AW631593	AW631593 AV763583	640	14	AG133284	AG133284 Pan trogl
682	196.8	15.2	624	7	AW963565	AW963565 EST375638	648	11	AQ080872	AQ080872 CIT-HSP-2
683	196.8	15.2	636	11	AQ266645	AQ266645 RPT11-174	667	8	CN392067	CN392067 170005998
C 684	196.8	15.2	777	2	BI766289	BI766289 603052764	704	8	CR789340	CR789340 DKF29459D
685	196.8	15.2	778	8	CN414760	CN414760 170006008	741	8	CR788532	CR788532 DKF29459C
686	196.8	15.2	825	6	CR592456	CR592456 full-1eng	770	4	AX953657	AX953657 DKF297810
687	196.8	15.2	846	11	AQ742931	AQ742931 HS 5386_B	818	5	CJ445618	CJ445618 CJ445618
C 688	196.8	15.2	873	3	BQ642657	BQ642657 AGENCOURT	836	14	CR972858	CR972858 Homo sapi
689	196.8	15.2	924	11	AQ748907	AQ748907 HS_5574_A	908	2	CG547829	CG547829 Homo sapi
C 690	196.8	15.2	946	3	BQ643124	BQ643124 AGENCOURT	1792	6	BC016631	BC016631 Homo sapi
C 691	196.8	15.2	1042	3	BQ054473	BQ054473 AGENCOURT	4146	6	HSN805210	HSN805210 Homo sapi
692	196.8	15.2	1372	14	DU800457	DU800457 LV01 fp00	295	11	AQ252011	AQ252011 HS 3024_B
693	196.6	15.2	317	3	BU564531	BU564531 AGENCOURT	310	3	BU928415	BU928415 AGENCOURT
694	196.6	15.2	349	5	CD173059	CD173059 AGENCOURT	319	10	DM411370	DM411370 HHAGE0144
695	196.6	15.2	395	11	AI811129	AI811129 HS_3218_A	371	3	BU752091	BU752091 UI-1-BBO-
C 696	196.6	15.2	413	7	AW162288	AW162288 au66a10.x	381	7	AV758967	AV758967 AV758967
697	196.6	15.2	427	5	CJ188900	CJ188900 CJ188900	416	2	BG474043	BG474043 602516603
C 698	196.6	15.2	431	4	CB296044	CB296044 12B22019	444	3	BU429807	BU429807 UI-HF-BNO
699	196.6	15.2	474	1	AL708756	AL708756 DKF29686B	489	4	CD085578	CD085578 MC1-0015T
C 700	196.6	15.2	495	1	AI963720	AI963720 wt66B04.x	491	1	AA455483	AA455483 zxf6906.e
C 701	196.6	15.2	547	7	AW504485	AW504485 UI-HF-BNO	523	3	BQ549779	BQ549779 iK91H01.x
C 702	196.6	15.2	617	11	AQ0506230	AQ0506230 RPT1-11-3	546	3	BM697526	BM697526 UI-E-DXO-
C 703	196.6	15.2	627	5	CF135611	CF135611 UI-HF-BNO	557	11	BE85764	BE85764 RPT11-20P1
704	196.6	15.2	695	5	CF126693	CF126693 UI-HF-ETO	578	7	BE252421	BE252421 601108224
C 705	196.6	15.2	698	4	BX645236	BX645236 DKF29781J	583	9	DB153528	DB153528 DB153528
706	196.6	15.2	803	3	BU570156	BU570156 AGENCOURT	647	14	AG148123	AG148123 Pan trogl
707	196.6	15.2	823	13	CZ459657	CZ459657 MCF748a18	718	7	AV763847	AV763847 AV763847
C 708	196.6	15.2	894	3	BU189287	BU189287 AGENCOURT	729	4	CB955963	CB955963 AGENCOURT
C 709	196.6	15.2	4640	6	AF370428	AF370428 Homo sapi	753	13	CZ455670	CZ455670 MCF738E05
C 710	196.4	15.2	358	2	BG236628	BG236628 na146b07.	763	13	CZ458978	CZ458978 MCF747a20
711	196.4	15.2	377	5	CD517567	CD517567 AGENCOURT	895	3	BQ437946	BQ437946 AGENCOURT
C 712	196.4	15.2	413	1	AI284092	AI284092 QC67b11.x	1073	12	BZ601227	BZ601227 WHADC897R
C 713	196.4	15.2	539	11	BI5409	BI5409 345A13_TV_C	318	3	BU590455	BU590455 AGENCOURT
C 714	196.4	15.2	546	8	CN427153	CN427153 170006000	448	9	DB166986	DB166986 DB166986
C 715	196.4	15.2	551	4	BX490659	BX490659 DKF29686B	504	11	AQ215853	AQ215853 HS_3238_B
C 716	196.4	15.2	560	4	BA501830	BA501830 DKF29779D	521	9	DB313056	DB313056 DB313056
717	196.4	15.2	565	11	AQ039455	AQ039455 CIT-HSP-2	535	3	BU076354	BU076354 Im50d04.x
718	196.4	15.2	567	7	AV761107	AV761107 AV761107	571	9	DA449721	DA449721 DA449721
C 719	196.4	15.2	568	9	DA527033	DA527033 DA527033	583	11	AQ389664	AQ389664 RPT11-14
720	196.4	15.2	570	9	DA820198	DA820198 DA820198	585	7	AV761810	AV761810 AV761810
721	196.4	15.2	583	9	DA339129	DA339129 DA339129	601	5	CF147171	CF147171 UI-HF-CB0
C 722	196.4	15.2	594	9	DA939402	DA939402 DA939402	620	4	AV773343	AV773343 AV773343
C 723	196.4	15.2	619	7	BF697673	BF697673 602131210	634	5	CD518590	CD518590 AGENCOURT
C 724	196.4	15.2	629	11	AQ900449	AQ900449 HS_2072_B	640	1	AL600819	AL600819 DKF29313G
C 725	196.4	15.2	650	14	AG147232	AG147232 Pan trogl	646	5	CK002065	CK002065 AGENCOURT
C 726	196.4	15.2	655	7	AV7660232	AV7660232 AV7660232	661	2	BG566535	BG566535 602585562
C 727	196.4	15.2	655	9	DA832740	DA832740 DA832740	696	11	BG5610	BG5610 CIT-HSP-202
728	196.4	15.2	655	11	AQ538235	AQ538235 RPT1-11-3	741	7	AV7733830	AV7733830 AV7733830
C 729	196.4	15.2	659	8	CN427152	CN427152 170005999	978	5	CD519410	CD519410 AGENCOURT
C 730	196.4	15.2	685	11	AQ039859	AQ039859 CIT-HSP-2	1068	2	BG433833	BG433833 602497357
C 731	196.4	15.2	735	3	BU942184	BU942184 AGENCOURT	1329	2	BF984807	BF984807 602308054
C 732	196.4	15.2	767	11	AQ779859	AQ779859 HS_3104_A	318	3	BU590087	BU590087 AGENCOURT
C 733	196.4	15.2	802	5	CD657112	CD657112 AGENCOURT	321	4	AX478293	AX478293 DKF29686N
C 734	196.4	15.2	824	5	CD657759	CD657759 AGENCOURT	388	7	AW069227	AW069227 cr41h09.x
735	196.4	15.2	878	11	AQ739539	AQ739539 HS 5381_B	391	11	AQ138631	AQ138631 HS 3070_B
736	196.4	15.2	891	11	AQ739551	AQ739551 HS_5381_B	419	11	AQ585850	AQ585850 RPT1-11-4
C 737	196.4	15.2	2176	6	HSN800440	HSN800440 Homo sapi	461	1	AL041706	AL041706 DKF29434N
738	196.4	15.2	6179	6	CR936621	CR936621 Homo sapi	463	4	CA427664	CA427664 UI-H-DF0-
739	196.2	15.2	319	3	BU536099	BU536099 AGENCOURT	466	9	DA222896	DA222896 DA222896
C 740	196.2	15.2	386	11	AY758723	AY758723 RP43-128n	483	9	DA222097	DA222097 DA222097
741	196.2	15.2	398	1	AL696113	AL696113 DKF29686A	507	11	AQ169564	AQ169564 HS 3176_B
C 742	196.2	15.2	421	11	AQ457148	AQ457148 HS_5162_A	521	9	DA440738	DA440738 DA440738
C 743	196.2	15.2	436	4	BX957111	BX957111 DKF29781A	551	11	AQ528700	AQ528700 RPT1-11-3
C 744	196.2	15.2	447	11	AQ017856	AQ017856 CIT-HSP-2	553	8	CR542795	CR542795 DKF29459I
C 745	196.2	15.2	448	2	BF948248	BF948248 CM2-NN15	562	1	AL704374	AL704374 DKF29686H
C 746	196.2	15.2	466	11	AQ583964	AQ583964 RPT1-11-4	564	2	BG529995	BG529995 60255883G
C 747	196.2	15.2	494	9	DA835526	DA835526	565	9	DA521789	DA521789 DA521789
748	196.2	15.2	539	9	DA524991	DA524991 DA524991	574	9	DB077301	DB077301 DB077301
C 749	196.2	15.2	548	9	DB272897	DB272897 DB272897	589	9	DB099308	DB099308 DB099308

823	195.6	15.1	593	11	AQ539538	AQ539538 RPCI-11-3	896	195.2	15.1	709	5	CD237477	CD237477 FNPAL12
c 824	195.6	15.1	640	14	D0839295	D0839295 MUQO CH25	c 897	195.2	15.1	721	3	BM679639	BM679639 UI-E-E00-
c 825	195.6	15.1	642	14	AG115950	AG115950 Pan trogl	898	195.2	15.1	757	5	CD511672	CD511672 AGENCOURT
826	195.6	15.1	653	11	AQ533785	AQ533785 RPCI-11-3	899	195.2	15.1	774	3	BQ010024	BQ010024 UI-H-E00-
827	195.6	15.1	655	11	AQ275774	AQ275774 CITBI-E1-	900	195.2	15.1	786	3	BU954286	BU954286 AGENCOURT
c 828	195.6	15.1	662	3	BU628843	BU628843 UI-H-FLO-	c 901	195.2	15.1	796	3	BU155118	BU155118 AGENCOURT
829	195.6	15.1	662	11	AQ308811	AQ308811 CITBI-E1-	902	195.2	15.1	797	4	CB311933	CB311933 AGENCOURT
830	195.6	15.1	705	2	BG103247	BG103247 602281277	c 903	195.2	15.1	824	5	CD518284	CD518284 AGENCOURT
831	195.6	15.1	712	1	AL700144	AL700144 DKFZp686H	c 904	195.2	15.1	865	3	BQ220903	BQ220903 AGENCOURT
c 832	195.6	15.1	721	11	AQ193445	AQ193445 CIT-HSP-2	c 905	195.2	15.1	869	7	BF692524	BF692524 602248058
833	195.6	15.1	772	12	CO606335	CO606335 HSC 00496	c 906	195.2	15.1	877	3	BU178040	BU178040 AGENCOURT
c 834	195.6	15.1	787	4	CA427811	CA427811 UI-H-DF0-	c 907	195.2	15.1	953	2	BM468204	BM468204 AGENCOURT
c 835	195.6	15.1	799	8	CN307564	CN307564 170006000	c 908	195.2	15.1	1012	2	BM469629	BM469629 AGENCOURT
836	195.6	15.1	861	11	AQ752077	AQ752077 HS 5570_B	c 909	195.2	15.1	1016	2	EG178784	EG178784 602327912
c 837	195.6	15.1	968	1	AL536593	AL536593 AL536593	c 910	195.2	15.1	1063	1	AL534346	AL534346
838	195.6	15.1	1029	1	AL554221	AL554221	c 911	195.2	15.1	1073	3	BQ058920	BQ058920 AGENCOURT
c 839	195.6	15.1	2329	6	CR593590	CR593590 full-leng	c 912	195	15.1	1336	3	AA904137	AA904137 od88a08_s
c 840	195.6	15.1	3577	4	CB617708	CB617708 OX-TES-2	913	195	15.1	337	1	AI284640	AI284640 qu23h09_x
841	195.4	15.1	340	10	DM409182	DM409182 HHAGE0099	914	195	15.1	361	2	BF746395	BF746395 PM2-BT082
842	195.4	15.1	344	12	CG509012	CG509012 OST59868	915	195	15.1	364	2	BF891585	BF891585 PM3-MT011
843	195.4	15.1	347	10	DM467224	DM467224 HHAGE0084	c 916	195	15.1	463	1	AI339845	AI339845 qq43b02_x
844	195.4	15.1	356	1	AV710066	AV710066 AV710066	c 917	195	15.1	487	4	EX954470	EX954470 DKFZp781N
845	195.4	15.1	395	2	BF948356	BF948356 CM2-NN115	c 918	195	15.1	497	1	AI080618	AI080618 ox54a09_x
c 846	195.4	15.1	426	11	AQ310151	AQ310151 CITBI-E1-	919	195	15.1	502	9	DA957835	DA957835
c 847	195.4	15.1	454	1	AI885572	AI885572 wm23h01_x	c 920	195	15.1	515	8	CR546036	CR546036 DKFZp470I
c 848	195.4	15.1	490	2	BI766535	BI766535 603052348	c 921	195	15.1	582	9	DA166100	DA166100
c 849	195.4	15.1	516	9	DA603759	DA603759 DA603759	c 922	195	15.1	599	5	CD690841	CD690841 EST7364_h
c 850	195.4	15.1	542	9	DB305045	DB305045 DB305045	c 923	195	15.1	649	14	AG036539	AG036539 Pan trogl
c 851	195.4	15.1	550	5	CD693660	CD693660 EST10183	c 924	195	15.1	657	7	BF573155	BF573155 602078620
c 852	195.4	15.1	565	9	DA824485	DA824485 DA824485	c 925	195	15.1	667	3	EQ183124	EQ183124 UI-H-E00-
c 853	195.4	15.1	567	9	DA1683682	DA1683682 tx76f07_x	c 926	195	15.1	694	11	AQ588584	AQ588584 CITBI-E1-
c 854	195.4	15.1	567	9	DA261198	DA261198 DA261198	c 927	195	15.1	695	14	DX104513	DX104513 MUQO CH25
c 855	195.4	15.1	591	7	AW979191	AW979191 EST391301	c 928	195	15.1	721	8	CN264428	CN264428 170004243
c 856	195.4	15.1	633	4	BK471308	BK471308 DKFZp686J	c 929	195	15.1	725	9	DA736618	DA736618
c 857	195.4	15.1	634	11	AQ543763	AQ543763 RPCI-11-3	930	195	15.1	727	14	AG145294	AG145294 Pan trogl
c 858	195.4	15.1	646	4	CB857198	CB857198 NISC-ra05	931	195	15.1	775	4	CB989598	CB989598 AGENCOURT
c 859	195.4	15.1	646	13	CZ454140	CZ454140 MCF736B22	c 932	195	15.1	854	13	CZ448805	CZ448805 MCF728P07
860	195.4	15.1	665	14	AG049305	AG049305 Pan trogl	c 933	195	15.1	859	9	DA732756	DA732756
861	195.4	15.1	671	2	DB289041	DB289041 602383913	934	194.8	15.0	385	3	BU568121	BU568121 AGENCOURT
c 862	195.4	15.1	791	4	BK439602	BK439602 BX439602	c 935	194.8	15.0	385	3	BU569664	BU569664 AGENCOURT
c 863	195.4	15.1	829	12	BZ609393	BZ609393 WHAC148TF	c 936	194.8	15.0	388	1	AI821918	AI821918 nt67e05_x
c 864	195.4	15.1	836	2	BG771122	BG771122 602719716	c 937	194.8	15.0	400	4	BX482403	BX482403 DKFZp686J
865	195.4	15.1	870	13	CZ448218	CZ448218 MCF728C15	c 938	194.8	15.0	403	11	BA0820	BA0820 HS-1052-B1-
866	195.4	15.1	889	5	CD515462	CD515462 AGENCOURT	c 939	194.8	15.0	410	1	AI821881	AI821881 nt63h02_x
c 867	195.4	15.1	927	2	BF792883	BF792883 602253372	c 940	194.8	15.0	487	12	BZ758465	BZ758465 UP 301-19
c 868	195.4	15.1	960	3	BQ226435	BQ226435 AGENCOURT	c 941	194.8	15.0	490	9	DN847473	DN847473 KECB32-02
c 869	195.4	15.1	3029	6	HSMB808025	HSMB808025 Homo sapi	c 942	194.8	15.0	535	4	BX488826	BX488826 DKFZp686C
c 870	195.4	15.1	3464	6	CR627410	CR627410 Homo sapi	c 943	194.8	15.0	552	9	DB125226	DB125226 DB125226
871	195.2	15.1	375	12	CG624086	CG624086 OST327063	c 944	194.8	15.0	556	14	CR959703	CR959703 Homo sapi
c 872	195.2	15.1	390	1	AI859946	AI859946 wm23h05_x	c 945	194.8	15.0	567	9	DB356885	DB356885 DB356885
c 873	195.2	15.1	441	11	AQ882986	AQ882986 HS 5450_B	c 946	194.8	15.0	598	4	BX498649	BX498649 DKFZp779J
c 874	195.2	15.1	445	11	AD480961	AD480961 RPCI-11-2	c 947	194.8	15.0	628	5	CD690152	CD690152 EST16675_h
875	195.2	15.1	455	5	QD702830	QD702830 EST19435	c 948	194.8	15.0	630	12	BZ603807	BZ603807 WHAC111TR
c 876	195.2	15.1	486	3	BM993751	BM993751 UI-H-DH0-	c 949	194.8	15.0	631	11	AQ899346	AQ899346 HS 3203_B
c 877	195.2	15.1	494	11	B52978	B52978 CIT-HSP-200	950	194.8	15.0	642	8	CN483194	CN483194 hw29d11_y
c 878	195.2	15.1	500	4	BK471878	BK471878 DKFZp686P	c 951	194.8	15.0	644	11	AZ502273	AZ502273 RPCI-11-1
c 879	195.2	15.1	507	13	CZ454271	CZ454271 MCF736E21	c 952	194.8	15.0	657	11	AQ782480	AQ782480 HS 3174_A
880	195.2	15.1	511	2	BG281960	BG281960 602403142	c 953	194.8	15.0	658	11	AQ393450	AQ393450 CITBI-E1-
881	195.2	15.1	513	4	BK642735	BK642735 DKFZp781F	c 954	194.8	15.0	669	14	AG148600	AG148600 Pan trogl
c 882	195.2	15.1	529	9	DB117803	DB117803 DB117803	c 955	194.8	15.0	692	4	CA442156	CA442156 UI-H-DH0-
c 883	195.2	15.1	533	9	DB311378	DB311378 DB311378	c 956	194.8	15.0	699	3	BU678175	BU678175 UI-CF-EC0
884	195.2	15.1	552	14	DU638226	DU638226 Cluflf-HI	c 957	194.8	15.0	707	4	BX953514	BX953514 DKFZp781A
c 885	195.2	15.1	557	9	DA273293	DA273293 DA273293	958	194.8	15.0	725	2	BG400733	BG400733 602464120
c 886	195.2	15.1	570	3	BP265868	BP265868 BP265868	c 959	194.8	15.0	780	9	CR866374	CR866374 HESCA_10
c 887	195.2	15.1	613	5	CD709038	CD709038 EST25565	960	194.8	15.0	860	11	AQ742827	AQ742827 HS 5482_B
c 888	195.2	15.1	627	8	CV571026	CV571026 oe08a10_y	961	194.8	15.0	887	5	CF454479	CF454479 AGENCOURT
889	195.2	15.1	632	7	AV761286	AV761286 AV761286	962	194.8	15.0	1148	7	AV761207	AV761207
c 890	195.2	15.1	651	11	B66038	B66038 CIT-HSP-202	963	194.8	15.0	1345	7	AV762220	AV762220
c 891	195.2	15.1	652	2	BJ044140	BJ044140 BJO44140	964	194.8	15.0	2940	6	CR858431	CR858431 Pongo pyg
c 892	195.2	15.1	657	1	AV711465	AV711465 AV711465	c 965	194.8	15.0	5689	6	HSMB06132	HSMB06132 Homo sapi
893	195.2	15.1	672	14	AG019427	AG019427 Homo sapi	c 966	194.6	15.0	239	3	BU752609	BU752609 UI-1-BC0-
894	195.2	15.1	673	14	AG068500	AG068500 Pan trogl	967	194.6	15.0	304	3	BQ949810	BQ949810 AGENCOURT
c 895	195.2	15.1	689	1	AL042771	AL042771 DKFZp434D	968	194.6	15.0	345	12	CG666529	CG666529 OST456665

C 969	194.6	15.0	363	7	AW166611	AW166611 xF64909.x	c1042	194.2	15.0	613	14	AG009040	Homo sapi
C 970	194.6	15.0	401	1	A1040051	ox28a11.x	1043	194.2	15.0	643	14	AG116440	Pan trogl
C 971	194.6	15.0	408	9	AW761519	AW761519	c1044	194.2	15.0	708	4	CB265374	1004279.H
C 972	194.6	15.0	438	7	DA640553	DA640553	1045	194.2	15.0	709	14	AG170809	Pan trogl
C 973	194.6	15.0	461	11	AQ478455	AQ478455 RPCI-11-2	1046	194.2	15.0	717	13	C2451438	MCP732106
C 974	194.6	15.0	470	8	CR752576	DKF2P459P	1047	194.2	15.0	746	14	AG179326	Pan trogl
C 975	194.6	15.0	473	7	AW613805	hA74301.x	1048	194.2	15.0	778	11	AQ741774	HS_5566.B
C 976	194.6	15.0	539	11	AQ423772	CITBI-EI-	1049	194.2	15.0	853	11	AQ747124	HS_5539.A
C 977	194.6	15.0	548	11	AQ423767	CITBI-EI-	1050	194.2	15.0	914	4	BX377240	BX377240
C 978	194.6	15.0	555	11	AQ029504	AQ029504 RPCI11-39	1051	194.2	15.0	1808	6	CR858461	Pongo pyg
C 979	194.6	15.0	558	3	BU928267	AGENCOURT	1052	194.2	15.0	3972	6	CR627413	Homo sapi
C 980	194.6	15.0	561	9	DA494323	DA494323	1053	194.2	15.0	6033	6	CR749486	Homo sapi
C 981	194.6	15.0	563	4	BX470745	DKF2P686C	1054	194	15.0	313	3	BU929784	AGENCOURT
C 982	194.6	15.0	575	11	A2521417	RPCI-11-3	1055	194	15.0	340	2	BF932982	IL5-NT022
C 983	194.6	15.0	577	9	DA219587	DA219587	1056	194	15.0	383	7	BE139267	xt-68A06.x
C 984	194.6	15.0	590	11	AQ426623	CITBI-EI-	1057	194	15.0	399	1	AL700720	DKF2P686B
C 985	194.6	15.0	604	11	AQ262198	CITBI-EI-	1058	194	15.0	399	11	AQ587593	CITBI-EI-
C 986	194.6	15.0	630	11	AQ628459	CITBI-EI-	1059	194	15.0	407	1	AI753113	cr05C11.x
C 987	194.6	15.0	649	14	CR960737	Homo sapi	1060	194	15.0	413	2	BG942897	ax30h12.x
C 988	194.6	15.0	700	14	AG087229	Pan trogl	1061	194	15.0	424	9	DA327318	DA327318
C 989	194.6	15.0	712	5	CD237852	FNPAGE02	1062	194	15.0	431	9	DN602005	HESC3_74
C 990	194.6	15.0	721	14	AG013872	Homo sapi	1063	194	15.0	435	1	AI588837	xt-68A02.x
C 991	194.6	15.0	727	14	AG014753	Homo sapi	1064	194	15.0	444	11	B89781	CIT-HSP-217
C 992	194.6	15.0	778	7	AW764490	AW764490	1065	194	15.0	446	1	AI630283	ad08A04.y
C 993	194.6	15.0	854	3	BU177531	BU177531	1066	194	15.0	450	11	AQ587553	CITBI-EI-
C 994	194.6	15.0	3084	6	CR857067	Pongo pyg	1067	194	15.0	471	11	A2695119	UP_572-21
C 995	194.4	15.0	350	2	BG944664	ax53C09.x	1068	194	15.0	472	2	BG576200	602597187
C 996	194.4	15.0	414	10	H90844	yu85C01.e1	1069	194	15.0	482	7	AW662543	hi29B01.x
C 997	194.4	15.0	441	1	AI732120	ac86A01.x	1070	194	15.0	487	11	CR741986	CR741986
C 998	194.4	15.0	441	1	AI732180	ac86A01.x	1071	194	15.0	487	11	A2694783	UP_310-20
C 999	194.4	15.0	446	11	AQ080889	CIT-HSP-2	1072	194	15.0	493	1	AL707211	DKF2P6861
C 1000	194.4	15.0	451	3	BQ181691	UT-H-EU0-	1073	194	15.0	510	2	BF965775	602277404
C 1001	194.4	15.0	506	8	CR538820	DKF2P459D	1074	194	15.0	513	9	DA390685	DA390685
C 1002	194.4	15.0	510	4	CA441782	UT-H-ED0-	1075	194	15.0	529	2	BG402924	602418727
C 1003	194.4	15.0	521	2	BF736198	PM4-KT000	1076	194	15.0	533	8	CR548320	DKF2P459B
C 1004	194.4	15.0	529	1	AA680243	ac86A01.s	1077	194	15.0	541	9	DA803349	DA803349
C 1005	194.4	15.0	540	3	BU617996	UT-H-DF0-	1078	194	15.0	545	9	DA405230	DA405230
C 1006	194.4	15.0	556	9	DA522627	DA522627	1079	194	15.0	554	9	DA436188	DA436188
C 1007	194.4	15.0	565	4	BX509789	DKF2P686U	1080	194	15.0	565	9	DA792584	DA792584
C 1008	194.4	15.0	572	9	DA129024	DA129024	1081	194	15.0	573	11	AQ585048	RPCI-11-4
C 1009	194.4	15.0	573	11	AQ537518	RPCI-11-3	1082	194	15.0	576	7	BE142930	MRO-HT015
C 1010	194.4	15.0	596	8	CR544076	DKF2P470K	1083	194	15.0	583	11	AQ391722	CITBI-EI-
C 1011	194.4	15.0	597	7	DA938247	DA938247	1084	194	15.0	590	13	C2451403	MCP736B03
C 1012	194.4	15.0	635	9	AW763418	AW763418	1085	194	15.0	591	11	AQ586921	RPCI-11-4
C 1013	194.4	15.0	636	7	AW759935	AW759935	1086	194	15.0	604	9	CR868054	HESCA_25
C 1014	194.4	15.0	642	7	AW975049	AW975049 EST387154	1087	194	15.0	650	14	AG116352	Pan trogl
C 1015	194.4	15.0	675	14	AG176894	AG176894	1088	194	15.0	653	14	AG159864	AG159864
C 1016	194.4	15.0	687	5	CK005591	AGENCOURT	1089	194	15.0	657	14	AG182991	Pan trogl
C 1017	194.4	15.0	711	11	AQ539088	RPCI-11-3	1090	194	15.0	659	14	AG076908	Pan trogl
C 1018	194.4	15.0	736	13	CZ460367	CZ460367 MCP749R03	1091	194	15.0	745	3	BQ028789	UT-H-DF0-
C 1019	194.4	15.0	756	8	CN419034	170004243	1092	194	15.0	789	11	AQ738908	HS_5382.B
C 1020	194.4	15.0	782	3	BQ775332	UT-H-FH0-	1093	194	15.0	831	3	BU567661	AGENCOURT
C 1021	194.4	15.0	822	2	BQ249643	602319736	1094	194	15.0	844	11	AQ748733	HS_5540.A
C 1022	194.4	15.0	836	3	BU567884	AGENCOURT	1095	194	15.0	936	14	DU710557	aaV01.fP0
C 1023	194.4	15.0	1011	3	BU561756	AGENCOURT	1096	194	15.0	1369	14	DU799773	lv01.fP00
C 1024	194.4	15.0	4325	6	CR857584	Pongo pyg	1097	194	15.0	3116	6	HSN804686	Homo sapi
C 1025	194.2	15.0	314	10	DM414862	DM414862 HHAGE0155	1098	193.8	15.0	300	2	BG434760	602507967
C 1026	194.2	15.0	352	4	BX485943	DKF2P686G	1099	193.8	15.0	310	3	BU560611	AGENCOURT
C 1027	194.2	15.0	368	3	BU430129	UT-HF-BNO	1100	193.8	15.0	318	3	BU531754	AGENCOURT
C 1028	194.2	15.0	463	3	BM989280	BM989280 UT-H-DF0-	1101	193.8	15.0	351	7	AW515437	xtU70C08.x
C 1029	194.2	15.0	497	9	DB234972	DB234972	1102	193.8	15.0	381	10	DM440994	HHAGE0037
C 1030	194.2	15.0	500	11	AQ394178	RPCI11-65	1103	193.8	15.0	388	11	AQ588707	CITBI-EI-
C 1031	194.2	15.0	507	7	AW277171	xg77c11.x	1104	193.8	15.0	418	11	AQ587801	CIT-HSP-2
C 1032	194.2	15.0	518	9	DB212365	DB212365	1105	193.8	15.0	450	7	AW571562	xx33B01..x
C 1033	194.2	15.0	539	9	DA3111387	DA3111387	1106	193.8	15.0	480	3	BM894065	i163A03.x
C 1034	194.2	15.0	540	2	BM456994	BM456994	1107	193.8	15.0	481	3	BM565475	i125e05.x
C 1035	194.2	15.0	552	11	AQ505983	AQ505983 RPCI-11-2	1108	193.8	15.0	501	9	DB228323	DB228323
C 1036	194.2	15.0	553	11	AQ462228	HS_4066.B	1109	193.8	15.0	506	7	AW970877	EST382960
C 1037	194.2	15.0	558	9	DB019422	DB019422	1110	193.8	15.0	518	9	DB341160	DB341160
C 1038	194.2	15.0	562	4	CA388905	ca03f11.x	1111	193.8	15.0	520	3	BM894337	i163A03.y
C 1039	194.2	15.0	577	11	AQ239882	CIT-HSP-2	1112	193.8	15.0	521	2	BM507206	i125e05.y
C 1040	194.2	15.0	586	11	AQ196559	CIT-HSP-2	1113	193.8	15.0	538	12	B2610864	WHADJ62TF
C 1041	194.2	15.0	587	11	AQ344455	RPCI11-11	1114	193.8	15.0	539	9	DB066718	DB066718

c1115	193.8	15.0	556	1	AU152561	AU152561	1188	193.4	14.9	910	3	BQ722917	BQ722917
c1116	193.8	15.0	558	9	DA949782	DA949782	c1189	193.4	14.9	928	3	BQ648991	BQ648991
c1117	193.8	15.0	564	9	DA017485	DA017485	c1190	193.4	14.9	937	7	BF312862	BF312862
c1118	193.8	15.0	581	9	DA236017	DA236017	c1191	193.4	14.9	997	2	BG547647	BG547647
c1119	193.8	15.0	582	9	DA235999	DA235999	c1192	193.4	14.9	1890	6	CR624170	CR624170
c1120	193.8	15.0	588	9	DA057126	DA057126	c1193	193.4	14.9	5957	6	HSM8000277	HSM8000277
c1121	193.8	15.0	593	1	AL1712739	AL1712739	c1194	193.2	14.9	305	3	BQ441427	BQ441427
c1122	193.8	15.0	669	1	AL133668	AL133668	c1195	193.2	14.9	352	1	A1915293	A1915293
c1123	193.8	15.0	680	2	BG924866	BG924866	c1196	193.2	14.9	369	3	BUS36852	BUS36852
c1124	193.8	15.0	706	13	CZ460513	CZ460513	c1197	193.2	14.9	393	1	AV703785	AV703785
c1125	193.8	15.0	712	4	BX508601	BX508601	c1198	193.2	14.9	401	1	A1635819	A1635819
c1126	193.8	15.0	864	1	AL574059	AL574059	c1199	193.2	14.9	409	1	A1216998	A1216998
c1127	193.8	15.0	866	6	CR590505	CR590505	c1200	193.2	14.9	423	7	AW819125	AW819125
c1128	193.8	15.0	883	13	CZ460349	CZ460349	c1201	193.2	14.9	424	2	BG056174	BG056174
c1129	193.8	15.0	1952	6	BC018692	BC018692	c1202	193.2	14.9	432	11	AQ659586	AQ659586
c1130	193.6	14.9	322	3	BU941317	BU941317	c1203	193.2	14.9	453	7	AW276814	AW276814
c1131	193.6	14.9	337	10	DAW09824	DAW09824	c1204	193.2	14.9	455	11	AQ508921	AQ508921
c1132	193.6	14.9	340	1	A1270117	A1270117	c1205	193.2	14.9	476	11	B18175	B18175
c1133	193.6	14.9	341	10	DAW08957	DAW08957	c1206	193.2	14.9	477	11	AQ133650	AQ133650
c1134	193.6	14.9	405	2	BF776617	BF776617	c1207	193.2	14.9	495	4	AX954422	AX954422
c1135	193.6	14.9	423	1	A1867058	A1867058	c1208	193.2	14.9	497	1	AL589495	AL589495
c1136	193.6	14.9	433	2	BG177715	BG177715	c1209	193.2	14.9	497	4	AX480039	AX480039
c1137	193.6	14.9	458	4	BX508242	BX508242	c1210	193.2	14.9	502	4	AX481465	AX481465
c1138	193.6	14.9	479	11	AQ225492	AQ225492	c1211	193.2	14.9	508	9	DA674463	DA674463
c1139	193.6	14.9	492	3	BM993628	BM993628	c1212	193.2	14.9	513	4	BX502388	BX502388
c1140	193.6	14.9	509	2	BF720424	BF720424	c1213	193.2	14.9	535	5	CD694741	CD694741
c1141	193.6	14.9	515	11	AQ019249	AQ019249	c1214	193.2	14.9	548	11	AQ636944	AQ636944
c1142	193.6	14.9	538	11	AQ547277	AQ547277	c1215	193.2	14.9	576	11	AQ546229	AQ546229
c1143	193.6	14.9	551	11	AQ441865	AQ441865	c1216	193.2	14.9	581	9	DA967079	DA967079
c1144	193.6	14.9	560	9	DB264370	DB264370	c1217	193.2	14.9	599	11	AQ390306	AQ390306
c1145	193.6	14.9	569	13	CZ459282	CZ459282	c1218	193.2	14.9	639	14	AG176411	AG176411
c1146	193.6	14.9	576	3	BU078633	BU078633	c1219	193.2	14.9	651	7	BE909125	BE909125
c1147	193.6	14.9	582	9	DA786925	DA786925	c1220	193.2	14.9	662	14	AG068637	AG068637
c1148	193.6	14.9	603	3	BP872932	BP872932	c1221	193.2	14.9	664	12	BZ599095	BZ599095
c1149	193.6	14.9	612	5	CK817709	CK817709	c1222	193.2	14.9	693	7	AV728425	AV728425
c1150	193.6	14.9	623	7	AV6762741	AV6762741	c1223	193.2	14.9	742	9	CK872706	CK872706
c1151	193.6	14.9	623	3	AV762741	AV762741	c1224	193.2	14.9	744	9	CK872706	CK872706
c1152	193.6	14.9	642	13	CZ454001	CZ454001	c1225	193.2	14.9	765	12	BZ607682	BZ607682
c1153	193.6	14.9	669	14	AG093329	AG093329	c1226	193.2	14.9	773	13	CZ450219	CZ450219
c1154	193.6	14.9	683	1	AL704146	AL704146	c1227	193.2	14.9	810	9	CK784348	CK784348
c1155	193.6	14.9	693	14	AG009058	AG009058	c1228	193.2	14.9	865	5	CD172255	CD172255
c1156	193.6	14.9	714	11	B16596	B16596	c1229	193.2	14.9	876	4	CR988102	CR988102
c1157	193.6	14.9	743	14	AG185468	AG185468	c1230	193.2	14.9	888	14	DU797654	DU797654
c1158	193.6	14.9	783	11	AQ740916	AQ740916	c1231	193.2	14.9	935	11	AQ743050	AQ743050
c1159	193.6	14.9	793	14	CR960646	CR960646	c1232	193.2	14.9	2435	6	AF289560	AF289560
c1160	193.6	14.9	834	2	BG427989	BG427989	c1233	193.2	14.9	5882	6	HSM808008	HSM808008
c1161	193.6	14.9	858	11	AQ742838	AQ742838	c1234	193	14.9	294	4	CB267559	CB267559
c1162	193.6	14.9	895	3	BU603620	BU603620	c1235	193	14.9	330	2	BG059450	BG059450
c1163	193.6	14.9	1110	4	BX378257	BX378257	c1236	193	14.9	340	10	DAW09180	DAW09180
c1164	193.4	14.9	306	7	BF681619	BF681619	c1237	193	14.9	342	10	DAW08757	DAW08757
c1165	193.4	14.9	308	10	F13749	F13749	c1238	193	14.9	378	11	AQ673092	AQ673092
c1166	193.4	14.9	320	3	BU959012	BU959012	c1239	193	14.9	413	11	AQ824174	AQ824174
c1167	193.4	14.9	321	3	BU945386	BU945386	c1240	193	14.9	460	11	B15692	B15692
c1168	193.4	14.9	345	10	DAW67571	DAW67571	c1241	193	14.9	460	11	AQ93511	AQ93511
c1169	193.4	14.9	346	7	AV762031	AV762031	c1242	193	14.9	464	3	BQ775040	BQ775040
c1170	193.4	14.9	375	7	AW303196	AW303196	c1243	193	14.9	513	12	CG605974	CG605974
c1171	193.4	14.9	398	4	EX494090	EX494090	c1244	193	14.9	516	4	AX470275	AX470275
c1172	193.4	14.9	400	7	AV758870	AV758870	c1245	193	14.9	523	9	DA957634	DA957634
c1173	193.4	14.9	418	1	AV738025	AV738025	c1246	193	14.9	543	9	DB231425	DB231425
c1174	193.4	14.9	522	3	BM993791	BM993791	c1247	193	14.9	544	11	AQ138917	AQ138917
c1175	193.4	14.9	523	8	CN479672	CN479672	c1248	193	14.9	546	11	AQ090485	AQ090485
c1176	193.4	14.9	527	7	AW970973	AW970973	c1249	193	14.9	548	9	DB351501	DB351501
c1177	193.4	14.9	528	11	AQ545181	AQ545181	c1250	193	14.9	557	9	AU147163	AU147163
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c1179	193.4	14.9	546	9	DB318900	DB318900	c1252	193	14.9	567	14	CR972773	CR972773
c1180	193.4	14.9	549	4	AX494048	AX494048	c1253	193	14.9	574	3	BQ898821	BQ898821
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c1182	193.4	14.9	643	14	AG052500	AG052500	c1255	193	14.9	581	1	AU144161	AU144161
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c1184	193.4	14.9	655	4	BX483067	BX483067	c1257	193	14.9	620	14	AG155321	AG155321
c1185	193.4	14.9	672	11	AQ542044	AQ542044	c1258	193	14.9	622	5	CD513591	CD513591
c1186	193.4	14.9	711	8	CN271783	CN271783	c1259	193	14.9	646	11	B49186	B49186
c1187	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1188	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1189	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1190	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1191	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1192	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1193	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1194	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1195	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1196	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1197	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
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c1199	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1200	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1201	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1202	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1203	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1204	193.4	14.9	807	9	CK786783	CK786783	c1260	193	14.9	656	8	CR559837	CR559837
c1205	193.4	14.9	807										

c1261 193 14.9 668 14 AG178682
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1263 193 700 14 AG135790
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1265 193 734 2 CA415300
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C1410	192.4	14.9	572	9	DB260896	DB260896	C1483	192	14.8	460	4	CA308447	CA308447 UI-H-PT1-
C1411	192.4	14.9	575	9	DA272243	DA272243	C1484	192	14.8	474	1	AL048925	AL048925 DKEZp434K
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ALIGNMENTS

RESULT 1	CR605305	1143 bp	mRNA	linear	HTC 21-JUL-2004
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DEFINITION	of Homo sapiens (human).				
ACCESSION	CR605305	1 GI:50486112			
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REFERENCE	1 (bases 1 to 1143)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2 (bases 1 to 1143)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)				
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
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RESULT 2
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LOCUS
DEFINITION
of Homo sapiens (human).
ACCESSION
CR618843
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VERSION CR618843.1 GI:50499650
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REFERENCE 1 (bases 1 to 1329)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope.
2 (bases 1 to 1329)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Best Local Similarity 97.6%; Pred. No. 1.4e-152;
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Db 178 CAGAGAGCGGCTGCGGCGCGGAGATGGCAGGAGAGCGCCACCGCCTCTCCT 237
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Db 358 AACCCCAAGAGAGCTGTTTCTCAGATTAGAGTGGAGAAACTGGGTCGGAGTGTCTC 417
Qy 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTCATTTTAAAAATCGAGCTGAGATGATAGA 360
Db 418 CTTTGTCTACTATCAACAGACTCTTCAAGGTCATTTTAAAAATCGAGCTGAGATGATAGA 477
Qy 361 TTTCAATATCCGGATCAAAAATGTGACAGAGTGTGATGCGGGGAAATATCGTTGTGAAGT 420
Db 478 TTTCAATATCCGGATCAAAAATGTGACAGAGTGTGATGCGGGGAAATATCGTTGTGAAGT 537
Qy 421 TAGTGCCCATCTGAGCAAGGCGCAAACTCTGGAAGAGATACAGTCACTCTGGAAGTATT 480
Db 538 TAGTGCCCATCTGAGCAAGGCGCAAACTCTGGAAGAGGATACAGTCACTCTGGAAGTATT 597
Qy 481 AGTGGCTCCAGCAGTTTCCATCATGTGAAGTACCTCTTCTGCTCAGTGGAGAACTGTGCT 540
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Db 598 AGTGGCTCCAGCAGTTCATCATGTGAAGTACCCTCTTCTGCTGAGTGGAACTGTGGT 657
Qy 541 AGAGCTACGATGTCAAGCAAGAGGAATCCAGCTCCTGAAATACATCATGTTTAAAGGA 600
Db 658 AGAGCTACGATGTCAAGCAAGAGGAATCCAGCTCCTGAAATACATCATGTTTAAAGGA 717
Qy 601 TGGCATCGTTTGTAGAAAATCCAGACTTTGGCTCCCAAGCACCACAGCTCATACAC 660
Db 718 TGGCATCGTTTGTAGAAAATCCAGACTTTGGCTCCCAAGCACCACAGCTCATACAC 777
Qy 661 AATGAATACAAAATCGAACTCTGCAATTTAAATCTGTTTCCAACTGGACACTGGAGA 720
Db 778 AATGAATACAAAATCGAACTCTGCAATTTAAATCTGTTTCCAACTGGACACTGGAGA 837
Qy 721 ATATTCTGTGAAGCCCGCAATTCCTGTTGGATATCGCAGGTGCTCGGAAACGAATGCA 780
Db 838 ATATTCTGTGAAGCCCGCAATTCCTGTTGGATATCGCAGGTGCTCGGAAACGAATGCA 897
Qy 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTGTGGCCTTTAGTGAT 840
Db 898 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTGTGGCCTTTAGTGAT 957
Qy 841 TTCGGTTTGGCCCTTGGTGTATGCTATGCTCAGAGGAAGGCTACTTTTCAAAAGAAAC 900
Db 958 TTCGGTTTGGCCCTTGGTGTATGCTATGCTCAGAGGAAGGCTACTTTTCAA----- 1010
Qy 901 CTCCTTCCAGAGAGTAATCTTCCATCTAAAGCCAGCAGCATGATGAAATGTGCAGTG 960
Db 1011 -----GTAAGAAGAGTAATCTTCCATCTAAAGCCAGCAGCATGATGAAATGTTCAA 1065
Qy 961 GCTCAC 966
Db 1066 GCACAC 1071

RESULT 3
CR621227 1511 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DB009YH07 of Neuroblastoma Cot
DEFINITION 10-normalized of Homo sapiens (human).
ACCESSION CR621227
VERSION CR621227.1 GI:50502034
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1511)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1511)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1511
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB009YH07"
/tissue_type="Neuroblastoma Cot 10-normalized"
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ORIGIN
Query Match 70.6%; Score 914.4; DB 6; Length 1511;
Best Local Similarity 97.6%; Pred. No. 1.4e-152;
Matches 943; Conservative 0; Mismatches 11; Indels 12; Gaps 1;

Qy 1 CCCAAGAGTTCAAGGGGCCCGGCTCTCTGCGCTCCTGCGCCGGGAGACCCCTCGACCTCCT 60
Db 307 CCCAAGAGTTCAAGGGGCCCGGCTCTCTGCGCTCCTGCGCCGGGAGACCCCTCGACCTCCT 366
Qy 61 CAGAGCAGCGGCTGCGCCCGGGAAGATGGCGAGGAGCGCCACCGCCTCCTCCT 120
Db 367 CAGAGCAGCGGCTGCGCCCGGGAAGATGGCGAGGAGCGCCACCGCCTCCTCCT 426
Qy 121 GCTGCTGCTGGCTACCTGCTGCTGCGCTGCGCTGCTATCATAGGCTATGGGTTTCTGC 180
Db 427 GCTGCTGCTGGCTACCTGCTGCTGCGCTGCGCTGCTATCATAGGCTATGGGTTTCTGC 486
Qy 181 CCCAAGAGCAACAAGTAGTACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA 240
Db 487 CCCAAGAGCAACAAGTAGTACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA 546
Qy 241 AACCCCAAGAGAGTCTTTCTCCAGATTAGAGTGGAAAGAACTGGGTGGAGTGTCTC 300
Db 547 AACCCCAAGAGAGTCTTTCTCCAGATTAGAGTGGAAAGAACTGGGTGGAGTGTCTC 606
Qy 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA 360
Db 607 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA 666
Qy 361 TTTCAATATCCGGATCAAAAATGACAGAAGTGTGCGGGGAAATATCTGTTGGAAGT 420
Db 667 TTTCAATATCCGGATCAAAAATGACAGAAGTGTGCGGGGAAATATCTGTTGGAAGT 726
Qy 421 TAGTGGCCCATCTGAGCAAGGCCAAAACCTGGAGAGGATACAGTCACTCTGGAAGTATT 480
Db 727 TAGTGGCCCATCTGAGCAAGGCCAAAACCTGGAGAGGATACAGTCACTCTGGAAGTATT 786
Qy 481 AGTGGCTCCAGCAGTGTCCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 540
Db 787 AGTGGCTCCAGCAGTGTCCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 846
Qy 541 AGAGCTACGATGTCAAGCAAGAGGAATCCAGCTCCTGGAATACATCATGTTTAAAGGA 600
Db 847 AGAGCTACGATGTCAAGCAAGAGGAATCCAGCTCCTGGAATACATCATGTTTAAAGGA 906
Qy 601 TGGCATCGTTTGTAGAAAATCCAGACTTTGGCTCCCAAGCACCACAGCTCATACAC 660
Db 907 TGGCATCGTTTGTAGAAAATCCAGACTTTGGCTCCCAAGCACCACAGCTCATACAC 966
Qy 661 AATGAATACAAAATCGAACTCTGCAATTTAAATCTGTTTCCAACTGGACACTGGAGA 720
Db 967 AATGAATACAAAATCGAACTCTGCAATTTAAATCTGTTTCCAACTGGACACTGGAGA 1026
Qy 721 ATATTCTGTGAAGCCCGCAATTCCTGTTGGATATCGCAGGTGCTCGGAAACGAATGCA 780
Db 1027 ATATTCTGTGAAGCCCGCAATTCCTGTTGGATATCGCAGGTGCTCGGAAACGAATGCA 1086
Qy 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTGTGGCCTTTAGTGAT 840
Db 1087 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTGTGGCCTTTAGTGAT 1146
Qy 841 TTCGGTTTGGCCTTGGTGTATGCTATGCTCAGAGGAAGGCTACTTTTCAAAAGAAAC 900
Db 1147 TTCGGTTTGGCCTTGGTGTATGCTATGCTCAGAGGAAGGCTACTTTTCAA----- 1199
Qy 901 CTCCTTCCAGAGAGTAATCTTCCATCTAAAGCCAGCAGCATGATGAAATGTGCAGTG 960
Db 1200 -----GTAAGAAGAGTAATCTTCCATCTAAAGCCAGCAGCATGATGAAATGTTCAA 1254
Qy 961 GCTCAC 966
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[illegible]

was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
source
1. .1465
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D022YA21"
/tissue type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 69.5%; Score 900.6; DB 6; Length 1465;
Best Local Similarity 97.4%; Pred. No. 3.9e-150;
Matches 915; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1 CCAGAGATTCAAGGGCCCCGGGCTCTGGCTCTCCGCGCGGAGACCCCTCGACCTCCT 60
Db 335 CCAGAGATTCAAGGGCCCCGGGCTCTGGCTCTCCGCGCGGAGACCCCTCGACCTCCT 394
Qy 61 CAGAGACCGCGCTGCCGCCCGGGAAGATGGCGAGGAGCGCCACCGCTCCTCCT 120
Db 395 CAGAGACCGCGCTGCCGCCCGGGAAGATGGCGAGGAGCGCCACCGCTCCTCCT 454
Qy 121 GCTGCTGCTGCTACCTGCTGCTGCTGCTGCTGCTATCATAAGGCTATGCGTTTCTGC 180
Db 455 GCTGCTGCTGCTACCTGCTGCTGCTGCTGCTGCTATCATAAGGCTATGCGTTTCTGC 514
Qy 181 CCMAAAGACAAGTAGTACAGCAGTAGATGACCAAGAGGCTATTTTAGCCTGCAA 240
Db 515 CCMAAAGACAAGTAGTACAGCAGTAGATGACCAAGAGGCTATTTTAGCCTGCAA 574
Qy 241 AACCCCAAGAGACTGTTTCTCCAGATTAGTGGAGGAGAACTGGGTGGAGTCTC 300
Db 575 AACCCCAAGAGACTGTTTCTCCAGATTAGTGGAGGAGAACTGGGTGGAGTCTC 634
Qy 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGTGAATGATAGA 360
Db 635 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGTGAATGATAGA 694
Qy 361 TTCAATATCCGATCAAAATGTGA CAAGAATGATGCGGGGAAATATCGTTGTGAAGT 420
Db 695 TTCAATATCCGATCAAAATGTGA CAAGAATGATGCGGGGAAATATCGTTGTGAAGT 754
Qy 421 TAGTGCCCATCTGAGCAAGCCAAACCTCGAGAGGATACAGTCACTCTGGAAGTATT 480
Db 755 TAGTGCCCATCTGAGCAAGCCAAACCTCGAGAGGATACAGTCACTCTGGAAGTATT 814
Qy 481 AGTGGCTCCAGCAGATTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTGTGGT 540
Db 815 AGTGGCTCCAGCAGATTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTGTGGT 874
Qy 541 AGAGCTACGATGTCAGACAAGAGGGAATCCAGCTCTCTGAAATACACATGTTTAAAGGA 600
Db 875 AGAGCTACGATGTCAGACAAGAGGGAATCCAGCTCTCTGAAATACACATGTTTAAAGGA 934
Qy 601 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATACAC 660
Db 935 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATACAC 994
Qy 661 AATGAATACAAAACCTGCAACTCTGCAATTTAATCTGTTTCAAACTGGACACTGGAGA 720
Db 995 AATGAATACAAAACCTGCAACTCTGCAATTTAATCTGTTTCAAACTGGACACTGGAGA 1054
Qy 721 ATATTCTGTGAAGCCCGCAATCTGTTGGATATCGCAGGTTGTCCTGGGAAACGGAATGCA 780
Db 1055 ATATTCTGTGAAGCCCGCAATCTGTTGGATATCGCAGGTTGTCCTGGGAAACGGAATGCA 1114
Qy 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTAGTTGTGGCCCTTAGTAT 840
Db 1115 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTAGTTGTGGCCCTTAGTAT 1174
Qy 841 TTCCGTTTGTGGCCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAC 900

Db 1175 TTCCGTTTGTGGCCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAGTAAGAT 1234
Qy 901 CTCTCTCCAGAGAGTAATTTCTTCATCTAAAGCCACGAC 939
Db 1235 TTCAAGCACACAAATCCTTTATAATTTAAAGACTCCAC 1273

RESULT 6
CR599894 1489 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DI025YK19 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR599894
VERSION CR599894.1 GI:50480701
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1489)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1489)
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
1. .1489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI025YK19"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 69.1%; Score 894.4; DB 6; Length 1489;
Best Local Similarity 95.2%; Pred. No. 4.9e-149;
Matches 922; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 CCAGAGATTCAAGGGCCCCGGGCTCTCTCGCTCTCTCGCGCGGAGACCCCTCGACCTCCT 60
Db 256 CCAGAGATTCAAGGGCCCCGGGCTCTCTCGCTCTCTCGCGCGGAGACCCCTCGACCTCCT 315
Qy 61 CAGAGACCGCGCTGCCGCCCGGGAAGATGGCGAGGAGCGCCACCGCTCCTCCT 120
Db 316 CAGAGACCGCGCTGCCGCCCGGGAAGATGGCGAGGAGCGCCACCGCTCCTCCT 375
Qy 121 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATCAAGGCTATGCGTTTCTGC 180
Db 376 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATCAAGGCTATGCGTTTCTGC 435
Qy 181 CCCAAAGACCAACAGTAGTACAGCAGTAGATGACCAAGAGGCTATTTTAGCCTGCAA 240
Db 436 CCCAAAGACCAACAGTAGTACAGCAGTAGATGACCAAGAGGCTATTTTAGCCTGCAA 495
Qy 241 AACCCCAAGAGACTGTTTCTTCCAGATTAGAGTGGAAGAACTGGGTGGAGTCTC 300
Db 496 AACCCCAAGAGACTGTTTCTTCCAGATTAGAGTGGAAGAACTGGGTGGAGTCTC 555

QY 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATTCGAGCTGAGATGATAGA 360
 DB 556 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATTCGAGCTGAGATGATAGA 615
 QY 361 TTTTCAATATCCGGATCAAAAATGTGACAAGAGTGTATCGGGGAAATATCGTTGTGAAGT 420
 DB 616 TTTTCAATATCCGGATCAAAAATGTGACAAGAGTGTATCGGGGAAATATCGTTGTGAAGT 675
 QY 421 TAGTGCCCATCTGACCAAGGCCCAAACTTGGAGAGGATACAGTCACTCTGGAAGTATT 480
 DB 676 TAGTGCCCATCTGACCAAGGCCCAAACTTGGAGAGGATACAGTCACTCTGGAAGTATT 735
 QY 481 AGTGGCTCAGCGATTCATCATCTGTAAGTACCTCTTCTGCTCAGTGGAACTGTGT 540
 DB 736 AGTGGCTCAGCGATTCATCATCTGTAAGTACCTCTTCTGCTCAGTGGAACTGTGT 795
 QY 541 AGAGCTACGATGTCAAGACAAGAGGAAATCCAGCTCTGTAATACACATGTTTAAAGGA 600
 DB 796 AGAGCTACGATGTCAAGACAAGAGGAAATCCAGCTCTGTAATACACATGTTTAAAGGA 855
 QY 601 TGGCATCCGTTTGTCTAGAAAATCCCAAGACTTGGCTCCCAAGCACCAAGCTCATACAC 660
 DB 856 TGGCATCCGTTTGTCTAGAAAATCCCAAGACTTGGCTCCCAAGCACCAAGCTCATACAC 915
 QY 661 AATGAATACAAAACCTGGAACCTCTGCAATTTAATCTGTTTCCAACTGGACACTGGAGA 720
 DB 916 AATGAATACAAAACCTGGAACCTCTGCAATTTAATCTGTTTCCAACTGGACACTGGAGA 975
 QY 721 ATATTCTGTGAAGCCCGCAATTTCTGTGATATCGCAGTGTCTTGGGAAAGCAATGCA 780
 DB 976 ATATTCTGTGAAGCCCGCAATTTCTGTGATATCGCAGTGTCTTGGGAAAGCAATGCA 1035
 QY 781 AGTAGATGATCTCAACATAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCCTTAGTGAT 840
 DB 1036 AGTAGATGATCTCAACATAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCCTTAGTGAT 1095
 QY 841 TTCCGTTTGTGGCTTGTGTATGCTATGCTCAGAGAAAGGCTACTTTTCAAAGAAAC 900
 DB 1096 TTCCGTTTGTGGCTTGTGTATGCTCAGAGAAAGGCTACTTTTCAAAGTAAATC 1155
 QY 901 CTCCTTCCAGAGAGTAATTTCTTCATCTAAAGCCACGACAAATGAGTGAAGTGCAGTG 960
 DB 1156 TGGCAGACCTTAATTTGGCTCTATGGCGTAGAGAGATGATGATGACAAACTATCTGAG 1215
 QY 961 GCTCAGCG 968
 DB 1216 GCTATGCG 1223

RESULT 7
 AL570767/c
 LOCUS
 DEFINITION
 clone CS0D1022YK04 3-PRIME, mRNA sequence.
 ACCESSION
 AL570767.3 GI:46236917
 VERSION
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 846)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 16, 2001 this sequence version replaced gi:31292182.
 CONTACT
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 10286.f

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?b=CS0D1022BF02NP1&c=10286.f.

FEATURES
 source
 1..846
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1022YK04"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and Ecor V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 60.0%; Score 777.6; DB 1; Length 846;
 Best Local Similarity 98.2%; Pred. No. 3.2e-128;
 Matches 780; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
 QY 173 TTTTCTGCCCCCAAGAGCCCAACAGTAGTCAAGAGTGTGAGTACCAAGAGGCTATTTTA 232
 DB 846 TTTTCTGCCCCCAAGAGCCCAACAGTAGTCAAGAGTGTGAGTACCAAGAGGCTATTTTA 787
 QY 233 GCCTGCAAAACCCCAAGAGAGACTGTTCTCCAGATTAGAGTGGAGAGAACTGGGTGCG 232
 DB 786 GCCTGCAAAACCCCAAGAGAGACTGTTCTCCAGATTAGAGTGGAGAGAACTGGGTGCG 727
 QY 293 AGTGTCTCTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATTCGAGCTGAG 352
 DB 726 AGTGTCTCTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATTCGAGCTGAG 667
 QY 353 ATGATAGATTTCAATATCCGGATCAAAATGTGACAAGAGTGTGAGTGGAGAAATTCGT 412
 DB 666 ATGATAGATTTCAATATCCGGATCAAAATGTGACAAGAGTGTGAGTGGAGAAATTCGT 607
 QY 413 TGTGAAGTTAGTGGCCCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTG 472
 DB 606 TGTGAAGTTAGTGGCCCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTG 547
 QY 473 GAAGTATTAGTGGCTCCAGAGTTCATCATGTGAAGTACCTCTTCTGCTGAGTGA 532
 DB 546 GAAGTATTAGTGGCTCCAGAGTTCATCATGTGAAGTACCTCTTCTGCTGAGTGA 487
 QY 533 ACTGTGGTAGAGCTAGGATGTCAAGACAAGAGGGAATCCAGCTCTCAATACACATGG 592
 DB 486 ACTGTGGTAGAGCTAGGATGTCAAGACAAGAGGGAATCCAGCTCTCAATACACATGG 427
 QY 593 TTTAAGGATGGCATCCGTTTGTCTAGAAAATCCAGACTTGGCTCCCAAGAGCACCACAGC 652
 DB 426 TTTAAGGATGGCATCCGTTTGTCTAGAAAATCCAGACTTGGCTCCCAAGAGCACCACAGC 367
 QY 653 TCATACACAATGAATACAAAACCTGGAACCTCTGCAATTTAATCTGTTTCCAACTGGAC 712
 DB 366 TCATACACAATGAATACAAAACCTGGAACCTCTGCAATTTAATCTGTTTCCAACTGGAC 307
 QY 713 ACTGAGAAATATTCTGTGAAGCCCGCAATTTCTGTTGGATATCGAGGTGCTCTGGGAAA 772
 DB 306 ACTGAGAAATATTCTGTGAAGCCCGCAATTTCTGTTGGATATCGAGGTGCTCTGGGAAA 247
 QY 773 CGAATGCAAGTAGATGATCTCAACATAAGTGCATCATAGCAGCCGTAGTAGTTGTGGCC 832
 DB 246 CGAATGCAAGTAGATGATCTCAACATAAGTGCATCATAGCAGCCGTAGTAGTTGTGGCC 187
 QY 833 TTAGTGATTTCCGTTTGTGGCCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCA 892
 DB 186 TTAGTGATTTCCGTTTGTGGCCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCA 127
 QY 893 AAAGAAACCTCTCTCCAGAGAGAGTAAATCTTCTCATCTTAAAGCCACGACATGAGTGAAT 952


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Db 126 AAGAAACCTCTTCCAGAGAGTAAATCTTTCATCTAAAGCCAGACAAATGAGTGAATAAT 67
Qy 953 GTGCAGTGGCTCAC 966
Db 66 GATTTCAGGCACAC 53

RESULT 8
AY610145 1184 bp mRNA linear HTC 31-JAN-2005
LOCUS AY610145
DEFINITION Sus scrofa clone Clu_80125.scr.mak.pl.Contigl, mRNA sequence.
ACCESSION AY610145
VERSION AY610145.1 GI:52351715
KEYWORDS HTC
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 1184)
AUTHORS Jorgensen,F.G., Hobolth,A., Hornshoj,H., Bendixen,C., Fredholm,M.
and Schierup,M.H.
TITLE Comparative analysis of protein coding sequences from human, mouse
and the domesticated pig
JOURNAL (er) BMC Biol. 3 (1), 2 (2005)
PUBMED 15679890
REFERENCE 2 (bases 1 to 1184)
AUTHORS Hornshoj,H., Bendixen,C. and Panitz,F.
TITLE Direct Submission
JOURNAL Submitted (28-APR-2004) Animal Breeding and Genetics, Danish
Institute of Agricultural Sciences, Research Centre Foulum, Postbox
50, Tjele DK-8930, Denmark
FEATURES
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1. .1184
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="Clu_80125.scr.mak.pl.Contigl"
misc_feature
1. .1184
/notes="similar to AF255910.1 Homo sapiens vascular
endothelial junction-associated molecule"

ORIGIN
Query Match 59.5%; Score 770.8; DB 6; Length 1184;
Best Local Similarity 88.2%; Pred. No. 4.9e-127;
Matches 836; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Qy 17 CCCCCGGCTCTCGCTCCGCGCCGGGAGCCCTCGACCTCTCTCAGAGCAGCGGCTGC 76
Db 110 CCGCGGCTCCAGCGGTCCGCGCCAGACCCCTCGGCTTTGAGGAGCGCCAGCTCC 169
Qy 77 CGCCCCGGGAAGTGGCGAGGAGGCGCCACCGCTCTCTCTGCTGCTCGCTAC 136
Db 170 GACCCCGGAAGTGGCGAGGAGGCGCCACCGCTCTCTGCTGCTCGCTAC 229
Qy 137 CTGTGTGCTCGCTCGGCTATCATAGAGCTATGGGTTTTCGCCCAAGAACCAACAA 196
Db 230 CTGTGTGCTCGCTCGGCTATCATAGAGCTGTGGATTCTGTGACCCCAAGATCATCAC 289
Qy 197 GTAGTACAGAGTAGATACCAAGAGCTATTTAGCTGCGCAAAACCCCAAGAGACT 256
Db 290 GTAGTACAGAAATAGAGTATCAAGAGGTATTTTAGCTGTAAATACCCCAAGAGACC 349
Qy 257 GTTTCTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTCTTTGTCTACTACAA 316
Db 350 GTGTCTCTCCAGATTAGATGAAGAACTGGGCGGGGTATCTCTTTGTCTACTACAA 409
Qy 317 CAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCGGATC 376
Db 410 CAGGCTCTTCAAGGTGCTTTTAAAGATCGAGCTGAGCTGATAGATTTTCAGCATACGGATC 469
Qy 377 AAAAAATGTGACAGAAGTATGTCGGGGAAATATCGTTGTGAAGTAGTGTGCCCCATCTGAG 436
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Db 470 AAAAAATGTTCAAGAAATGATGCGGGAAGTATCGTTGTGAAATTAGTGTCTCCATCCGAA 529
Qy 437 CAAGGCCAARACCTTGAAGAGGATACAGTCACTCTGGAAGTATTATTAGTGGCTCCAGCAGATT 496
Db 530 CAAGGTCAAAACCTGGCAGAGGATACGGTCACTTGGAGATATTAGTGGCTCCAGCAGATT 589
Qy 497 CCATCATGTGAAGTACCCCTCTTCTGCTCTGAGTGGAACTGTGGTAGAGTACGATGTCAA 556
Db 590 CCATCATGTGAAGTACCCAGTTCTGCTCTGAGCGGCACCTACGGTAGAGTACGATGTCAA 649
Qy 557 GACAAAGAAAGGAAATCAGCTCTCTGAATACATCATGTTTAAAGATGGCATCCGTTTGCTA 616
Db 650 GACAAAGAAAGCAATCCAGCTCCGGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTA 709
Qy 617 GAAAATCCAGAGCTTGGCTCCCAAGCACCACCAAGCTCATACACAATGATAAAACT 676
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LOCUS BX375908
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ACCESSION BX375908
VERSION BX375908.2 GI:46573233
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 864)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30448456.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10286.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DC019CB12NP1&c=10286.f.
Location/Qualifiers
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DN994893	772 bp	mRNA	linear	EST 17-MAY-2005
LOCUS	TC108217	Human adult whole brain, large insert, pCMV expression		
DEFINITION	Library Homo sapiens cDNA clone TC108217 5' similar to Homo sapiens junctional adhesion molecule 2 (JAM2), mRNA sequence.			
ACCESSION	DN994893			
VERSION	DN994893.1	GI:66254724		
KEYWORDS	EST.			
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ORGANISM	Homo sapiens			
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REFERENCE	1 (bases 1 to 772)			
AUTHORS	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.			
TITLE	High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts			
JOURNAL	Unpublished (2005)			
COMMENT	Contact: Kovacs, KF High Throughput cDNA Cloning Origene Technologies, Inc. (www.origene.com) 6 Taft Court, Suite 100, Rockville, MD 20850, USA Tel: 301 340 3188 Fax: 301 340 8606 Email: CDNA@origene.com This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc. Please contact Origene for access. Origene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850 Tel: (301) 340-3188 http://www.origene.com Seq primer: pCMV6 5prime forward vector primer, Origene Technologies Inc.			
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QY	121	GCTGCTGCTGCGCTACCTGCTGCTGCTGCTATCATAGCCCTATGCGTTTCTGC	180	
Db	174	GCTGCTGCTGCGCTACCTGCTGCTGCTGCTATCATAGCCCTATGCGTTTCTGC	233	
QY	181	CCCAAGACCAACAGTAGTCACAGCAGTAGTAGTACCAAGAGGCTATTTAGCCTGCA	240	

DN994893	772 bp	mRNA	linear	EST 17-MAY-2005
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ACCESSION	DN994893			
VERSION	DN994893.1	GI:66254724		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
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REFERENCE	1 (bases 1 to 772)			
AUTHORS	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.			
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JOURNAL	Unpublished (2005)			
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ORIGIN				
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QY	121	GCTGCTGCTGCGCTACCTGCTGCTGCTGCTATCATAGCCCTATGCGTTTCTGC	180	
Db	174	GCTGCTGCTGCGCTACCTGCTGCTGCTGCTATCATAGCCCTATGCGTTTCTGC	233	
QY	181	CCCAAGACCAACAGTAGTCACAGCAGTAGTAGTACCAAGAGGCTATTTAGCCTGCA	240	

DN994893	772 bp	mRNA	linear	EST 17-MAY-2005
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ACCESSION	DN994893			
VERSION	DN994893.1	GI:66254724		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
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REFERENCE	1 (bases 1 to 772)			
AUTHORS	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.			
TITLE	High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts			
JOURNAL	Unpublished (2005)			
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Db	174	GCTGCTGCTGCGCTACCTGCTGCTGCTGCTATCATAGCCCTATGCGTTTCTGC	233	
QY	181	CCCAAGACCAACAGTAGTCACAGCAGTAGTAGTACCAAGAGGCTATTTAGCCTGCA	240	

DN994893	772 bp	mRNA	linear	EST 17-MAY-2005
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VERSION	DN994893.1	GI:66254724		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
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REFERENCE	1 (bases 1 to 772)			
AUTHORS	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.			
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Db	174	GCTGCTGCTGCGCTACCTGCTGCTGCTGCTATCATAGCCCTATGCGTTTCTGC	233	
QY	181	CCCAAGACCAACAGTAGTCACAGCAGTAGTAGTACCAAGAGGCTATTTAGCCTGCA	240	

DN994893	772 bp	mRNA	linear	EST 17-MAY-2005
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ACCESSION	DN994893			
VERSION	DN994893.1	GI:66254724		
KEYWORDS	EST.			
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ORGANISM	Homo sapiens			
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REFERENCE	1 (bases 1 to 772)			
AUTHORS	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.			
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REFERENCE	1 (bases 1 to 772)			
AUTHORS	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.			
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REFERENCE	1 (bases 1 to 772)			
AUTHORS	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.			
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Db 654 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATACAC 713
Qy 661 AATGAATACAAAACCTGGAACTCTGCAATTTAACTACTGTTTCCAAACTGGACACTGGAG 719
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RESULT 11
BX463390/c 984 bp mRNA linear EST 05-MAY-2004
LOCUS BX463390 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN001YD24 3-PRIME, mRNA sequence.
```

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ACCESSION BX463390
VERSION BX463390.2 GI:47055037
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31025510.
```

```
CONTACT Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 10286.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DN001YD24&c=10286.f.
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FEATURES
Location/Qualifiers
1. 984
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/notes="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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ORIGIN
Query Match 54.2%; Score 702.2; DB 4; Length 984;
Best Local Similarity 96.8%; Pred. No. 8.1e-115;
Matches 721; Conservative 6; Mismatches 14; Indels 4; Gaps 1;
Qy 222 AGGCTATTTAGCCTGCAAAACCCCAAGAAAGACTGTTTCTCCAGATTAGAGTGGAAAGA 281
Db 978 AGRGCTTTTAGCCTGCAAAACCCCAAGAAAGACTGTTTCTCCAGATTAGAGTGGAAAGA 919
Qy 282 AACTGGGTCCGAGTGTCTCCCTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAA 341
Db 918 AACTGGGTCCGAGTGTCTCCCTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAA 859
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Db 858 ATCGAGCTGAGATGATAGATTTCAATATCCGGATCAAAATATGTCAGAAAGTATGCGG 799
Qy 402 GGAATAATCGTTGTGAAGTTAGTGCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATA 461
Db 798 GGAATAATCGTTGTGAAGTTAGTGCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATA 739
Qy 462 CAGTCACTCTGGAAGTATTAGTGGCTCAGCAGTTCATCATGTGAAGTACCTCTTCTG 521
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Qy 522 CTCTGAGTGGAACTGTGCTAGAGCTACGATGTCAAGCAAAAGAGGGAATCCAGCTCCTG 581
Db 678 CTCTGAGTGGAACTGTGCTAGAGCTACGATGTCAAGCAAAAGAGGGAATCCAGCTCCTG 619
Qy 582 AATACACATGGTTTAAAGATGGCATCCGTTTGTGTAGAAAATCCAGACTTGGCTCCCAA 641
Db 618 AATACACATGGTTTAAAGATGGCATCCGTTTGTGTAGAAAATCCAGACTTGGCTCCCAA 559
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Db 498 CCAAACTGGACACTGGAGAAATATTCCTGTGAAGCCCGCAATTCCTGTGGATATCGCAGGT 439
Qy 762 GTCTCGGAAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAG 821
Db 438 GTCTCGGAAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAG 383
Qy 822 TAGTGTGGCTTAGTGAATTTCCGTTTGGCCCTTGGTGTATGTATGCTCAGAGGAAAG 881
Db 382 TAGTGTGGCTTAGTGAATTTCCGTTTGGCCCTTGGTGTATGTATGCTCAGAGGAAAG 323
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Db 322 GCTACTTTTCAAAAGAAACCTCTTCCAGAGAGTAAATTTCTTCACTTAAAGCCAGACAA 263
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Db 262 TGAGTGAATAATGTATDTCAGGACAC 238
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RESULT 12
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DEFINITION 1700600180567 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN347901
VERSION CN347901.1 GI:47347835
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
AUTHORS Brandenberger R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 716 Std Error: 0.00.
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mitogen-treated hES cell line H7"
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notes="oligo dt primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic and mitogens."

ORIGIN
Query Match 53.2%; Score 688.6; DB 8; Length 716;
Best Local Similarity 99.6%; Pred. No. 2.1e-112;
Matches 701; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DB 64 GCGCCCCGGGAGATGGCGAGAGAGCGCCACCGCTCTCTCTCTCTCTCTCTCTCTCTCT 123
QY 135 ACCTGTGTGGCTGGCTATCATAGGCTCTATGGCTTTCTGCCCCCAAGAGACAAC 194
DB 124 ACCTGTGTGGCTGGCTATCATAGGCTATGGCTTTCTGCCCCCAAGAGACAAC 183
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DB 184 AGTAGTCAAGAGTAGAGTACCAAGAGCTATTTTAGCCTGCACAAACCCCAAGAGA 243
QY 255 CTGTTTCTCCAGATTAGAGTGAAGAACTGGTGGAGTGCTCTCTTGTCTACTATC 314
DB 244 CTGTTTCTCCAGATTAGAGTGAAGAACTGGTGGAGTGCTCTCTTGTCTACTATC 303
QY 315 ACAGACTCTTCAAGTGATTTTAAATAACGAGCTGAGATGATAGATTTCAATATCCGGA 374
DB 304 ACAGACTCTTCAAGTGATTTTAAATAACGAGCTGAGATGATAGATTTCAATATCCGGA 363
QY 375 TCAAAATGTGAAGAAGTGTGCGGGAAATATCGTTGTGAAGTTAGTGCCCACTCTG 434
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QY 495 TTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGGTGGAGTACAGATGTC 554
DB 484 TTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGGTGGAGTACAGATGTC 543
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RESULT 13
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DEFINITION IMAGE:30334613 5', mRNA sequence.
ACCESSION CB992775
VERSION CB992775.1 GI:30287295
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 811)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsbbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM355 row: c column: 06
High quality sequence stop: 673.
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directionally cloned using primer
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size 2.3 kb and normalized to 50x. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
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QY 1 CCCAAGATTCAAGGGCCCCCGGCTCTCTGCGCTCTCTGCGGGGACCTCGACCTCT 60
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QY 61 CAGAGAGCCGCTGCGGGCCCCCGGAGAGATGGCGAGGAGAGCCGCCACCGCTCTCT 120
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DT809612
 LOCUS
 DEFINITION
 DB0164.CR.B12 GC_BGC-16 Bos taurus mRNA linear EST 12-OCT-2005
 mRNA sequence.
 DB09612
 DB09612.1 GI:75741488
 EST.
 Bos taurus (cattle)
 Bos taurus
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 830)
 Moore,S., Alexander,L., Brownstein,M., Guan,L., Lobo,S., Meng,Y.,
 Tanaguchi,M., Wang,Z., Yu,J., Prange,C., Schreiber,K., Shenmen,C.,
 Wagner,L., Bala,M., Barbasuk,S., Barber,S., Babakiaiff,R.,
 Beland,J., Chun,E., Del Rio,L., Gibson,S., Hanson,R.,
 Kirkpatrick,R., Liu,J., Matsuo,C., Mayo,M., Santos,R.R., Stott,J.,
 Tsai,M., Wong,D., Siddiqui,A., Holt,R., Jones,S.J. and Marra,M.A.
 Bovine Genome Sequencing Program: Full-length cDNA Sequencing
 Unpublished (2005)
 Contact: Robert Kirkpatrick
 Canada's Michael Smith Genome Sciences Centre
 BC Cancer Agency
 Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
 Canada, V5Z 4S6
 Tel: 1-604-707-5900 x5406
 Fax: 1-604-876-3561
 Email: robertk@bcgsc.ca
 Plate: LB0164 row: B column: 12
 High quality sequence stop: 830.
 Location/Qualifiers
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 Query Match 51.9%; Score 672.6; DB 10; Length 830;
 Best Local Similarity 88.9%; Pred. No. 1.5e-109;
 Matches 738; Conservative 0; Mismatches 90; Indels 2; Gaps 1;
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 Db 1 GGACCTTCAGCTCCGAGGAGGCCAGCTCCCGACCCCAACGAAGATGGCAAGGAGG 60
 QY 103 CCGCCACCGCTCCTCCTGCTGCTGCTGCGGTACTCTGCTGCTGCCCTCGGCTATCA 162
 Db 61 CCGCCACCACTCCTGCTTCTTCGCTGGGTACTCTGGTGGTGGCTGGCTGACTATCA 120
 QY 163 GGCTATGGGTTTTCGCCCAAAAGACCAACAAGTAGTCACACGCTAGAGTACCAAGA 222
 Db 121 GGCTATGGATTCTCTGCCTCAAAAGATCATCAAGTGGTCACACCAATAGATATCA 180
 QY 223 GGCTATTTTAGCCTGCAAAACCCCAAGAGACTGTTTCTCCAGATTAGAGTGAAGAA 282
 Db 181 GGCTATTTTAGCCTGTAATACCCCAAGAGACCGTTTCTCCAGATTGGAGTGGAA 240
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 Db 241 ATGGGGCGGGTGTTCCTTTGCTACTATCAACAGGCTCTTCAAGTGAATTTAGGA 300
 QY 343 TCGAGCTGAGATGATGATTTCAATATCCGGATCAAAAATGTGCAAGAAAGTGTATCG 402

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2006, 20:15:30 ; Search time 7778 Seconds
(without alignments)
10646.941 Million cell updates/sec

Title: US-10-785-221-8
Perfect score: 1295
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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 1

Total number of hits satisfying chosen parameters: 12730834

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :

- GenEmbl.*
1: gb_env.*
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4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_ats.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1295	100.0	1295	2	BD173237
6	1295	100.0	1295	2	BD175271
7	1295	100.0	1295	2	CQ957874
8	1295	100.0	1295	2	CQ957936
9	1295	100.0	1295	2	AR216160
10	1295	100.0	1295	2	AR410649
11	1295	100.0	1295	2	AR439013
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13	1295	100.0	1295	2	AR527019
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16	1295	100.0	1295	2	AR604344
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18	1295	100.0	1295	2	AR613595

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C 94	61	4.7	110000	5	BA000041_03	Continuation (4 of	C 167	56	4.3	193559	12	AC137500	AC137500 Homo sapi
C 95	61	4.7	113388	5	AL773544	Human DNA	C 168	56	4.3	194029	12	AC135059	AC135059 Homo sapi
96	61	4.7	119255	12	AC169884	Macaca mu	C 169	56	4.3	198582	5	AC005291	AC005291 Homo sapi
97	61	4.7	121659	5	CR388229	Human DNA	C 170	56	4.3	199102	5	AC129507	AC129507 Homo sapi
98	61	4.7	124255	5	AC125435	Homo sapi	C 171	56	4.3	205463	5	AL355388	AL355388 Human DNA
99	61	4.7	132600	12	AL355675	Homo sapi	C 172	56	4.3	208396	5	AC003101	AC003101 Homo sapi
C 100	61	4.7	141213	5	AL145982	Pan trogl	C 173	56	4.3	208609	5	HS389A20	293442 Human DNA
101	61	4.7	143039	5	AC016559	Homo sapi	C 174	56	4.3	297898	5	AC004526	AC004526 Homo sapi
102	61	4.7	154859	5	AC012596	Homo sapi	C 175	55	4.2	10988	5	AL592286	AL592286 Human DNA
103	61	4.7	163318	5	AC114772	Homo sapi	C 176	55	4.2	59638	12	AP000630	AP000630 Homo sapi
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C 106	61	4.7	167942	5	AC021654	Homo sapi	C 179	55	4.2	195950	5	AC012003	AC012003 Homo sapi
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124	60	4.6	698	7	BS578243	G591P6094	C 197	54	4.2	191950	12	AC022307	AC022307 Homo sapi
125	60	4.6	37934	5	AC151807	Homo sapi	C 198	53	4.1	710	7	BS641645	BS641645 S215P6153
126	60	4.6	37971	5	AC151808	Homo sapi	C 199	53	4.1	6644	2	AX060290	AX060290 Sequence
C 127	60	4.6	139918	12	AC146345	Pan trogl	C 200	53	4.1	38324	5	HSB4T2	215025 Homo sapien
C 128	60	4.6	154413	5	AC021989	Homo sapi	C 201	53	4.1	81631	5	HS745114	AL033532 Human DNA
C 129	60	4.6	183974	5	AC093421	Homo sapi	C 202	53	4.1	128228	5	AL355598	AL355598 Human DNA
C 130	58	4.5	45291	5	AL445605	Human DNA	C 203	53	4.1	144228	5	AC068599	AC068599 Homo sapi
C 131	58	4.5	147924	12	AC036186	Homo sapi	C 204	53	4.1	147489	12	AC139366	AC139366 Homo sapi
C 132	58	4.5	163978	5	AC022724	Homo sapi	C 205	53	4.1	150636	12	AC027529	AC027529 Homo sapi
C 133	58	4.5	164403	5	AC027097	Homo sapi	C 206	53	4.1	159123	5	AC007739	AC007739 Homo sapi
C 134	58	4.5	172185	12	AC068072	Homo sapi	C 207	53	4.1	167732	5	AC091092	AC091092 Papio anu
C 135	58	4.5	227139	12	AP001780	Homo sapi	C 208	53	4.1	170639	5	AL391065	AL391065 Human DNA
C 136	57	4.4	167208	12	AC034190	Homo sapi	C 209	53	4.1	173375	12	AC044815	AC044815 Homo sapi
C 137	57	4.4	173534	5	AL007920	Homo sapi	C 210	53	4.1	174715	12	AC026587	AC026587 Homo sapi
C 138	57	4.4	174196	5	AL353140	Human DNA	C 211	53	4.1	178058	5	AC009139	AC009139 Homo sapi
C 139	57	4.4	207841	12	AC072019	Homo sapi	C 212	53	4.1	189326	5	AL355490	AL355490 Human DNA
C 140	56	4.3	723	7	BS624808	S216P6231	C 213	53	4.1	190803	5	AL355490	AL355490 Human DNA
C 141	56	4.3	46213	5	AC005387	Homo sapi	C 214	53	4.1	204230	7	BS633048	BS633048 Homo sapi
C 142	56	4.3	46504	12	AC009100	Homo sapi	C 215	52	4.0	631	7	BS633048	BS633048 Homo sapi
C 143	56	4.3	57304	5	AC004802	Homo sapi	C 216	52	4.0	709	7	BS602665	BS602665 S216P6152
C 144	56	4.3	81674	5	HS722E9	Human DNA	C 217	52	4.0	741	7	BS549134	BS549134 S215P6585
C 145	56	4.3	82995	5	AC005183	Homo sapi	C 218	52	4.0	850	7	BS513965	BS513965 rgg02h03
C 146	56	4.3	94420	5	AC116493	Homo sapi	C 219	52	4.0	31766	2	AX354725	AX354725 Sequence
C 147	56	4.3	104395	5	AC092469	Homo sapi	C 220	52	4.0	55417	12	AL390915	AL390915 Homo sapi
C 148	56	4.3	110000	12	AC140129_1	Continuation (2 of	C 221	52	4.0	62319	12	AC132200	AC132200 Homo sapi
C 149	56	4.3	125973	12	AC010353	Homo sapi	C 222	52	4.0	62319	12	AC132200	AC132200 Homo sapi
C 150	56	4.3	135005	5	HS860F19	Human DNA	C 223	52	4.0	65608	12	AC132197	AC132197 Homo sapi
C 151	56	4.3	137831	5	AC010335	Homo sapi	C 224	52	4.0	68446	12	AC131939	AC131939 Homo sapi
C 152	56	4.3	140126	5	AC141424	Homo sapi	C 225	52	4.0	84591	5	AC096655	AC096655 Homo sapi
C 153	56	4.3	143516	5	AC083783	Homo sapi	C 226	52	4.0	88883	5	AC107911	AC107911 Homo sapi
C 154	56	4.3	146500	5	AC099480	Homo sapi	C 227	52	4.0	92339	5	AL365362	AL365362 Human DNA
C 155	56	4.3	150636	12	AC027529	Homo sapi	C 228	52	4.0	95692	12	AC015534	AC015534 Homo sapi
C 156	56	4.3	152161	5	AL359074	Human DNA	C 229	52	4.0	104435	5	AC016292	AC016292 Homo sapi
C 157	56	4.3	160515	5	AC135724	Homo sapi	C 230	52	4.0	104485	5	AC069439	AC069439 Homo sapi
C 158	56	4.3	169650	5	CNS0000U	Human chr	C 231	52	4.0	106373	5	HS128017	AC031654 Human DNA
C 159	56	4.3	170536	5	AC093914	Homo sapi	C 232	52	4.0	107462	12	AC068208	AC068208 Homo sapi
C 160	56	4.3	174545	5	AC103801	Homo sapi	C 233	52	4.0	111500	5	AC121344	AC121344 Homo sapi
C 161	56	4.3	179139	12	AC022484	Homo sapi	C 234	52	4.0	119883	5	AL929554	AL929554 Human DNA
C 162	56	4.3	179452	5	AC116010	Homo sapi	C 235	52	4.0	122839	5	AL161898	AL161898 Human DNA
C 163	56	4.3	180718	5	AL596087	Human DNA	C 236	52	4.0	129553	5	AC013448	AC013448 Homo sapi
C 164	56	4.3	189271	5	AL138752	Human DNA	C 237	52	4.0	137072	12	AL353893	AL353893 Homo sapi

238	52	4.0	138839	5	HUAC002400	AC002400 Human Chr	c 311	51	3.9	92946	12	AC140020_3	Continuation (4 of
239	52	4.0	144000	5	AC123764	AC123764 Homo sapi	312	51	3.9	97868	5	AC090425	AC005425 Homo sapi
240	52	4.0	144515	5	AC005831	AC005831 Homo sapi	313	51	3.9	102112	5	AC005231	AC005231 Homo sapi
241	52	4.0	146515	12	AC146981	AC146981 Homo sapi	314	51	3.9	106277	5	AC068792	AC068792 Homo sapi
242	52	4.0	146810	5	HS179115A	Z95240 Human DNA s	315	51	3.9	108523	5	AC000159	AC000159 Homo sapi
243	52	4.0	150481	5	HS061140A	AL121753 Human DNA	c 316	51	3.9	110000	12	AC011600_2	Continuation (3 of
244	52	4.0	150522	5	AC008870	AC008870 Homo sapi	317	51	3.9	110000	12	AC125619_0	AC125619 Homo sapi
245	52	4.0	151133	5	AC013355	AC013355 Homo sapi	318	51	3.9	110000	12	AC139803_1	Continuation (2 of
246	52	4.0	157173	5	AC009501	AC009501 Homo sapi	c 319	51	3.9	116882	5	AL512785	AL512785 Human DNA
247	52	4.0	157871	5	AC104365	AC104365 Homo sapi	320	51	3.9	119151	12	AP000655	AP000655 Homo sapi
248	52	4.0	158090	5	AC006353	AC006353 Homo sapi	321	51	3.9	120628	5	AC012153	AC012153 Homo sapi
249	52	4.0	158588	12	AC170814	AC170814 Macaca mu	322	51	3.9	124015	5	AC006509	AC006509 Homo sapi
250	52	4.0	159692	5	AC016727	AC016727 Homo sapi	c 323	51	3.9	127925	5	AC135593	AC135593 Homo sapi
251	52	4.0	161164	12	AC022278	AC022278 Homo sapi	c 324	51	3.9	128117	5	AC004000	AC004000 Human PAC
252	52	4.0	161416	12	AC026857	AC026857 Homo sapi	c 325	51	3.9	134459	12	AC026632	AC026632 Homo sapi
253	52	4.0	162692	12	AC016171	AC016171 Homo sapi	c 326	51	3.9	135237	12	AP000814	AP000814 Homo sapi
254	52	4.0	163772	5	AC093165	AC093165 Homo sapi	327	51	3.9	137541	5	AC079068	AC079068 Homo sapi
255	52	4.0	163805	5	AC010956	AC010956 Homo sapi	328	51	3.9	141899	5	AC006334	AC006334 Homo sapi
256	52	4.0	164125	5	AC018693	AC018693 Homo sapi	329	51	3.9	142712	5	AC112175	AC112175 Homo sapi
257	52	4.0	164855	12	AC063942	AC063942 Homo sapi	c 330	51	3.9	144432	12	AF276983	AF276983 Homo sapi
258	52	4.0	165003	12	AC021592	AC021592 Homo sapi	331	51	3.9	146174	12	AC138823	AC138823 Homo sapi
259	52	4.0	166357	5	AC091559	AC091559 Homo sapi	c 332	51	3.9	146469	12	AL355991	AL355991 Homo sapi
260	52	4.0	169598	5	AC087650	AC087650 Homo sapi	c 333	51	3.9	147123	12	AC027030	AC027030 Homo sapi
261	52	4.0	169862	12	AC025530	AC025530 Homo sapi	c 334	51	3.9	149915	12	AC021637	AC021637 Homo sapi
262	52	4.0	171941	12	AC026531	AC026531 Homo sapi	c 335	51	3.9	150129	12	AC023816	AC023816 Homo sapi
263	52	4.0	172346	12	AC016349	AC016349 Homo sapi	336	51	3.9	151970	12	AC040905	AC040905 Homo sapi
264	52	4.0	177710	5	AL592294	AL592294 Human DNA	337	51	3.9	152395	5	AL161907	AL161907 Human DNA
265	52	4.0	177965	12	AC151389	AC151389 Callithrix	338	51	3.9	154376	5	AC137803	AC137803 Homo sapi
266	52	4.0	178151	5	AL136123	AL136123 Human DNA	c 339	51	3.9	154455	12	AC021844	AC021844 Homo sapi
267	52	4.0	181571	5	BS000206	BS000206 Pan trogl	c 340	51	3.9	155017	12	AC068583	AC068583 Homo sapi
268	52	4.0	183293	12	AC148883	AC148883 Pan trogl	c 341	51	3.9	155394	12	AC092328	AC092328 Homo sapi
269	52	4.0	185376	5	AC005096	AC005096 Homo sapi	342	51	3.9	155828	12	AC142084	AC142084 Homo sapi
270	52	4.0	189767	5	AL137145	AL137145 Human DNA	343	51	3.9	157809	5	AC146394	AC146394 Pan trogl
271	52	4.0	190194	5	AC068025	AC068025 Homo sapi	344	51	3.9	158351	5	BS000090	BS000090 Pan trogl
272	52	4.0	190863	12	AC173750	AC173750 Macaca mu	345	51	3.9	159153	5	AC020757	AC020757 Homo sapi
273	52	4.0	193047	5	CNS00000Q	AL049874 Human chr	c 346	51	3.9	159347	12	AC138971	AC138971 Homo sapi
274	52	4.0	193316	5	AC163761	AC163761 Pan trogl	c 347	51	3.9	160371	12	AC068793	AC068793 Homo sapi
275	52	4.0	194244	12	BX322553	BX322553 Homo sapi	c 348	51	3.9	162189	5	AL592295	AL592295 Human DNA
276	52	4.0	195161	5	AC013464	AC013464 Homo sapi	349	51	3.9	163427	5	AC009053	AC009053 Homo sapi
277	52	4.0	195773	12	AC073134	AC073134 Homo sapi	c 350	51	3.9	163621	5	AC112129	AC112129 Homo sapi
278	52	4.0	196603	5	AC087721	AC087721 Homo sapi	c 351	51	3.9	164168	5	AL135927	AL135927 Human DNA
279	52	4.0	197652	5	AC012074	AC012074 Homo sapi	352	51	3.9	164179	5	AC007227	AC007227 Homo sapi
280	52	4.0	203050	12	HS44N10	Z97197 Homo sapien	353	51	3.9	165672	12	AC111324	AC111324 Homo sapi
281	52	4.0	203521	5	BS000205	BS000205 Pan trogl	c 354	51	3.9	166224	12	AC137792	AC137792 Homo sapi
282	52	4.0	206204	12	AC161277	AC161277 Pan trogl	c 355	51	3.9	166532	12	AC022279	AC022279 Homo sapi
283	52	4.0	207822	12	AC109321	AC109321 Homo sapi	356	51	3.9	166774	5	AC005225	AC005225 Homo sapi
284	52	4.0	210204	5	AC007954	AC007954 Homo sapi	357	51	3.9	168395	12	AC092678	AC092678 Homo sapi
285	52	4.0	210672	12	HS179115	Z84464 Homo sapien	c 358	51	3.9	169074	12	AC148830	AC148830 Pan trogl
286	52	4.0	217807	12	AC079469	AC079469 Homo sapi	c 359	51	3.9	169259	5	AP006288	AP006288 Homo sapi
287	52	4.0	231464	5	AF111168	AF111168 Homo sapi	360	51	3.9	170141	12	AL611928	AL611928 Homo sapi
288	52	4.0	349980	2	AX711180	AX711180 Sequence	c 361	51	3.9	171148	5	AL359195	AL359195 Human DNA
289	51	3.9	816	7	BV472208	BV472208 GS91P6167	c 362	51	3.9	171480	5	AC016542	AC016542 Homo sapi
290	51	3.9	825	7	BV615512	BV615512 S21P6130	363	51	3.9	171656	5	AL136380	AL136380 Human DNA
291	51	3.9	891	7	BV462699	BV462699 rop03h09.	c 364	51	3.9	171793	5	AP001187	AP001187 Homo sapi
292	51	3.9	6277	2	CQ881062	CQ881062 Sequence	365	51	3.9	172123	5	AC060809	AC060809 Homo sapi
293	51	3.9	17001	5	AP005669	AP005669 Homo sapi	c 366	51	3.9	172276	5	AC139795	AC139795 Homo sapi
294	51	3.9	22038	5	HSPMPG2	AF141309 Homo sapi	367	51	3.9	172571	12	AC027484	AC027484 Homo sapi
295	51	3.9	22845	5	HSA309943	AX039943 Homo sapi	368	51	3.9	172579	5	AL596385	AL596385 Human DNA
296	51	3.9	39198	2	AX078379	AX078379 Sequence	c 369	51	3.9	172600	5	AL359644	AL359644 Human DNA
297	51	3.9	40223	5	AC119403	AC119403 Homo sapi	370	51	3.9	172615	12	AC139765	AC139765 Homo sapi
298	51	3.9	40927	5	AV388614	AV388614 Homo sapi	c 371	51	3.9	172790	12	AC126184	AC126184 Homo sapi
299	51	3.9	41303	5	AC1353602	AC1353602 Human DNA	c 372	51	3.9	173091	12	AC122689	AC122689 Homo sapi
300	51	3.9	43739	5	AC144573	AC144573 Homo sapi	c 373	51	3.9	173525	12	AC067893	AC067893 Homo sapi
301	51	3.9	55442	5	BX119919	BX119919 Human DNA	c 374	51	3.9	173637	5	AC046185	AC046185 Homo sapi
302	51	3.9	60163	5	AC012018	AC012018 Homo sapi	c 375	51	3.9	174195	12	AC072035	AC072035 Homo sapi
303	51	3.9	66363	12	AC106828	AC106828 Homo sapi	c 376	51	3.9	174923	12	AC169789	AC169789 Macaca mu
304	51	3.9	66363	12	AC106828	AC106828 Homo sapi	c 377	51	3.9	176002	12	AC139262	AC139262 Homo sapi
305	51	3.9	70946	5	AL161614	AL161614 Human DNA	c 378	51	3.9	176798	12	AC010944	AC010944 Homo sapi
306	51	3.9	73454	5	AL136988	AL136988 Human DNA	379	51	3.9	177479	5	AC009153	AC009153 Homo sapi
307	51	3.9	76447	5	AC116354	AC116354 Homo sapi	c 380	51	3.9	178100	12	AP001558	AP001558 Homo sapi
308	51	3.9	84780	5	AC005885	AC005885 Homo sapi	c 381	51	3.9	178348	5	AP000501	AP000501 Homo sapi
309	51	3.9	89171	5	AC008404	AC008404 Homo sapi	c 382	51	3.9	178651	5	CNS05TDY	AL358275 Human chr
310	51	3.9	89642	12	AC005136	AC005136 Homo sapi	383	51	3.9	178796	12	AC020667	AC020667 Homo sapi

C 384	51	3.9	179509	5	AC113554	AC113554 Homo sapi	C 457	50	3.9	18722	2	DD211105	DD211105 EXPRESSIO
385	51	3.9	182118	5	AL356287	AL356287 Human DNA	C 458	50	3.9	18722	2	AX828196	AX828196 Sequence
386	51	3.9	182175	5	AC138819	AC138819 Homo sapi	C 459	50	3.9	13501	5	BX649378	BX649378 Human DNA
C 387	51	3.9	182847	12	AC126229	AC126229 Papio anu	C 460	50	3.9	32887	5	AC118535	AC118535 Homo sapi
C 388	51	3.9	184313	5	AL445584	AL445584 Human DNA	C 461	50	3.9	33112	2	AP700267	AP700267 Sequence
C 389	51	3.9	184511	5	AC009032	AC009032 Homo sapi	C 462	50	3.9	34029	2	AR000531	AR000531 Homo sapi
C 390	51	3.9	184595	5	AC079465	AC079465 Homo sapi	C 463	50	3.9	34565	5	AC003064	AC003064 Homo sapi
391	51	3.9	184649	12	AC025185	AC025185 Homo sapi	C 464	50	3.9	36246	5	AC092316	AC092316 Homo sapi
C 392	51	3.9	185796	12	AC138857	AC138857 Homo sapi	C 465	50	3.9	37225	5	AC005954	AC005954 Homo sapi
C 393	51	3.9	185986	12	AC140123	AC140123 Homo sapi	C 466	50	3.9	37599	5	AP000532	AP000532 Homo sapi
C 394	51	3.9	186448	12	AC034129	AC034129 Homo sapi	C 467	50	3.9	38140	5	AC002991	AC002991 Homo sapi
C 395	51	3.9	186759	5	AL645608	AL645608 Human DNA	C 468	50	3.9	38147	5	AC087539	AC087539 Homo sapi
C 396	51	3.9	187005	5	BX664735	BX664735 Human DNA	C 469	50	3.9	38149	5	AC022154	AC022154 Homo sapi
397	51	3.9	187483	12	AC090316	AC090316 Homo sapi	C 470	50	3.9	39263	5	AF129077	AF129077 Homo sapi
C 398	51	3.9	188639	5	AC011236	AC011236 Homo sapi	C 471	50	3.9	40162	5	US8675	US8675 Homo sapien
C 399	51	3.9	188897	12	AC140146	AC140146 Homo sapi	C 472	50	3.9	40986	5	BX640514	BX640514 Human DNA
400	51	3.9	189076	12	AC023788	AC023788 Homo sapi	C 473	50	3.9	40992	5	AC002471	AC002471 Homo sapi
C 401	51	3.9	190430	12	AC118987	AC118987 Pan trogl	C 474	50	3.9	41144	5	AC174062	AC174062 Homo sapi
C 402	51	3.9	190517	5	CNS01DX4	AL139022 Human chr	C 475	50	3.9	41378	5	AC005381	AC005381 Homo sapi
C 403	51	3.9	190544	5	AC005768	AC005768 Homo sapi	C 476	50	3.9	41958	5	AC005374	AC005374 Homo sapi
C 404	51	3.9	190874	12	AC139830	AC139830 Homo sapi	C 477	50	3.9	42027	5	AC106042	AC106042 Homo sapi
405	51	3.9	191746	5	AC079325	AC079325 Homo sapi	C 478	50	3.9	42104	5	AY206865	AY206865 Homo sapi
C 406	51	3.9	192525	12	AC012475	AC012475 Homo sapi	C 479	50	3.9	42303	5	AL355133	AL355133 Human DNA
C 407	51	3.9	192993	12	AC145108	AC145108 Homo sapi	C 480	50	3.9	42380	5	AL672237	AL672237 Human DNA
C 408	51	3.9	193953	12	AC149623	AC149623 Papio anu	C 481	50	3.9	43190	5	AC005777	AC005777 Homo sapi
C 409	51	3.9	195280	5	AC073869	AC073869 Homo sapi	C 482	50	3.9	43593	5	AL954659	AL954659 Human DNA
410	51	3.9	196603	5	AC087721	AC087721 Homo sapi	C 483	50	3.9	43715	5	AC092398	AC092398 Homo sapi
411	51	3.9	196742	5	AC087884	AC087884 Homo sapi	C 484	50	3.9	44718	12	AC158318	AC158318 Homo sapi
C 412	51	3.9	197866	12	AC138895	AC138895 Homo sapi	C 485	50	3.9	44769	5	DQ314888	DQ314888 Homo sapi
C 413	51	3.9	197972	5	AC138865	AC138865 Homo sapi	C 486	50	3.9	45421	5	AC078826	AC078826 Homo sapi
414	51	3.9	198084	12	AC0119339	AC0119339 Homo sapi	C 487	50	3.9	46165	12	AC092564	AC092564 Hylobates
415	51	3.9	198857	5	AC012404	AC012404 Homo sapi	C 488	50	3.9	46225	5	AC069305	AC069305 Homo sapi
416	51	3.9	199021	5	AC139236	AC139236 Homo sapi	C 489	50	3.9	46765	5	AL354863	AL354863 Human DNA
C 417	51	3.9	199288	5	AC090950	AC090950 Homo sapi	C 490	50	3.9	50829	5	AL558444	AL558444 Human DNA
C 418	51	3.9	200026	12	AC090368	AC090368 Homo sapi	C 491	50	3.9	53402	5	AL158844	AL158844 Homo sapi
C 419	51	3.9	200409	12	AC097331	AC097331 Pan trogl	C 492	50	3.9	55265	5	AC137631	AC137631 Homo sapi
C 420	51	3.9	200491	12	AB107102	AB107102 Homo sapi	C 493	50	3.9	57408	5	AL670471	AL670471 Human DNA
C 421	51	3.9	200791	12	AC125507	AC125507 Papio anu	C 494	50	3.9	60036	12	AC009610	AC009610 Homo sapi
C 422	51	3.9	201638	12	AC144987	AC144987 Homo sapi	C 495	50	3.9	60940	2	AX695473	AX695473 Sequence
423	51	3.9	204182	12	AC097271	AC097271 Pan trogl	C 496	50	3.9	61797	12	AC023094	AC023094 Homo sapi
C 424	51	3.9	209521	5	AC021649	AC021649 Homo sapi	C 497	50	3.9	63264	5	AL359511	AL359511 Human DNA
C 425	51	3.9	210668	12	AC139257	AC139257 Homo sapi	C 498	50	3.9	63332	5	AC024938	AC024938 Homo sapi
C 426	51	3.9	212387	5	AC140504	AC140504 Homo sapi	C 499	50	3.9	65466	12	AC124246	AC124246 Homo sapi
C 427	51	3.9	216546	12	AC138863	AC138863 Homo sapi	C 500	50	3.9	65608	2	AX330738	AX330738 Sequence
C 428	51	3.9	217623	2	CS200152	CS200152 Sequence	C 501	50	3.9	65608	2	AX332242	AX332242 Sequence
429	51	3.9	219673	12	AC139263	AC139263 Homo sapi	C 502	50	3.9	65608	2	AX335496	AX335496 Sequence
C 430	51	3.9	220599	12	AL357792	AL357792 Homo sapi	C 503	50	3.9	65608	5	HSU62293	HSU62293 Human LIM-k
431	51	3.9	230895	12	AC110872	AC110872 Homo sapi	C 504	50	3.9	66867	12	AC073170	AC073170 Homo sapi
432	51	3.9	246333	12	AC163739	AC163739 Pan trogl	C 505	50	3.9	67046	5	HSU63721	HSU63721 Human elast
C 433	51	3.9	254112	12	CR762382	CR762382 Homo sapi	C 506	50	3.9	67372	5	AL138741	AL138741 Human DNA
C 434	51	3.9	255963	12	AC025153	AC025153 Homo sapi	C 507	50	3.9	68984	5	AC135592	AC135592 Homo sapi
C 435	51	3.9	273376	12	CT027841	CT027841 Homo sapi	C 508	50	3.9	69013	12	AC133559	AC133559 Homo sapi
C 436	51	3.9	316406	12	AC122691	AC122691 Homo sapi	C 509	50	3.9	69912	12	AC010322	AC010322 Homo sapi
C 437	51	3.9	327883	12	BX571684	BX571684 Homo sapi	C 510	50	3.9	74371	5	AC005369	AC005369 Homo sapi
C 438	50	3.9	227	2	AX908415	AX908415 Sequence	C 511	50	3.9	75224	5	AC134510	AC134510 Homo sapi
C 439	50	3.9	227	2	BD043948	BD043948 Sequence	C 512	50	3.9	78816	12	AC145755	AC145755 Pan trogl
C 440	50	3.9	271	2	AR744209	AR744209 Sequence	C 513	50	3.9	79555	5	AL583856	AL583856 Human DNA
441	50	3.9	421	7	AX935073	AX935073 Sequence	C 514	50	3.9	80142	5	AL645465	AL645465 Human DNA
442	50	3.9	434	2	AB140881	AB140881 Homo sapi	C 515	50	3.9	80696	5	HS384D21	HS384D21 Human DNA
443	50	3.9	434	2	CQ518466	CQ518466 Sequence	C 516	50	3.9	82101	5	AC005694	AC005694 Homo sapi
444	50	3.9	574	7	BV645429	BV645429 S217P6166	C 517	50	3.9	89312	5	AC091400	AC091400 Pan trogl
C 445	50	3.9	773	7	BV637268	BV637268 S217P6063	C 518	50	3.9	90159	5	AC067855	AC067855 Homo sapi
446	50	3.9	824	7	BV460700	BV460700 q2199d01	C 519	50	3.9	90724	5	AL353673	AL353673 Human DNA
C 447	50	3.9	833	7	BV628711	BV628711 S217P6066	C 520	50	3.9	92068	12	AL672077	AL672077 Homo sapi
C 448	50	3.9	1644	2	CQ734738	CQ734738 Homo sapi	C 521	50	3.9	93744	5	AC097724	AC097724 Homo sapi
449	50	3.9	1762	5	BC001028	BC001028 Homo sapi	C 522	50	3.9	93876	5	AL390240	AL390240 Human DNA
C 450	50	3.9	1912	2	CS176116	CS176116 Sequence	C 523	50	3.9	95445	12	AC016175	AC016175 Homo sapi
C 451	50	3.9	2525	2	CQ843357	CQ843357 Sequence	C 524	50	3.9	95556	5	HSDJ73H14	HSDJ73H14 Human DNA
C 452	50	3.9	2525	5	AK126294	AK126294 Homo sapi	C 525	50	3.9	97465	5	AL157820	AL157820 Human DNA
C 453	50	3.9	3450	5	BC101058	BC101058 Homo sapi	C 526	50	3.9	98078	5	AL451083	AL451083 Human DNA
C 454	50	3.9	12178	5	AY736284	AY736284 Homo sapi	C 527	50	3.9	98188	5	AC005056	AC005056 Homo sapi
455	50	3.9	13203	5	AY898800	AY898800 Homo sapi	C 528	50	3.9	98391	5	AC106733	AC106733 Homo sapi
456	50	3.9	15765	2	AX377200	AX377200 Sequence	C 529	50	3.9	98413	5	HSU1083G3	HSU1083G3 Human DNA

c 530	50	3.9	98835	5	AC073195	Homo sapi	AC073195 Homo sapi	c 603	50	3.9	143366	12	AC027112	Homo sapi	AC027112 Homo sapi
c 531	50	3.9	99973	5	AC124259	Homo sapi	AC124259 Homo sapi	c 604	50	3.9	143712	5	HS917N8	Human DNA	AL031684 Human DNA
c 532	50	3.9	100120	5	AC090454	Homo sapi	AC090454 Homo sapi	c 605	50	3.9	143805	5	HS033551	Human DNA	AL109920 Human DNA
c 533	50	3.9	100139	5	AC021752	Homo sapi	AC021752 Homo sapi	c 606	50	3.9	144189	5	AC023891	Homo sapi	AC023891 Homo sapi
c 534	50	3.9	101500	5	AL365505	Homo sapi	AL365505 Homo sapi	c 607	50	3.9	144659	5	AC006145	Homo sapi	AC006145 Homo sapi
c 535	50	3.9	102424	5	AC026790	Homo sapi	AC026790 Homo sapi	c 608	50	3.9	145101	12	AC021775	Homo sapi	AC021775 Homo sapi
c 536	50	3.9	104632	5	AL136124	Human DNA	AL136124 Human DNA	c 609	50	3.9	146219	5	AC023855	Homo sapi	AC023855 Homo sapi
c 537	50	3.9	105321	5	AL928711	Human DNA	AL928711 Human DNA	c 610	50	3.9	146437	5	AC010489	Homo sapi	AC010489 Homo sapi
c 538	50	3.9	106172	5	AC004111	Homo sapi	AC004111 Homo sapi	c 611	50	3.9	146502	5	AC116456	Homo sapi	AC116456 Homo sapi
c 539	50	3.9	107165	12	AC080120	Homo sapi	AC080120 Homo sapi	c 612	50	3.9	146735	5	AF165147	Homo sapi	AF165147 Homo sapi
c 540	50	3.9	107415	5	AL513365	Human DNA	AL513365 Human DNA	c 613	50	3.9	146756	12	AC002348	Homo sapi	AC002348 Homo sapi
c 541	50	3.9	107868	5	AL445686	Human DNA	AL445686 Human DNA	c 614	50	3.9	146923	12	AC124063	Homo sapi	AC124063 Homo sapi
c 542	50	3.9	109138	5	AC104084	Homo sapi	AC104084 Homo sapi	c 615	50	3.9	146969	5	AC092945	Homo sapi	AC092945 Homo sapi
c 543	50	3.9	110000	12	AC007194	1	Continuation (2 of	c 616	50	3.9	147261	5	AP003475	Homo sapi	AP003475 Homo sapi
c 544	50	3.9	110000	12	AL359456	2	Continuation (3 of	c 617	50	3.9	147401	12	AC067778	Homo sapi	AC067778 Homo sapi
c 545	50	3.9	110000	12	AL732359	-03	Continuation (4 of	c 618	50	3.9	147555	12	AC142206	Homo sapi	AC142206 Homo sapi
c 546	50	3.9	110312	5	AC005215	Homo sapi	AC005215 Homo sapi	c 619	50	3.9	147710	12	AC090070	Homo sapi	AC090070 Homo sapi
c 547	50	3.9	110608	2	CQ861560	Sequence	CQ861560 Sequence	c 620	50	3.9	147945	12	AC084735	Homo sapi	AC084735 Homo sapi
c 548	50	3.9	110608	5	HS283E3	Human DNA	AL031282 Human DNA	c 621	50	3.9	148876	5	AC011455	Homo sapi	AC011455 Homo sapi
c 549	50	3.9	110654	5	HS243L18	Human DNA	AL034395 Human DNA	c 622	50	3.9	149115	5	AC010317	Homo sapi	AC010317 Homo sapi
c 550	50	3.9	112219	12	AL390315	Homo sapi	AL390315 Homo sapi	c 623	50	3.9	149308	5	AC005527	Homo sapi	AC005527 Homo sapi
c 551	50	3.9	112539	5	AL691482	Human DNA	AL691482 Human DNA	c 624	50	3.9	149726	5	AC016394	Homo sapi	AC016394 Homo sapi
c 552	50	3.9	113693	5	HS0J1C16	Human DNA	AL049614 Human DNA	c 625	50	3.9	150193	12	AC027360	Homo sapi	AC027360 Homo sapi
c 553	50	3.9	114104	5	AC128712	Homo sapi	AC128712 Homo sapi	c 626	50	3.9	150199	5	AC087568	Pan trogl	AC087568 Pan trogl
c 554	50	3.9	115935	2	CQ861608	Sequence	CQ861608 Sequence	c 627	50	3.9	150298	2	CS086347	Sequence	CS086347 Sequence
c 555	50	3.9	115935	5	HS963K23	Human DNA	AL031685 Human DNA	c 628	50	3.9	150525	2	CS086332	Sequence	CS086332 Sequence
c 556	50	3.9	120029	12	HSJ282H10	Homo sapi	AL132672 Homo sapi	c 629	50	3.9	150762	5	AC106739	Homo sapi	AC106739 Homo sapi
c 557	50	3.9	120376	5	HS271G9	Human DNA	Z92543 Human DNA	c 630	50	3.9	150902	12	AC023106	Homo sapi	AC023106 Homo sapi
c 558	50	3.9	121272	12	AC004956	Homo sapi	AC004956 Homo sapi	c 631	50	3.9	151386	12	AC015731	Homo sapi	AC015731 Homo sapi
c 559	50	3.9	122279	5	HS215D11	Human DNA	AL034417 Human DNA	c 632	50	3.9	151501	12	AC073543	Homo sapi	AC073543 Homo sapi
c 560	50	3.9	122553	12	CR753417	Homo sapi	CR753417 Homo sapi	c 633	50	3.9	151933	12	AC073199	Homo sapi	AC073199 Homo sapi
c 561	50	3.9	123372	5	AC104120	Homo sapi	AC104120 Homo sapi	c 634	50	3.9	152393	12	AC021765	Homo sapi	AC021765 Homo sapi
c 562	50	3.9	124025	5	AL160169	Human DNA	AL160169 Human DNA	c 635	50	3.9	152966	5	AL359713	Human DNA	AL359713 Human DNA
c 563	50	3.9	124581	5	EX649364	Human DNA	EX649364 Human DNA	c 636	50	3.9	153334	5	AC185855	Pan trogl	AC185855 Pan trogl
c 564	50	3.9	124821	5	AC097109	Homo sapi	AC097109 Homo sapi	c 637	50	3.9	153482	5	AC087498	Homo sapi	AC087498 Homo sapi
c 565	50	3.9	125836	12	AC137629	Human DNA	AC137629 Human DNA	c 638	50	3.9	153539	12	AL591168	Homo sapi	AL591168 Homo sapi
c 566	50	3.9	126474	5	HS181N1	Human DNA	Z82899 Human DNA	c 639	50	3.9	153762	5	AL355338	Human DNA	AL355338 Human DNA
c 567	50	3.9	126722	12	AC145401	Pongo pyg	AC145401 Pongo pyg	c 640	50	3.9	154818	5	AL157711	Human DNA	AL157711 Human DNA
c 568	50	3.9	126753	12	AF252826	Homo sapi	AF252826 Homo sapi	c 641	50	3.9	154970	12	AC106808	Homo sapi	AC106808 Homo sapi
c 569	50	3.9	127677	5	AC102945	Homo sapi	AC102945 Homo sapi	c 642	50	3.9	155112	12	AC124847	Homo sapi	AC124847 Homo sapi
c 570	50	3.9	128312	5	AL591885	Human DNA	AL591885 Human DNA	c 643	50	3.9	155218	12	AC021879	Homo sapi	AC021879 Homo sapi
c 571	50	3.9	131611	5	AC005099	Homo sapi	AC005099 Homo sapi	c 644	50	3.9	155332	12	AL365439	Homo sapi	AL365439 Homo sapi
c 572	50	3.9	132003	5	AC138779	Homo sapi	AC138779 Homo sapi	c 645	50	3.9	156072	12	AC016077	Homo sapi	AC016077 Homo sapi
c 573	50	3.9	132179	5	AL672142	Human DNA	AL672142 Human DNA	c 646	50	3.9	156169	5	AP005062	Homo sapi	AP005062 Homo sapi
c 574	50	3.9	132444	5	AC091878	Homo sapi	AC091878 Homo sapi	c 647	50	3.9	156601	5	HS212G6	Human DNA	AL009172 Human DNA
c 575	50	3.9	132755	5	AC092536	Homo sapi	AC092536 Homo sapi	c 648	50	3.9	156997	5	AC011465	Homo sapi	AC011465 Homo sapi
c 576	50	3.9	132764	5	AC073842	Homo sapi	AC073842 Homo sapi	c 649	50	3.9	157566	5	AC022517	Homo sapi	AC022517 Homo sapi
c 577	50	3.9	133568	5	HS16915	Human DNA	Z93015 Human DNA	c 650	50	3.9	157981	5	AC005184	Homo sapi	AC005184 Homo sapi
c 578	50	3.9	133955	5	AC011380	Homo sapi	AC011380 Homo sapi	c 651	50	3.9	158113	12	AC011159	Homo sapi	AC011159 Homo sapi
c 579	50	3.9	134040	12	AC044856	Homo sapi	AC044856 Homo sapi	c 652	50	3.9	158433	12	AC026460	Homo sapi	AC026460 Homo sapi
c 580	50	3.9	134680	5	AC015726	Homo sapi	AC015726 Homo sapi	c 653	50	3.9	158434	5	AL500527	Human DNA	AL500527 Human DNA
c 581	50	3.9	134793	5	AC020922	Homo sapi	AC020922 Homo sapi	c 654	50	3.9	158529	5	AC027157	Homo sapi	AC027157 Homo sapi
c 582	50	3.9	135161	12	AL357494	Homo sapi	AL357494 Homo sapi	c 655	50	3.9	158730	5	BS000166	Pan trogl	BS000166 Pan trogl
c 583	50	3.9	135369	12	AC090557	Homo sapi	AC090557 Homo sapi	c 656	50	3.9	159156	12	AC133241	Homo sapi	AC133241 Homo sapi
c 584	50	3.9	135820	5	AL513497	Human DNA	AL513497 Human DNA	c 657	50	3.9	159824	12	AC141062	Homo sapi	AC141062 Homo sapi
c 585	50	3.9	136088	5	AL139426	Human DNA	AL139426 Human DNA	c 658	50	3.9	159974	5	AL139008	Human DNA	AL139008 Human DNA
c 586	50	3.9	137111	5	HS202J23	Human DNA	AL022576 Human DNA	c 659	50	3.9	160138	5	AC008551	Homo sapi	AC008551 Homo sapi
c 587	50	3.9	137716	5	AC104068	Homo sapi	AC104068 Homo sapi	c 660	50	3.9	160511	12	AC022786	Homo sapi	AC022786 Homo sapi
c 588	50	3.9	137806	12	AC026372	Homo sapi	AC026372 Homo sapi	c 661	50	3.9	160655	5	AC064874	Homo sapi	AC064874 Homo sapi
c 589	50	3.9	137899	12	AC146067	Pan trogl	AC146067 Pan trogl	c 662	50	3.9	160854	5	AC110602	Homo sapi	AC110602 Homo sapi
c 590	50	3.9	138752	5	AL161627	Human DNA	AL161627 Human DNA	c 663	50	3.9	160892	12	AC023910	Homo sapi	AC023910 Homo sapi
c 591	50	3.9	138779	5	AC008120	Homo sapi	AC008120 Homo sapi	c 664	50	3.9	161161	12	AC150294	Callithr	AC150294 Callithr
c 592	50	3.9	138997	5	HS0J383P5	Human DNA	AL121947 Human DNA	c 665	50	3.9	161695	12	AC079849	Homo sapi	AC079849 Homo sapi
c 593	50	3.9	139049	5	AC007314	Homo sapi	AC007314 Homo sapi	c 666	50	3.9	161776	5	AL133229	Human DNA	AL133229 Human DNA
c 594	50	3.9	139376	5	HSU95742	Human chrom	U95742 Human chrom	c 667	50	3.9	161813	5	CNS01RIG	Human chr	AL163194 Human chr
c 595	50	3.9	139512	5	HSJ1169J3	Human DNA	AL049652 Human DNA	c 668	50	3.9	162129	12	AC016429	Homo sapi	AC016429 Homo sapi
c 596	50	3.9	139979	5	AC109449	Homo sapi	AC109449 Homo sapi	c 669	50	3.9	162377	12	AC142205	Homo sapi	AC142205 Homo sapi
c 597	50	3.9	140287	5	HS0J40754	Human DNA	AL121949 Human DNA	c 670	50	3.9	162554	5	AC079354	Homo sapi	AC079354 Homo sapi
c 598	50	3.9	140556	12	AC078807	Homo sapi	AC078807 Homo sapi	c 671	50	3.9	162704	12	AC016289	Homo sapi	AC016289 Homo sapi
c 599	50	3.9	141092	12	AC016013	Homo sapi	AC016013 Homo sapi	c 672	50	3.9	162953	5	AC145985	Pan trogl	AC145985 Pan trogl
c 600	50	3.9	141704	5	AC007993	Homo sapi	AC007993 Homo sapi	c 673	50	3.9	162973	12	AC016307	Homo sapi	AC016307 Homo sapi
c 601	50	3.9	142185	12	AC022656	Homo sapi	AC022656 Homo sapi	c 674	50	3.9	162975	12	AC025225	Homo sapi	AC025225 Homo sapi
c 602	50	3.9	143210	5	AC022407	Homo sapi	AC022407 Homo sapi	c 675	50	3.9	163279	5	AC160024	Pan trogl	AC160024 Pan trogl

676	50	3.9	163350	2	AX839844	Sequence	749	50	3.9	175136	5	AC104984	Homo sapi
677	50	3.9	163404	12	AC009614	AC009614 Homo sapi	750	50	3.9	175167	12	AC116044	Papio ham
678	50	3.9	163621	5	AC112129	AC112129 Homo sapi	c 751	50	3.9	175465	12	AL356783	Homo sapi
679	50	3.9	163844	5	AC009048	AC009048 Homo sapi	752	50	3.9	175917	12	AC022191	Homo sapi
680	50	3.9	163994	12	AL136108	AL136108 Homo sapi	c 753	50	3.9	175945	12	AC022147	Homo sapi
681	50	3.9	164084	12	AC026580	AC026580 Homo sapi	754	50	3.9	176121	5	AC131011	Homo sapi
682	50	3.9	164116	5	AC141418	AC141418 Pan trogl	c 755	50	3.9	176425	5	AC107075	Homo sapi
683	50	3.9	164299	5	AC027541	AC027541 Pan trogl	c 756	50	3.9	176459	5	AC147314	Pan trogl
684	50	3.9	164365	12	CT573324	CT573324 Pan trogl	c 757	50	3.9	176597	12	AC149622	Papio anu
685	50	3.9	164435	5	AC021937	AC021937 Homo sapi	c 758	50	3.9	176622	5	AL954245	Pan trogl
686	50	3.9	164566	12	AC068559	AC068559 Homo sapi	c 759	50	3.9	177115	5	AC091805	Homo sapi
687	50	3.9	164910	2	CS086348	CS086348 Sequence	760	50	3.9	177301	12	AC078868	Homo sapi
688	50	3.9	165178	12	AC025355	AC025355 Homo sapi	c 761	50	3.9	177469	12	AC019283	Homo sapi
689	50	3.9	165572	5	AL356785	AL356785 Human DNA	c 762	50	3.9	177910	12	AC018357	Homo sapi
690	50	3.9	165673	12	AL354765	AL354765 Homo sapi	c 763	50	3.9	177987	12	AC129881	Papio anu
691	50	3.9	165871	5	CNS01DVO	AL135998 Human chr	764	50	3.9	178042	12	AC036168	Homo sapi
692	50	3.9	166109	5	AC107990	AC107990 Homo sapi	c 765	50	3.9	178252	12	AL356386	Homo sapi
693	50	3.9	166117	12	AC020988	AC020988 Homo sapi	766	50	3.9	178311	5	AC104795	Homo sapi
694	50	3.9	166439	5	AC010325	AC010325 Homo sapi	c 767	50	3.9	178975	12	AP001500	Homo sapi
695	50	3.9	166536	2	CS086331	CS086331 Sequence	768	50	3.9	179138	5	CNS078GV	Human chr
696	50	3.9	166643	5	AL392104	AL392104 Human DNA	769	50	3.9	179372	12	AC040922	Homo sapi
697	50	3.9	166669	5	AC113191	AC113191 Homo sapi	c 770	50	3.9	179650	5	AP003476	Homo sapi
698	50	3.9	166669	12	AC022883	AC022883 Homo sapi	c 771	50	3.9	180290	5	AC005081	Homo sapi
699	50	3.9	167357	12	AC025342	AC025342 Homo sapi	c 772	50	3.9	180415	12	AC152026	Papio anu
700	50	3.9	167642	12	AC015945	AC015945 Homo sapi	773	50	3.9	180526	12	AC078866	Homo sapi
701	50	3.9	167854	12	AC092483	AC092483 Homo sapi	774	50	3.9	180545	5	AL355333	Human DNA
702	50	3.9	168268	5	AC009124	AC009124 Homo sapi	775	50	3.9	180918	5	AC098680	Homo sapi
703	50	3.9	168498	12	AL583847	AL583847 Homo sapi	776	50	3.9	181112	12	AL360012	Homo sapi
704	50	3.9	168578	12	AL359756	AL359756 Homo sapi	777	50	3.9	181300	5	AC011742	Homo sapi
705	50	3.9	168587	5	AC090810	AC090810 Homo sapi	c 778	50	3.9	181683	12	HSBA512N4	Human DNA
706	50	3.9	169082	12	AC163241	AC163241 Callicebu	c 779	50	3.9	181799	5	AC021618	Homo sapi
707	50	3.9	169223	12	AL353675	AL353675 Homo sapi	c 780	50	3.9	181932	5	AC145923	Pan trogl
708	50	3.9	169424	12	AL50291	AL50291 Callithri	c 781	50	3.9	181942	5	AC135106	Pan trogl
709	50	3.9	169540	5	AC024288	AC024288 Homo sapi	c 782	50	3.9	181927	5	AC114980	Homo sapi
710	50	3.9	169540	12	AC026041	AC026041 Homo sapi	c 783	50	3.9	182201	5	AC012498	Homo sapi
711	50	3.9	169697	5	AC009299	AC009299 Homo sapi	784	50	3.9	182639	5	AC104307	Homo sapi
712	50	3.9	169869	12	AC005867	AC005867 Homo sapi	c 785	50	3.9	183625	5	AC053503	Homo sapi
713	50	3.9	169892	12	AC037483	AC037483 Homo sapi	c 786	50	3.9	183664	5	AC009084	Homo sapi
714	50	3.9	169950	12	AC084049	AC084049 Homo sapi	787	50	3.9	184349	5	AC113189	Homo sapi
715	50	3.9	170043	5	AC122718	AC122718 Homo sapi	788	50	3.9	184864	5	AC013553	Homo sapi
716	50	3.9	170203	12	AL714002	AL714002 Homo sapi	c 789	50	3.9	185167	12	AC009077	Homo sapi
717	50	3.9	170284	5	AL359739	AL359739 Human DNA	c 790	50	3.9	185171	12	AC023098	Homo sapi
718	50	3.9	170397	5	AC119677	AC119677 Homo sapi	791	50	3.9	185638	5	AC006210	Homo sapi
719	50	3.9	170400	12	AC048331	AC048331 Homo sapi	792	50	3.9	185980	5	AC090610	Homo sapi
720	50	3.9	170591	12	AC022936	AC022936 Homo sapi	793	50	3.9	186011	12	AC079461	Homo sapi
721	50	3.9	170823	12	AC133549	AC133549 Homo sapi	c 794	50	3.9	186239	12	AC022286	Homo sapi
722	50	3.9	171116	12	AC164943	AC164943 Callicebu	c 795	50	3.9	186482	5	AL691432	Human DNA
723	50	3.9	171123	5	AC020779	AC020779 Homo sapi	c 796	50	3.9	186561	5	AC093159	Homo sapi
724	50	3.9	171374	5	AC010980	AC010980 Homo sapi	c 797	50	3.9	186687	5	AC134943	Homo sapi
725	50	3.9	171419	5	AC013469	AC013469 Homo sapi	798	50	3.9	186892	12	AC148839	Pan trogl
726	50	3.9	171480	12	AC097333	AC097333 Pan trogl	c 799	50	3.9	186829	5	BX640519	Human DNA
727	50	3.9	171574	12	AC012300	AC012300 Homo sapi	c 800	50	3.9	186883	12	AC040991	Homo sapi
728	50	3.9	171941	12	AC114305	AC114305 Homo sapi	c 801	50	3.9	188065	12	AC018689	Homo sapi
729	50	3.9	171951	5	CNS05TDA	AL356020 Human chr	c 802	50	3.9	188534	12	AC022913	Homo sapi
730	50	3.9	171966	12	AC092516	AC092516 Papio anu	803	50	3.9	188868	5	AC023232	Homo sapi
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732	50	3.9	172334	5	AC010650	AC010650 Homo sapi	c 805	50	3.9	188921	5	AC096730	Homo sapi
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737	50	3.9	173198	5	AC0108132	AC0108132 Homo sapi	810	50	3.9	189817	5	AC073160	Homo sapi
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740	50	3.9	173717	5	AC005695	AC005695 Homo sapi	c 813	50	3.9	190129	12	AP001814	Homo sapi
741	50	3.9	173770	5	AC138724	AC138724 Cercopith	814	50	3.9	190221	5	AC025741	Homo sapi
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AC104984 Homo sapi

AC116044 Papio ham

AL356783 Homo sapi

AC022191 Homo sapi

AC022147 Homo sapi

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AC107075 Homo sapi

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AC149622 Papio anu

AL954245 Pan trogl

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AC078868 Homo sapi

AC019283 Homo sapi

AC018357 Homo sapi

AC129881 Papio anu

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AL356386 Homo sapi

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AC145923 Pan trogl

AC135106 Pan trogl

AC114980 Homo sapi

AC012498 Homo sapi

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AC06210 Homo sapi

AC090610 Homo sapi

AC079461 Homo sapi

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AL691432 Human DNA

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C 885	50	3.9	286332	12	AC022105	Homo sapi	C 958	49	3.8	97217	5	AC116565	Homo sapi
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c1006	49	3.8	133629	12	CT574562	CT574562 Pan trogl	c1079	49	3.8	165010	5	HSJ089B84	AL109754 Human DNA
c1007	49	3.8	133954	5	AL355493	AL355493 Human DNA	1080	49	3.8	165021	12	AC107019	AC107019 Homo sapi
c1008	49	3.8	135978	5	CNS01DV8	AL133485 Human chr	1081	49	3.8	165150	12	AP001585	AP001585 Homo sapi
c1009	49	3.8	138094	12	AC009417	AC009417 Homo sapi	1082	49	3.8	165347	5	AF252827	AF252827 Homo sapi
c1010	49	3.8	138435	5	AC073468	AC073468 Homo sapi	c1083	49	3.8	165558	5	AC146348	AC146348 Pan trogl
c1011	49	3.8	138875	5	AC124210	AC124210 Homo sapi	c1084	49	3.8	165558	5	AC103776	AC103776 Homo sapi
c1012	49	3.8	139049	5	AC007314	AC007314 Homo sapi	1085	49	3.8	166234	5	HS273F12	AL034372 Human DNA
c1013	49	3.8	139966	5	AC004820	AC004820 Homo sapi	1086	49	3.8	166329	5	AL139187	AL139187 Human DNA
c1014	49	3.8	141612	5	AC079093	AC079093 Homo sapi	1087	49	3.8	166684	5	AC161287	AC161287 Pan trogl
c1015	49	3.8	142018	5	HS1033H22	AL109613 Human DNA	c1088	49	3.8	167613	5	AC012148	AC012148 Homo sapi
c1016	49	3.8	142064	5	AC091193	AC091193 Homo sapi	c1089	49	3.8	167702	12	AL390916	AL390916 Homo sapi
c1017	49	3.8	142698	5	AC025429	AC025429 Homo sapi	c1090	49	3.8	168042	12	AC025931	AC025931 Homo sapi
c1018	49	3.8	143887	12	AC027819	AC027819 Homo sapi	c1091	49	3.8	168424	5	AC103863	AC103863 Homo sapi
c1019	49	3.8	144407	5	HSJ799P18	AL122008 Human DNA	1092	49	3.8	168610	12	AC073503	AC073503 Homo sapi
c1020	49	3.8	144431	5	AC079376	AC079376 Homo sapi	c1093	49	3.8	169713	12	AC015919	AC015919 Homo sapi
c1021	49	3.8	146552	5	AC090753	AC090753 Homo sapi	1094	49	3.8	169775	5	AL139120	AL139120 Human DNA
c1022	49	3.8	146712	5	AF252828	AF252828 Homo sapi	1095	49	3.8	170026	12	AC016421	AC016421 Homo sapi
c1023	49	3.8	147242	12	AC079084	AC079084 Homo sapi	1096	49	3.8	170233	5	AC018663	AC018663 Human Chr
c1024	49	3.8	148507	12	AC011263	AC011263 Homo sapi	1097	49	3.8	170502	5	AC140485	AC140485 Homo sapi
c1025	49	3.8	148845	5	HS1114A1	AL035684 Human DNA	1098	49	3.8	170624	5	AC022096	AC022096 Homo sapi
c1026	49	3.8	150125	5	AP000437	AP000437 Homo sapi	c1099	49	3.8	170788	5	AC024678	AC024678 Homo sapi
c1027	49	3.8	150354	5	AC091920	AC091920 Homo sapi	1100	49	3.8	171024	12	AC149250	AC149250 Papio anu
c1028	49	3.8	150397	12	CNS050D2	AL355923 Homo sapi	c1101	49	3.8	171076	5	AC090231	AC090231 Homo sapi
c1029	49	3.8	150453	5	AC015920	AC015920 Homo sapi	c1102	49	3.8	171183	5	AL358876	AL358876 Human DNA
c1030	49	3.8	151123	5	AC005520	AC005520 Homo sapi	c1103	49	3.8	171403	5	AC092701	AC092701 Homo sapi
c1031	49	3.8	151128	5	AC015871	AC015871 Homo sapi	1104	49	3.8	171467	5	AL449223	AL449223 Human DNA
c1032	49	3.8	151316	5	AC005039	AC005039 Homo sapi	1105	49	3.8	171653	5	AC080162	AC080162 Homo sapi
c1033	49	3.8	151640	12	AC015816	AC015816 Homo sapi	1106	49	3.8	173041	12	AC069320	AC069320 Homo sapi
c1034	49	3.8	151833	12	AC016875	AC016875 Homo sapi	1107	49	3.8	173268	5	AL138760	AL138760 Human DNA
c1035	49	3.8	151834	5	AP004195	AP004195 Homo sapi	1108	49	3.8	173336	5	AC025168	AC025168 Homo sapi
c1036	49	3.8	152132	5	AC011592	AC011592 Homo sapi	1109	49	3.8	174378	5	AC020983	AC020983 Homo sapi
c1037	49	3.8	153000	12	AC010934	AC010934 Homo sapi	1110	49	3.8	174537	12	AC022917	AC022917 Homo sapi
c1038	49	3.8	153071	12	AC104155	AC104155 Pan trogl	1111	49	3.8	174902	5	AC099811	AC099811 Homo sapi
c1039	49	3.8	153716	12	AC069187	AC069187 Homo sapi	1112	49	3.8	175543	12	AC073378	AC073378 Homo sapi
c1040	49	3.8	154140	5	CNS06C7P	AL390798 Human chr	1113	49	3.8	175666	5	AL356481	AL356481 Human DNA

cl114	49	3.8	175797	5	AL390760	AL390760 Human DNA	cl187	49	3.8	208010	12	AC129927	AC129927 Homo sapi
cl115	49	3.8	175870	5	AC007637	AC007637 Homo sapi	cl188	49	3.8	208360	5	AC020708	AC020708 Homo sapi
cl116	49	3.8	176017	5	AP002748	AP002748 Homo sapi	cl189	49	3.8	208924	5	AC018735	AC018735 Homo sapi
cl117	49	3.8	177067	12	AC016516	AC016516 Homo sapi	cl190	49	3.8	211291	5	AC107959	AC107959 Homo sapi
cl118	49	3.8	177334	5	AP006216	AP006216 Homo sapi	cl191	49	3.8	211345	5	AP002453	AP002453 Homo sapi
cl119	49	3.8	177901	5	AC011893	AC011893 Homo sapi	cl192	49	3.8	211770	12	AC159578	AC159578 Papio anu
cl120	49	3.8	177995	5	AC016700	AC016700 Homo sapi	cl193	49	3.8	212036	12	AC163770	AC163770 Pan trogl
cl121	49	3.8	178097	12	AC016704	AC016704 Homo sapi	cl194	49	3.8	212643	5	AC098807	AC098807 Papio anu
cl122	49	3.8	178105	5	AC073057	AC073057 Homo sapi	cl195	49	3.8	212643	5	AC112504	AC112504 Homo sapi
cl123	49	3.8	178199	12	AC018772	AC018772 Homo sapi	cl196	49	3.8	215077	5	AC100871	AC100871 Homo sapi
cl124	49	3.8	178453	5	AC072044	AC072044 Homo sapi	cl197	49	3.8	215314	5	AC106791	AC106791 Homo sapi
cl125	49	3.8	178714	12	AC017008	AC017008 Homo sapi	cl198	49	3.8	216877	5	AC108791	AC108791 Homo sapi
cl126	49	3.8	178820	5	AC020552	AC020552 Homo sapi	cl199	49	3.8	217413	12	AC158240	AC158240 Pan trogl
cl127	49	3.8	178908	5	AL157392	AL157392 Human DNA	cl200	49	3.8	217521	12	AC016047	AC016047 Homo sapi
cl128	49	3.8	178928	5	AC142315	AC142315 Pan trogl	cl201	49	3.8	220004	12	AC004795	AC004795 Homo sapi
cl129	49	3.8	179222	12	AC090270	AC090270 Homo sapi	cl202	49	3.8	220084	12	AL445221	AL445221 Homo sapi
cl130	49	3.8	179441	12	AC044879	AC044879 Homo sapi	cl203	49	3.8	221085	5	AC090359	AC090359 Homo sapi
cl131	49	3.8	179959	5	AL160395	AL160395 Human DNA	cl204	49	3.8	222408	12	AP001566	AP001566 Homo sapi
cl132	49	3.8	180957	5	AF267168	AF267168 Homo sapi	cl205	49	3.8	222730	5	CNS01DUU	AL133246 BAC seque
cl133	49	3.8	181031	12	AC169832	AC169832 Macaca mu	cl206	49	3.8	223044	12	AC104158	AC104158 Pan trogl
cl134	49	3.8	181034	12	AC016377	AC016377 Homo sapi	cl207	49	3.8	224098	5	BS000242	BS000242 Pan trogl
cl135	49	3.8	181102	5	AC090058	AC090058 Homo sapi	cl208	49	3.8	224931	5	AC008540	AC008540 Homo sapi
cl136	49	3.8	181133	12	AC073478	AC073478 Homo sapi	cl209	49	3.8	231313	12	CT009513	CT009513 Homo sapi
cl137	49	3.8	181412	12	AC113242	AC113242 Pan trogl	cl210	49	3.8	248281	5	AC008737	AC008737 Homo sapi
cl138	49	3.8	181946	12	AC097330	AC097330 Pan trogl	cl211	49	3.8	280140	12	AC055751	AC055751 Homo sapi
cl139	49	3.8	182350	5	BS000243	BS000243 Pan trogl	cl212	49	3.8	280483	12	AL627109	AL627109 Homo sapi
cl140	49	3.8	182848	5	AC145207	AC145207 Homo sapi	cl213	49	3.8	282718	5	AF130343	AF130343 Homo sapi
cl141	49	3.8	182945	12	AC069004	AC069004 Homo sapi	cl214	49	3.8	300658	12	BX649447	BX649447 Mus muscu
cl142	49	3.8	182828	12	AC020999	AC020999 Homo sapi	cl215	49	3.8	303248	12	AL161660	AL161660 Homo sapi
cl143	49	3.8	184295	12	AC021138	AC021138 Homo sapi	cl216	49	3.8	339168	12	AC078987	AC078987 Homo sapi
cl144	49	3.8	184520	5	AC009220	AC009220 Homo sapi	cl217	49	3.8	340000	5	AP001710	AP001710 Homo sapi
cl145	49	3.8	184597	12	AC161624	AC161624 Pan trogl	cl218	48	3.7	48	2	BD075423	BD075423 Homo sapi
cl146	49	3.8	184788	5	AF003627	AF003627 Homo sapi	cl219	48	3.7	48	2	BD172283	BD172283 Secreted
cl147	49	3.8	184981	5	AC008659	AC008659 Homo sapi	cl220	48	3.7	48	2	BD172602	BD172602 Secreted
cl148	49	3.8	185759	5	AC084026	AC084026 Homo sapi	cl221	48	3.7	48	2	BD172921	BD172921 Secreted
cl149	49	3.8	186202	5	AC108516	AC108516 Homo sapi	cl222	48	3.7	48	2	BD173240	BD173240 Secreted
cl150	49	3.8	186394	12	AC012551	AC012551 Homo sapi	cl223	48	3.7	48	2	BD175274	BD175274 Secretory
cl151	49	3.8	186538	5	AL158069	AL158069 Human DNA	cl224	48	3.7	48	2	CQ957896	CQ957896 Sequence
cl152	49	3.8	186608	5	AC125453	AC125453 Homo sapi	cl225	48	3.7	48	2	CQ957896	CQ957896 Sequence
cl153	49	3.8	187064	5	AC011476	AC011476 Homo sapi	cl226	48	3.7	48	2	AR216176	AR216176 Sequence
cl154	49	3.8	187102	12	AC090217	AC090217 Homo sapi	cl227	48	3.7	48	2	AR410652	AR410652 Sequence
cl155	49	3.8	187578	5	AC096952	AC096952 Homo sapi	cl228	48	3.7	48	2	AR439016	AR439016 Sequence
cl156	49	3.8	188295	5	AC098869	AC098869 Homo sapi	cl229	48	3.7	48	2	AR473036	AR473036 Sequence
cl157	49	3.8	188504	2	AR659670	AR659670 Sequence	cl230	48	3.7	48	2	AR527022	AR527022 Sequence
cl158	49	3.8	188963	5	AC007707	AC007707 Homo sapi	cl231	48	3.7	48	2	AR566055	AR566055 Sequence
cl159	49	3.8	189485	12	AC141268	AC141268 Homo sapi	cl232	48	3.7	48	2	AR592073	AR592073 Sequence
cl160	49	3.8	189825	5	AL683807	AL683807 Human DNA	cl233	48	3.7	48	2	AR604347	AR604347 Sequence
cl161	49	3.8	190152	12	AC149183	AC149183 Papio anu	cl234	48	3.7	48	2	AR604933	AR604933 Sequence
cl162	49	3.8	190776	5	AC146029	AC146029 Pan trogl	cl235	48	3.7	48	2	AR613598	AR613598 Sequence
cl163	49	3.8	192688	12	AC021881	AC021881 Homo sapi	cl236	48	3.7	48	2	AR629938	AR629938 Sequence
cl164	49	3.8	192802	5	AC011753	AC011753 Homo sapi	cl237	48	3.7	48	2	AR635769	AR635769 Sequence
cl165	49	3.8	193559	12	AC137500	AC137500 Homo sapi	cl238	48	3.7	48	2	AR650498	AR650498 Sequence
cl166	49	3.8	194612	5	AL357354	AL357354 Human DNA	cl239	48	3.7	48	2	AR657439	AR657439 Sequence
cl167	49	3.8	194719	12	AC026173	AC026173 Homo sapi	cl240	48	3.7	48	2	AR720391	AR720391 Sequence
cl168	49	3.8	194976	5	AL513165	AL513165 Human DNA	cl241	48	3.7	48	2	AR770950	AR770950 Sequence
cl169	49	3.8	195858	12	AC074265	AC074265 Homo sapi	cl242	48	3.7	48	2	AR771317	AR771317 Sequence
cl170	49	3.8	196264	12	AC145548	AC145548 Homo sapi	cl243	48	3.7	48	2	AX055382	AX055382 Sequence
cl171	49	3.8	196451	5	AC112784	AC112784 Homo sapi	cl244	48	3.7	48	2	AX098391	AX098391 Sequence
cl172	49	3.8	196662	5	AP001107	AP001107 Homo sapi	cl245	48	3.7	48	2	AX697476	AX697476 Sequence
cl173	49	3.8	196990	12	AC156839	AC156839 Pan trogl	cl246	48	3.7	234	2	AX322337	AX322337 Sequence
cl174	49	3.8	197456	12	AC005054	AC005054 Homo sapi	cl247	48	3.7	401	7	BV189852	BV189852 sqm16518
cl175	49	3.8	197786	5	AL450326	AL450326 Human DNA	cl248	48	3.7	433	2	AX386522	AX386522 Sequence
cl176	49	3.8	197992	12	AC020715	AC020715 Homo sapi	cl249	48	3.7	722	7	BV598079	BV598079 S217P6668
cl177	49	3.8	198588	12	AC166519	AC166519 Callithri	cl250	48	3.7	757	7	BV625487	BV625487 S217P6605
cl178	49	3.8	199661	12	AC166197	AC166197 Callithri	cl251	48	3.7	760	7	BV636657	BV636657 S217P6116
cl179	49	3.8	200688	12	AC073266	AC073266 Homo sapi	cl252	48	3.7	10500	2	AX360285	AX360285 Sequence
cl180	49	3.8	200918	2	AR659606	AR659606 Sequence	cl253	48	3.7	15382	5	AF222689	AF222689 Homo sapi
cl181	49	3.8	201981	12	AC073640	AC073640 Homo sapi	cl254	48	3.7	31694	5	AC053606	AC053606 Human DNA
cl182	49	3.8	202142	5	AF254981	AF254981 Homo sapi	cl255	48	3.7	36301	5	AC092166	AC092166 Homo sapi
cl183	49	3.8	202539	12	AC090559	AC090559 Homo sapi	cl256	48	3.7	37406	12	AL405916	AL405916 Macaca mu
cl184	49	3.8	203158	12	AC149169	AC149169 Papio anu	cl257	48	3.7	39383	5	AL592218	AL592218 Human DNA
cl185	49	3.8	206777	12	AC153303	AC153303 Pan trogl	cl258	48	3.7	40926	5	HSB10B1	HSB10B1 Human DNA
cl186	49	3.8	207653	12	AL355614	AL355614 Homo sapi	cl259	48	3.7	41257	5	AC005330	AC005330 Homo sapi

1260	48	3.7	41502	5	ALS13262	ALS13262 Human DNA	1333	48	3.7	167079	5	AL606489	AL606489 Human DNA
1261	48	3.7	49996	5	HSDJ816K9	AL117349 Human DNA	1334	48	3.7	167266	12	AC130273	AC130273 Papio anu
1262	48	3.7	55965	5	DQ003720	DQ003720 Homo sapi	c1335	48	3.7	167563	12	AC069280	AC069280 Homo sapi
c1263	48	3.7	57729	5	AL449284	AL449284 Human DNA	1336	48	3.7	167941	12	AC058804	AC058804 Homo sapi
1264	48	3.7	64851	5	AL139105	AL139105 Human DNA	1337	48	3.7	169587	5	AC109597	AC109597 Homo sapi
1265	48	3.7	68451	5	AL162384	AL162384 Human DNA	1338	48	3.7	170520	5	AC012064	AC012064 Homo sapi
c1266	48	3.7	70000	5	AY064247	AY064247 Homo sapi	c1339	48	3.7	170579	12	AC020985	AC020985 Homo sapi
c1267	48	3.7	76200	5	AC008616	AC008616 Homo sapi	1340	48	3.7	171559	12	AC067919	AC067919 Homo sapi
c1268	48	3.7	79913	12	AC133557	AC133557 Homo sapi	c1341	48	3.7	171655	12	AC055782	AC055782 Homo sapi
c1269	48	3.7	81872	5	AL134818	AL134818 Homo sapi	1342	48	3.7	172597	5	AC055782	AC146065 Pan trogl
c1270	48	3.7	83827	5	AL157369	AL157369 Human DNA	c1343	48	3.7	172757	5	AC146065	AL133523 Human chr
1271	48	3.7	87903	5	AL732364	AL732364 Human DNA	c1344	48	3.7	173039	5	CNS01DVB	AX335950 Sequence
1272	48	3.7	98753	12	AP000434	AP000434 Homo sapi	1345	48	3.7	174424	2	AX335950	AC018494 Homo sapi
1273	48	3.7	102926	5	AC004230	AC004230 Homo sapi	1346	48	3.7	174512	5	ALS90103	ALS90103 Human DNA
c1274	48	3.7	107717	5	AC137055	AC137055 Homo sapi	c1347	48	3.7	175162	5	AC040995	AC040995 Homo sapi
c1275	48	3.7	108711	5	AC097523	AC097523 Homo sapi	1348	48	3.7	177176	12	AC069221	AC069221 Homo sapi
1276	48	3.7	108930	5	ALS13122	ALS13122 Human DNA	c1349	48	3.7	177464	12	AC018811	AC018811 Homo sapi
c1277	48	3.7	109472	5	ALS131363	ALS131363 Human DNA	c1350	48	3.7	177834	5	AC008406	AC008406 Homo sapi
1278	48	3.7	109885	5	HS523G1	AL034375 Human DNA	1351	48	3.7	178030	5	AC008406	AL355501 Human DNA
1279	48	3.7	110000	5	AC005079 ³	Continuation (4 of	c1352	48	3.7	179380	5	AL355501	AP003043 Homo sapi
c1280	48	3.7	110000	12	AC004085 ⁰	AC004085 Homo sapi	c1353	48	3.7	180648	5	CNS01R69	AL157871 Human chr
1281	48	3.7	110542	12	AL732359 ⁰⁸	Continuation (9 of	c1354	48	3.7	180688	5	U52112	U52112 Homo sapien
c1282	48	3.7	112050	12	AC090777	AC090777 Homo sapi	c1355	48	3.7	181343	5	AC009965	AC009965 Homo sapi
1283	48	3.7	112643	12	AC009187	AC009187 Homo sapi	1356	48	3.7	181700	5	AC009965	AL365365 Homo sapi
c1284	48	3.7	112846	5	AC004991	AC004991 Homo sapi	c1357	48	3.7	181773	12	AC024052	AC024052 Homo sapi
c1285	48	3.7	113036	5	AL158160	AL158160 Human DNA	c1358	48	3.7	182403	12	AC073476	AC073476 Homo sapi
1286	48	3.7	119024	5	AL159987	AL159987 Human DNA	1359	48	3.7	182559	5	AC008462	AC008462 Homo sapi
1287	48	3.7	120917	5	HSJ583P15	AL121845 Human DNA	c1360	48	3.7	183591	5	AC008474	AC008474 Homo sapi
c1288	48	3.7	123016	12	AF189001	AF189001 Homo sapi	c1361	48	3.7	186115	5	AC008474	AC068151 Homo sapi
1289	48	3.7	124060	5	AC087793	AC087793 Homo sapi	1362	48	3.7	187399	12	AC091231	AC091231 Homo sapi
1290	48	3.7	124086	5	AC008882	AC008882 Homo sapi	1363	48	3.7	187779	5	AC091231	AC009146 Homo sapi
c1291	48	3.7	124086	5	AC008882	AC008882 Homo sapi	1364	48	3.7	188249	12	AC009146	AC022254 Homo sapi
c1292	48	3.7	124536	12	AC149107	AC149107 Papio anu	c1365	48	3.7	188249	12	AC009146	AC022254 Homo sapi
c1293	48	3.7	124990	5	HS434P1	297056 Human DNA e	1366	48	3.7	188601	5	AC022254	AC068090 Homo sapi
c1294	48	3.7	127171	12	AC008777	AC008777 Homo sapi	1367	48	3.7	189245	12	AC068090	AC068769 Homo sapi
1295	48	3.7	130932	5	AC0932658	AC0932658 Homo sapi	1368	48	3.7	191246	5	AC068769	AC068769 Homo sapi
c1296	48	3.7	132337	5	AC104798	AC104798 Homo sapi	c1369	48	3.7	191925	5	AC008736	AC008736 Homo sapi
1297	48	3.7	133478	5	AL037066	AL137066 Human DNA	1370	48	3.7	193168	12	AC011969	AC011969 Homo sapi
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24-NOV-1997 US	60/066511,24-NOV-1997 US	60/066453 PR
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PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI JEAN CHEN,		
PI JEAN YUAN		
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PC C12N1/19,		
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VERSION	BD172280.1 GI:28413580	
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REFERENCE	1 (bases 1 to 1295)	
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.	
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same	
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24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
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RESULT 3
BD172599
LOCUS
DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.
ACCSSION BD172599
VERSION BD172599.1 GI:28413901
KEYWORDS JP 2002238586-A/53.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1295)
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
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TITLE	Yuan, J.	Db	181	CCCCAAAGACCAACAGTAGTACAGCAGTACAGTACCAAGAGGCTATTTTACCGCTGCAA	240
JOURNAL	Secreted and transmembrane polypeptides and nucleic acids encoding the same	Qy	241	AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGAAGAACTCGGTGCGAGTGCTC	300
COMMENT	Patent: JP 2002238586-A 53 27-AUG-2002; GENENTECH INC	Db	241	AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGAAGAACTCGGTGCGAGTGCTC	300
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	PD 27-AUG-2002	Qy	361	TTTTCATATCCCGATCAAAATGTGCAAGAAGTGTGCGGGGAAATATCGTTGTGAAGT	420
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Db	61	CAGAGCAGCGGCTGCGCGCCCCGGGAAGATGGGAGGAGGAGCGCCACCGCTCTCTCT	120		
Qy	121	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	180		
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DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding
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ACCESSION  BD175271
VERSION    BD175271.1 GI:29120967
KEYWORDS   JP 2002253280-A/53.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 1295)
AUTHORS   Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
            Yuan,J.
TITLE      Secretory and transmembrane polypeptide and nucleic acid encoding
            the same
JOURNAL    Patent: JP 2002253280-A 53 10-SEP-2002;
            GENENTECH INC
COMMENT    OS Homo sapiens (human)
            PN JP 2002253280-A/53
            PD 10-SEP-2002
            PF 18-DEC-2001 JP 2001385319
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DEFINITION	Sequence 8 from patent US 6410708.				
ACCESSION	AR216160				
VERSION	AR216160.1	GI:23314515			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1295)				
AUTHORS	Ashkenazi, A., Fong, S., Goddard, A., Gurney, A.L., Napier, M.A., Tumas, D. and Wood, W.I.				
TITLE	Nucleic acids encoding A-33 related antigen polypeptides				
JOURNAL	Patent: US 6410708-A 8 25-JUN-2002;				
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SOURCE	Unknown.			
ORGANISM	Unclassified.			
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AUTHORS	Ashkenazi, A., Botstein, D., Deenoyers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.			
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same			
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ACCESSION AR473033
VERSION AR473033.1 GI:42708408
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1295)
AUTHORS Desnovers, L.; Goddard, A.; Godowski, P.J.; Gurney, A.L.; Mather, J.P.;
Williams, P.M. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding

JOURNAL	the same						
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Search completed: May 18, 2006, 00:20:36
Job time : 7865 secs

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Run on: May 17, 2006, 19:58:15 ; Search time 915 Seconds
(without alignments)
9867.827 Million cell updates/sec

Title: US-10-785-221-8
Perfect score: 1295
Sequence: 1 ccagaagtcaggcccc.....ataaatagcttgatattc 1295
Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0
Total number of hits satisfying chosen parameters: 10489196
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

1: Genesegm1980s:*
2: Genesegm1990s:*
3: Genesegm2000s:*
4: Genesegm2001as:*
5: Genesegm2001bs:*
6: Genesegm2002as:*
7: Genesegm2002bs:*
8: Genesegm2003as:*
11: Genesegm2003ds:*
12: Genesegm2004as:*
13: Genesegm2004bs:*
14: Genesegm2005s:*
15: Genesegm2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AA37664	standard;	CDNA;	1295	BP.	
DE	Human PRO245	CDNA.				
PN	WO914241-A2.					
PD	23-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 2;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 2						
ID	AA35225	standard;	DNA;	1295	BP.	
DE	Protein PRO245	CDNA clone DNA35638-1141.				
PN	WO914328-A2.					
PD	25-MAR-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 2;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 3						
ID	AAC5856	standard;	CDNA;	1295	BP.	
DE	Human PRO245	protein UNQ219 encoding CDNA SEQ ID NO:35.				
PN	WO200053758-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 3;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 4						
ID	AA25202	standard;	CDNA;	1295	BP.	
DE	Human PRO245	protein encoding CDNA, UNQ219.				
PN	WO200015797-A2.					
PD	23-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 3;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 5						
ID	AA77562	standard;	CDNA;	1295	BP.	
DE	Human PRO245	CDNA sequence SEQ ID NO:66.				
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1295;	DB 3;	Length 1295;		
Best Local Similarity	100.0%;	Pred. No. 0;				
RESULT 6						
ID	ADC78383	standard;	CDNA;	1295	BP.	
DE	Human PRO245	CDNA.				

us-10-785-221-8.oligo.rng.spd1

PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 7
ID AAF72383 standard; CDNA; 1295 BP.
DE Human PRO245 CDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 4; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 8
ID AA521411 standard; CDNA; 1295 BP.
DE Human CDNA sequence encoding for PRO245 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 4; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 9
ID AAC97437 standard; CDNA; 1295 BP.
DE Human angiogenesis-associated protein PRO245 CDNA, SEQ ID NO:90.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 4; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 10
ID AAC91463 standard; CDNA; 1295 BP.
DE Human PRO245 CDNA.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 5; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 11
ID ACA60052 standard; CDNA; 1295 BP.
DE Human CDNA for secreted/transmembrane protein PRO245.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 12
ID ACD07452 standard; CDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 CDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 13
ID ACA03770 standard; CDNA; 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ABX71500 standard; CDNA; 1295 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO245.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ACH06832 standard; CDNA; 1295 BP.
DE Human secreted/transmembrane polypeptide PRO245 CDNA.
PN US2003044839-A1.

PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ABX89308 standard; cDNA; 1295 BP.
DE DNA encoding novel secreted and transmembrane protein PRO245.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ACD41962 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #168.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ABX96069 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ACA05190 standard; cDNA; 1295 BP.
DE cDNA encoding human secreted protein PRO245.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ACD20057 standard; cDNA; 1295 BP.
DE Human secreted / transmembrane polypeptide PRO245 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ABX93348 standard; cDNA; 1295 BP.
DE cDNA encoding human A-33 related antigen PRO245.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID ACA04191 standard; cDNA; 1295 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 335.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ACA54860 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 8; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ACD19695 standard; cDNA; 1295 BP.
DE Human secreted / transmembrane polypeptide PRO245 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ADA45854 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ADA76285 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ADB29268 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ADA18935 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ADA61558 standard; cDNA; 1295 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ADB19343 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ADB27884 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ADA86363 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ADB15927 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.


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Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ADA47713 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ADA18124 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ACD66842 standard; cDNA; 1295 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO245.
PN US2003045693-A1.
PD 08-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ADA67508 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ADB30515 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ADA85811 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ADA97023 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ADA79327 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ADA87466 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ADB16668 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ACD83003 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ADA16099 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ADA91760 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ADB14823 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ADB18784 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ADA93999 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ADB19895 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ADB13207 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ADA87466 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 52
ID ACD98591 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ADA74461 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ADA42244 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ADB24694 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077113-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ADA82218 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ADA75181 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ADA85259 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ADA84707 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ACD23181 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ADB29963 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ADA80491 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ADA75733 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ADA46958 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ADB25254 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077115-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ADA93430 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ADB26780 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ADB31067 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADA60995 standard; cDNA; 1295 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADB24142 standard; cDNA; 1295 BP.
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DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ADA96471 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ADA81043 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADA95919 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADB26228 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADB21713 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ADA77492 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ADB18232 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADA86915 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADA16523 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003059909-A1.

PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADA12952 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ADA41820 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ADA88018 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ADA46406 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ADA17167 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ADA42670 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ADB28436 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ADB28988 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ADA76940 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003059909-A1.
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PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ADA88570 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ADA97575 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ADB27332 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US200302239-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ADB2265 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ACD23543 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ADA66956 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ADB22817 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ADB23590 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ADA92312 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ADB15375 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ADB38627 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ADB38075 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 9; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ADB66547 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ADB89627 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ADB90359 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ADB77589 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ADB39460 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ADB74725 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 107
ID ADB47083 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ADB86690 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ADB77295 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ADB34452 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ADB35556 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ADB33900 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ADB35004 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ADB36108 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ADB46503 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ADB47083 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ADC39571 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ADC40085 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ADC18913 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ADC34209 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 121
ID ADC29264 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 122
ID ADC28795 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ADC4680 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 124
ID ADC19337 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ADC33785 standard; cDNA; 1295 BP.
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DE Human secreted/transmembrane protein cDNA, #13.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ADC12855 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 127
ID ADC50376 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 128
ID ADC71923 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 129
ID ADC5902 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID ADC52909 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 131
ID ADC57263 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 132
ID ADC60454 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 133
ID ADC50929 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 134
ID ADC65456 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194770-A1.

DE Human secreted/transmembrane protein cDNA, #13.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 135
ID ADC54554 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ADC5515 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ADC59038 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ADC55916 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ADC58486 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID335.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ADC12307 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID ADD03160 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ADC90152 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ADC69571 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003194770-A1.
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PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID ADC48460 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 145
ID ADD09989 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID ADD04564 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID ADC80520 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID ADD11027 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID ADC47908 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ADD04862 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID ADC79968 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID ADD09437 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID ADD03868 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID ADD03444 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID ADD41150 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ADD52289 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ADD53029 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ADD53581 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ADD51737 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ADD02536 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ADD01970 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.


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Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ADD54152 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ADD92469 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ADD91365 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ADE03979 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ADE32276 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ADE22208 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ADD79432 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ADE41968 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ADE17785 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ADD91917 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ADE33380 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ADE33932 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ADD79984 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ADD93021 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ADE19441 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ADE34696 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ADE18889 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ADE43085 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 180
ID ADE95874 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ADE22760 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ADD78878 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ADE32828 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ADE4520 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ADD80536 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207418-A1.
PD 08-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ADD89564 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ADE40848 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ADE04647 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ADE92776 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ADG21485 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ADG23126 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ADE97461 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ADG80525 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ADG79973 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ADH62535 standard; cDNA; 1295 BP.
DE Human DNA35638 cDNA encoding PRO245 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ADH59179 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ADH55265 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207381-A1.
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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ADH55817 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ADI37958 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ADI64036 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ADI64985 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ADI63484 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ADH81898 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ADH81346 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ACA58948 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ACD24020 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ACA58345 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #11.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ACA67161 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ADJ26226 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 10; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 210
ID ADM82515 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ADN15914 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ADN16543 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ADN15362 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
ID ADN14810 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 11; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ADC81072 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 216
ID ADE79141 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 217
ID ADD76520 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 218
ID ADD87884 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 219
ID ADD86288 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 220
ID ADE79565 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 221
ID ADE75736 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 222
ID ADE73241 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 223
ID ADE23312 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 224
ID ADE23864 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 225
ID ADE24507 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 226
ID ADD87332 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 227
ID ADE89198 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 228
ID ADE73776 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 229
ID ADE18337 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 230
ID ADE88646 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 231
ID ADE99330 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 232
ID ADE94666 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 233
ID ADE91077 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;
RESULT 234
ID ADE23864 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 12; Length 1295;

RESULT 234
ID ADE95218 standard; cDNA; 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 235
ID ADE93328 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 236
ID ADF34909 standard; cDNA; 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 237
ID ADE98449 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 238
ID ADE92224 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 239
ID ADE90525 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 240
ID ADE91672 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 241
ID ADE98876 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 242
ID ADG40346 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODN/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 243
ID ADF73740 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 244
ID ADG02251 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 245
ID ADG22037 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 246
ID ADG20107 standard; cDNA; 1295 BP.
DE CDNA encoding human PRO polypeptide #168.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 247
ID ADF98013 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 248
ID ADG24230 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 249
ID ADF98584 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 250
ID ADG03415 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 251
ID ADF99136 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207353-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 252
ID ADG16721 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 253
ID ADG05180 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 254
ID ADG19447 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 255
ID ADF73316 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 256
ID ADG13284 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 257
ID ADG08341 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 258
ID ADG15511 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 259
ID ADF96909 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 260
ID ADG06094 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207374-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 261
ID ADG23678 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 262
ID ADG03967 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 263
ID ADG24868 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 264
ID ADG07165 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 265
ID ADG07717 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 266
ID ADG55212 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 267
ID ADG60876 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 268
ID ADG61980 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 269
ID ADG92159 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.

ID ADG61428 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 289
ID ADH28515 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ADG54660 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ADG59700 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ADH20375 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ADH07230 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GDD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ADH59775 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ADH06803 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GDD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ADH18124 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ADI18545 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ADI65265 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ADI37528 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ADG09867 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ADH97332 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ADI15338 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ADG09215 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ADI65692 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ADI14670 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ADH60435 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US200402331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ADI18265 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 308
ID ADJ99492 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ADL08685 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ADM25030 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ADJ63546 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ADM29776 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ADJ77441 standard; cDNA; 1295 BP.

DE Human PRO polynucleotide #168.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ADJ55563 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ADM27699 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ADM42423 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ADO06098 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #13.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ADN35291 standard; DNA; 1295 BP.
DE Human PRO245 gene.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ADM28285 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ADR10950 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 12; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 321
ID ADR17859 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.

PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
Pred. No. 0;
RESULT 322
ID ADI95767 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
Pred. No. 0;
RESULT 323
ID ADI96319 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
Pred. No. 0;
RESULT 324
ID ADT94236 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane cDNA sequence.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
Pred. No. 0;
RESULT 325
ID ADS74498 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane cDNA #13.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
Pred. No. 0;
RESULT 326
ID ADS32271 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
Pred. No. 0;
RESULT 327
ID ADT03255 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
Pred. No. 0;
RESULT 328
ID ADT03535 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 13; Length 1295;
Pred. No. 0;
RESULT 329
ID ADZ03306 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane PRO245 cDNA.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 14; Length 1295;
Pred. No. 0;
RESULT 330
ID AEA37773 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 14; Length 1295;
Pred. No. 0;
RESULT 331
ID AEB14052 standard; cDNA; 1295 BP.
DE Cancer cell diagnosis method-related human cDNA sequence - SEQ ID 335.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFOGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 14; Length 1295;
Pred. No. 0;
RESULT 332
ID AED23807 standard; cDNA; 1295 BP.
DE Human secreted protein PRO 245 encoding gene, SEQ ID 63.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1295; DB 14; Length 1295;
Pred. No. 0;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 333
ID AED86250 standard; cDNA; 1295 BP.
DE Human PRO cDNA, seq id 335.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 14; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 334
ID ABE68976 standard; cDNA; 1295 BP.
DE Tyrosine kinase homologous PRO245 encoding gene, SEQ ID 63.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1295; DB 15; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 335
ID AAX81770 standard; cDNA; 1295 BP.
DE cDNA DNA35638 encoding A33 related antigen PRO245.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 96.1%; Score 1244; DB 2; Length 1295;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 336
ID AAS00157 standard; cDNA; 1295 BP.
DE Human cDNA clone DNA35638-1141 encoding PRO245 (UNQ219).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 96.1%; Score 1244; DB 4; Length 1295;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 337
ID ACN40835 standard; cDNA; 1721 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326887, SEQ ID NO:5879.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 73.6%; Score 953; DB 13; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 338
ID AAV82780 standard; cDNA; 1076 BP.
DE Clone ct684_4 isolated from human adult brain cDNA library.
PN WO9842739-A2.
PD 01-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 73.4%; Score 951; DB 2; Length 1076;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 339
ID ABQ92017 standard; cDNA; 1076 BP.
DE Human polynucleotide SEQ ID NO 14.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (WERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match 73.4%; Score 951; DB 6; Length 1076;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 340
ID ADP56686 standard; cDNA; 972 BP.
DE Human junction adhesion molecule 2 splice variant (huJAM2sv) cDNA.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELT.
Query Match 71.5%; Score 926; DB 12; Length 972;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 341

ID AAS00512 standard; cDNA; 1131 BP.
DE Human junctional adhesion protein (JAM2) cDNA.
PN WO200114404-A1.
PD 01-MAR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 70.3%; Score 910; DB 4; Length 1131;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 342
ID ACC72652 standard; cDNA; 1397 BP.
DE Human vascular endothelial junction-associated molecule cDNA.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 69.7%; Score 902; DB 10; Length 1397;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 343
ID ADV43971 standard; cDNA; 897 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1599.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 66.8%; Score 865; DB 14; Length 897;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 344
ID AAV34310 standard; DNA; 1022 BP.
DE Human secreted protein gene 25 clone HTEEB42.
PN WO9840483-A2.
PD 17-SEP-1998.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 63.4%; Score 821; DB 2; Length 1022;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 345
ID AAD44660 standard; cDNA; 1022 BP.
DE Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
PN US2002077287-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
Query Match 63.4%; Score 821; DB 6; Length 1022;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 346
ID AAD44878 standard; cDNA; 1022 BP.
DE Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
PN US2002076756-A1.
PD 20-JUN-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
Query Match 63.4%; Score 821; DB 6; Length 1022;
Best Local Similarity 99.8%; Pred. No. 0;

RESULT 347
ID ACC50637 standard; cDNA; 1022 BP.
DE Human secreted protein coding sequence, SEQ ID 304.
PN W0200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 63.4%; Score 821; DB 8; Length 1022;
Pred. No. 0;
RESULT 348
ID AB2711351 standard; cDNA; 1022 BP.
DE Secreted protein-encoding gene 162 cDNA clone HTEB42, SEQ ID NO:172.
PN W0200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 63.4%; Score 821; DB 8; Length 1022;
Pred. No. 0;
RESULT 349
ID ABX96990 standard; cDNA; 1022 BP.
DE Human secreted protein gene 25, cDNA.
PN US2002172994-A1.
PD 21-NOV-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
Query Match
Best Local Similarity 63.4%; Score 821; DB 8; Length 1022;
Pred. No. 0;
RESULT 350
ID ADB91286 standard; cDNA; 1022 BP.
DE Human secreted protein cDNA #SEQ ID 232.
PN W02003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 63.4%; Score 821; DB 9; Length 1022;
Pred. No. 0;
RESULT 351
ID ADC73716 standard; DNA; 1022 BP.
DE Human secreted protein-related DNA - SEQ ID 349.
PN W02003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 63.4%; Score 821; DB 10; Length 1022;
Pred. No. 0;
RESULT 352
ID ADG89762 standard; cDNA; 1022 BP.
DE Human cDNA from secreted protein gene 25.
PN US2003225009-A1.
PD 04-DEC-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.

Query Match
Best Local Similarity 63.4%; Score 821; DB 12; Length 1022;
Pred. No. 0;
RESULT 353
ID AED10199 standard; cDNA; 1022 BP.
DE Human secreted protein encoding cDNA clone, SEQ ID 35.
PN US2005208621-A1.
PD 22-SEP-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 63.4%; Score 821; DB 14; Length 1022;
Pred. No. 0;
RESULT 354
ID AAL51599 standard; DNA; 897 BP.
DE Human junctional adhesion molecule 2 (hujam2) coding sequence.
PN W02003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 60.9%; Score 789; DB 8; Length 897;
Pred. No. 0;
RESULT 355
ID AAL60897 standard; cDNA; 1389 BP.
DE Human novel splice variant of VEJAM (NOJAM) cDNA.
PN W02003046180-A2.
PD 05-JUN-2003.
PA (GEST) GENSET SA.
Query Match
Best Local Similarity 60.3%; Score 781; DB 9; Length 1389;
Pred. No. 0;
RESULT 356
ID AAI61103 standard; cDNA; 930 BP.
DE Human polynucleotide SEQ ID NO 5092.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 49.3%; Score 638; DB 4; Length 930;
Pred. No. 0;
RESULT 357
ID AAF74414 standard; DNA; 905 BP.
DE Angiogenesis protein AAA1 nucleotide sequence (Fig 7).
PN W020011086-A2.
PD 15-FEB-2001.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 47.6%; Score 617; DB 5; Length 905;
Pred. No. 1.1e-274;
RESULT 358
ID AAH98352 standard; cDNA; 1416 BP.
DE Human EST-derived coding sequence SEQ ID NO: 209.
PN W0200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 37.2%; Score 482; DB 4; Length 1416;
Pred. No. 2.7e-212;
RESULT 359
ID AAS86528 standard; cDNA; 1430 BP.
DE DNA encoding novel human diagnostic protein #22332.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 34.5%; Score 447; DB 5; Length 1430;
Pred. No. 4.1e-196;
RESULT 360
ID AAI59317 standard; cDNA; 561 BP.
DE Human polynucleotide SEQ ID NO 1520.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 34.4%; Score 446; DB 4; Length 561;
Pred. No. 1.2e-195;
RESULT 361
ID ACH37074 standard; cDNA; 450 BP.
DE Human endothelial cell cDNA #5207.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 30.0%; Score 389; DB 9; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.8e-169;
RESULT 362
ID AAX81783 standard; DNA; 413 BP.
DE Consensus sequence DNA30954 encoding an A33 related antigen.
PN W09927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 373; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 6.9e-162;
RESULT 363
ID AAX37665 standard; cDNA; 413 BP.
DE Human PRO protein derived EST consensus sequence DNA30954.
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 373; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 6.9e-162;
RESULT 364
ID AAX93489 standard; cDNA; 413 BP.
DE Consensus sequence expressed sequence tag, EST, DNA30954.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 373; DB 8; Length 413;
Best Local Similarity 100.0%; Pred. No. 6.9e-162;
RESULT 365
ID ADH62554 standard; DNA; 413 BP.
DE Human DNA30954 consensus sequence DNA.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 373; DB 10; Length 413;
Best Local Similarity 100.0%; Pred. No. 6.9e-162;
RESULT 366
ID ADN35306 standard; DNA; 413 BP.
DE Human PRO245 consensus DNA fragment DNA30954.
PN W02004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 373; DB 12; Length 413;
Best Local Similarity 100.0%; Pred. No. 6.9e-162;
RESULT 367
ID AAL35849 standard; DNA; 3762 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2214.
PN W0200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.5%; Score 343; DB 4; Length 3762;
Best Local Similarity 100.0%; Pred. No. 4.8e-148;
RESULT 368
ID AAL35848 standard; DNA; 3762 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2213.
PN W0200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.5%; Score 343; DB 4; Length 3762;
Best Local Similarity 100.0%; Pred. No. 4.8e-148;
RESULT 369
ID AAL35847 standard; DNA; 3762 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2212.
PN W0200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

ID ADP28230 standard; DNA; 270 BP.
DE Human secreted protein encoding sequence SEQ ID #228.
FN WO2004035732-A2.
PA 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 20.0%; Score 259; DB 12; Length 270;
Best Local Similarity 100.0%; Pred. No. 3.6e-109;
RESULT 379
ID ACH29690 standard; cDNA; 433 BP.
DE Human testis cDNA #76.
FN US2003073623-A1.
PA 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 19.8%; Score 257; DB 9; Length 433;
Best Local Similarity 100.0%; Pred. No. 2.9e-108;
RESULT 380
ID AAX37669 standard; cDNA; 253 BP.
DE Human PRO protein derived EST DNA sequence 1861250.
FN WO9914241-A2.
PA 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 19.5%; Score 253; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.1e-106;
RESULT 381
ID AAX37666 standard; cDNA; 228 BP.
DE Human PRO protein derived EST DNA sequence 2715631.
FN WO9914241-A2.
PA 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 228; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 7.7e-95;
RESULT 382
ID AAS86525 standard; cDNA; 493 BP.
DE DNA encoding novel human diagnostic protein #22329.
FN WO200175067-A2.
PA 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 17.6%; Score 228; DB 5; Length 493;
Best Local Similarity 100.0%; Pred. No. 7.5e-95;
RESULT 383
ID AAS86526 standard; cDNA; 208 BP.
DE DNA encoding novel human diagnostic protein #22330.
FN WO200175067-A2.
PA 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.1%; Score 208; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.4e-85;
RESULT 384
ID ACH03847 standard; cDNA; 604 BP.
DE Human cDNA differentially expressed in lung cancer #52.
FN US2003065157-A1.
PA 03-APR-2003.
PA (LASE/) LASEK A W.
Query Match 12.9%; Score 167; DB 9; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.2e-66;
RESULT 385
ID AAS86527 standard; cDNA; 581 BP.
DE DNA encoding novel human diagnostic protein #22331.
FN WO200175067-A2.
PA 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.0%; Score 156; DB 5; Length 581;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
RESULT 386
ID ABU65580 standard; DNA; 427 BP.
DE Lung cancer related gene sequence SEQ ID NO:3917.
FN WO200194629-A2.
PA 13-DEC-2001.
PA (AVAL-) AVALON PHARM.

Query Match 11.0%; Score 142; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.3e-55;
RESULT 387
ID ABL68041 standard; DNA; 427 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6378.
FN WO200194629-A2.
PA 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 11.0%; Score 142; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 4.3e-55;
RESULT 388
ID AAX37667 standard; cDNA; 241 BP.
DE Human PRO protein derived EST DNA sequence 1622388.
FN WO9914241-A2.
PA 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 9.6%; Score 124; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 9.2e-47;
RESULT 389
ID AAD35981 standard; DNA; 36998 BP.
DE Human transporter gene.
FN WO200222678-A2.
PA 21-MAR-2002.
PA (PEKE) PE CORP NY.
Query Match 5.0%; Score 65; DB 6; Length 36998;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
RESULT 390
ID AQ080838 standard; DNA; 14468 BP.
DE Human SPARC gene SEQ ID NO:7.
FN WO2004064785-A2.
PA 05-AUG-2004.
PA (DAND) DANA FARBER CANCER INST.
Query Match 4.7%; Score 61; DB 13; Length 14468;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
RESULT 391
ID ABN40786 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:13534.
FN WO200210449-A2.
PA 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 4.6%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
RESULT 392
ID ABV48272 standard; cDNA; 531 BP.
DE Human prostate expression marker cDNA 48263.
FN WO200160860-A2.
PA 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 60; DB 5; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.5e-17;
RESULT 393
ID ABV18488 standard; cDNA; 628 BP.
DE Human prostate expression marker cDNA 18479.
FN WO200160860-A2.
PA 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.6%; Score 60; DB 5; Length 628;
Best Local Similarity 100.0%; Pred. No. 3.5e-17;
RESULT 394
ID ACN45138 standard; DNA; 23694 BP.
DE Human genomic sequence hCG17175.
FN WO2003073826-A2.
PA 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.3%; Score 56; DB 11; Length 23694;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
RESULT 395
ID ADQ19501 standard; DNA; 135005 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.
FN WO2004048938-A2.
PA 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.3%; Score 56; DB 12; Length 135005;

Best Local Similarity 100.0%; Pred. No. 2e-15;
RESULT 396
ID ACN41055 standard; cDNA; 2706 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA327070, SEQ ID NO:6241.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.2%; Score 54; DB 13; Length 2706;
Best Local Similarity 100.0%; Pred. No. 2e-14;
RESULT 397
ID ACH28643 standard; cDNA; 465 BP.
DE Human adult ovary cDNA #7023.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.1%; Score 53; DB 9; Length 465;
Best Local Similarity 100.0%; Pred. No. 6e-14;
RESULT 398
ID ACH14407 standard; cDNA; 483 BP.
DE Human adult brain cDNA #1619.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.1%; Score 53; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 6e-14;
RESULT 399
ID AAK67660 standard; DNA; 4542 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22472.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 53; DB 4; Length 4542;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
RESULT 400
ID AAF31479 standard; DNA; 6644 BP.
DE ZALPHA associated DNA.
PN WO200100831-A1.
PD 04-JAN-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.1%; Score 53; DB 5; Length 6644;
Best Local Similarity 100.0%; Pred. No. 5.5e-14;
RESULT 401
ID ADF18591 standard; DNA; 6644 BP.
DE Human zalpha29 partial DNA.
PN US2003153050-A1.
PD 14-AUG-2003.
PA (CONK/) CONKLIN D C.
PA (GAOZ/) GAO Z.
Query Match 4.1%; Score 53; DB 10; Length 6644;
Best Local Similarity 100.0%; Pred. No. 5.5e-14;
RESULT 402
ID AAK67659 standard; DNA; 9360 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22471.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 53; DB 4; Length 9360;
Best Local Similarity 100.0%; Pred. No. 5.4e-14;
RESULT 403
ID AAK67658 standard; DNA; 16347 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22470.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 53; DB 4; Length 16347;

Best Local Similarity 100.0%; Pred. No. 5.3e-14;
RESULT 404
ID ABZ71971 standard; DNA; 16347 BP.
DE Secreted protein gene 126 genomic fragment HCFPE20, SEQ ID NO:1118.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 53; DB 8; Length 16347;
Best Local Similarity 100.0%; Pred. No. 5.3e-14;
RESULT 405
ID ADA44316 standard; DNA; 16347 BP.
DE Human secreted protein DNA SEQ ID 509.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 53; DB 8; Length 16347;
Best Local Similarity 100.0%; Pred. No. 5.3e-14;
RESULT 406
ID AAK89247 standard; DNA; 21010 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2823.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 52; DB 4; Length 21010;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
RESULT 407
ID AAL05888 standard; DNA; 21010 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8576.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 52; DB 4; Length 21010;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
RESULT 408
ID ABL98452 standard; DNA; 21010 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3104.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 52; DB 4; Length 21010;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
RESULT 409
ID ABZ74628 standard; DNA; 21010 BP.
DE Secreted protein gene 376 genomic fragment HWDAG96, SEQ ID NO:1775.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 52; DB 8; Length 21010;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
RESULT 410
ID ABZ68148 standard; DNA; 21010 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1671.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 52; DB 10; Length 21010;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
RESULT 411
ID AAK89248 standard; DNA; 21024 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2824.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 52; DB 4; Length 21024;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
RESULT 412
ID AAL05889 standard; DNA; 21024 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8577.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 52; DB 4; Length 21024;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22738.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 51; DB 4; Length 46553;
Best Local Similarity 100.0%; Pred. No. 4.3e-13;
RESULT 433
ID ADO97727 standard; DNA; 73063 BP.
DE Human cancer associated sequence HD10-034, SEQ ID 704.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.9%; Score 51; DB 12; Length 73063;
Best Local Similarity 100.0%; Pred. No. 4.2e-13;
RESULT 434
ID AED18395 standard; DNA; 128117 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 646.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 3.9%; Score 51; DB 14; Length 128117;
Best Local Similarity 100.0%; Pred. No. 4.2e-13;
RESULT 435
ID ACN44898 standard; DNA; 144723 BP.
DE Human genomic sequence HCG18129.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 51; DB 11; Length 144723;
Best Local Similarity 100.0%; Pred. No. 4.1e-13;
RESULT 436
ID ADL13501 standard; DNA; 167932 BP.
DE Osteoarthritis-associated polymorphic nucleotide #33.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 51; DB 10; Length 167932;
Best Local Similarity 100.0%; Pred. No. 4.1e-13;
RESULT 437
ID AED89393 standard; DNA; 217623 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 33.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 3.9%; Score 51; DB 14; Length 217623;
Best Local Similarity 100.0%; Pred. No. 4.1e-13;
RESULT 438
ID ACN45174 standard; DNA; 235070 BP.
DE Human genomic sequence HCG15927.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 51; DB 11; Length 235070;
Best Local Similarity 100.0%; Pred. No. 4.1e-13;
RESULT 439
ID AAS36075 standard; DNA; 112 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1575.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 440
ID AAS36074 standard; DNA; 112 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1574.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 441
ID AAK82885 standard; DNA; 112 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37697.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 442
ID ADE46768 standard; DNA; 112 BP.
DE Human cardiovascular system related genomic DNA #334.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 10; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 443
ID ADE46769 standard; DNA; 112 BP.
DE Human cardiovascular system related genomic DNA #335.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 10; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 444
ID ADJ08187 standard; DNA; 112 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1575.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 13; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 445
ID ADJ08186 standard; DNA; 112 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1574.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 13; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 446
ID AAK80057 standard; DNA; 151 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34869.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 447
ID AAC20203 standard; cDNA; 227 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 24278.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 50; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 448
ID ACD93907 standard; cDNA; 271 BP.
DE Human colon cancer cell expressed cDNA #2319.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
Query Match 3.9%; Score 50; DB 10; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 449
ID ACH21666 standard; cDNA; 364 BP.
DE Human adult ovary cDNA #46.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRWA/) DRWANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.

Query Match 3.9%; Score 50; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 450
ID ABV50314 standard; cDNA: 434 BP.
DE Human prostate expression marker cDNA 50305.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 50; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
RESULT 451
ID AAK66487 standard; DNA; 922 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21299.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 922;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
RESULT 452
ID AAK66488 standard; DNA; 1386 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21300.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 1386;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
RESULT 453
ID AAK67221 standard; DNA; 1386 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22033.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 1386;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
RESULT 454
ID AED17540 standard; DNA; 1912 BP.
DE Haplotype SNP7 associated with obesity.
PN WO2005090600-A2.
PD 29-SEP-2005.
PA (INTE-) INTEGRAGEN.
Query Match 3.9%; Score 50; DB 14; Length 1912;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
RESULT 455
ID AQ64843 standard; cDNA; 2525 BP.
DE Novel human cDNA sequence #2004.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.9%; Score 50; DB 12; Length 2525;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
RESULT 456
ID AAK74001 standard; DNA; 2786 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28813.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 2786;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
RESULT 457
ID AAK84144 standard; DNA; 7152 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38956.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 7152;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 458
ID AAK84002 standard; DNA; 15413 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38814.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 15413;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 459
ID AAD32327 standard; DNA; 15765 BP.
DE Human NFKB1B gene, alternative version.
PN WO200212497-A2.
PD 14-FEB-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 3.9%; Score 50; DB 6; Length 15765;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 460
ID AAD32179 standard; DNA; 15765 BP.
DE Human NFKB1B gene.
PN WO200212497-A2.
PD 14-FEB-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 3.9%; Score 50; DB 6; Length 15765;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 461
ID ADC18734 standard; DNA; 18722 BP.
DE 18722bp human desmin gene related DNA.
PN WO2003074711-A1.
PD 12-SEP-2003.
PA (TRGE) TRANSGENE SA.
Query Match 3.9%; Score 50; DB 10; Length 18722;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 462
ID AEB96529 standard; DNA; 20001 BP.
DE Human SUT2B1 gene, SEQ ID 13.
PN JP2005204549-A.
PD 04-AUG-2005.
PA (HYUB-) HYUBITTO GENOMICS KK.
PA (KAWA/) KAWADA Y.
Query Match 3.9%; Score 50; DB 14; Length 20001;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 463
ID ACC85730 standard; DNA; 33112 BP.
DE Human kinase enzyme gene.
PN WO2003095612-A2.
PD 20-NOV-2003.
PA (APPL-) APPLERA CORP.
Query Match 3.9%; Score 50; DB 10; Length 33112;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 464
ID AAD56159 standard; DNA; 38045 BP.
DE Human salvador genomic DNA.
PN WO2003035845-A2.
PD 01-MAY-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 3.9%; Score 50; DB 9; Length 38045;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 465
ID ADI38715 standard; DNA; 39001 BP.
DE Human LIM domain kinase 1 polynucleotide #4.
PN US2004014047-A1.
PD 22-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.9%; Score 50; DB 12; Length 39001;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 466
ID AAK84729 standard; DNA; 48037 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39541.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 48037;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 467
ID AAK85983 standard; DNA; 48037 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40795.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 48037;

Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 468
ID AAK84730 standard; DNA; 48045 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39542.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 48045;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 469
ID AAK85984 standard; DNA; 48045 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40796.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 50; DB 4; Length 48045;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 470
ID ACN44518 standard; DNA; 52510 BP.
DE Human genomic sequence hCG222647.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 50; DB 11; Length 52510;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 471
ID ADA02582 standard; DNA; 60940 BP.
DE Human REL carcinoma associated gene, SEQ ID NO:1100.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 50; DB 9; Length 60940;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 472
ID ADB72320 standard; DNA; 60940 BP.
DE Human REL gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 50; DB 10; Length 60940;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 473
ID ADE95830 standard; DNA; 60940 BP.
DE Human REL gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 50; DB 10; Length 60940;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 474
ID ABL62910 standard; DNA; 65608 BP.
DE Breast cancer related gene sequence SEQ ID NO:1247.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 50; DB 6; Length 65608;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 475
ID ABL64414 standard; DNA; 65608 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2751.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 50; DB 6; Length 65608;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 476
ID ABL67668 standard; DNA; 65608 BP.
DE Oesophagus cancer related gene sequence SEQ ID NO:6005.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 50; DB 6; Length 65608;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;

RESULT 477
ID AED18320 standard; DNA; 74371 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 571.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 3.9%; Score 50; DB 14; Length 74371;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 478
Query Match 3.9%; Score 50; DB 14; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 479
ID ABK83572 standard; cDNA; 110608 BP.
DE Human cDNA differentially expressed in granulocytic cells #143.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.9%; Score 50; DB 6; Length 110608;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 480
ID ADR52842 standard; DNA; 110608 BP.
DE Drug therapy altered expressed gene #193.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A. J.
PA (TREP/) TREPICCHIO W. L.
Query Match 3.9%; Score 50; DB 13; Length 110608;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 481
ID AED18211 standard; DNA; 110608 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 462.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 3.9%; Score 50; DB 14; Length 110608;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 482
ID AEF75271 standard; DNA; 110608 BP.
DE Human polynucleotide #785.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 3.9%; Score 50; DB 15; Length 110608;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 483
ID ADR52890 standard; DNA; 115935 BP.
DE Drug therapy altered expressed gene #241.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A. J.
PA (TREP/) TREPICCHIO W. L.
Query Match 3.9%; Score 50; DB 13; Length 115935;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 484
ID ACN45206 standard; DNA; 139214 BP.
DE Human genomic sequence hCG23831.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 50; DB 11; Length 139214;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 485
ID AAD46127 standard; DNA; 163350 BP.
DE Human tumour suppressor gene.
PN WO200268468-A2.
PD 06-SEP-2002.

PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 50; DB 6; Length 163350;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 486
ID ADL13775 standard; DNA; 173805 BP.
DE Osteoarthritis-associated polymorphic nucleotide #307.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 50; DB 10; Length 173805;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 487
ID ADM69029 standard; DNA; 191150 BP.
DE Human platelet derived growth factor receptor alpha wild-type gDNA.
PN WO20030105773-A2.
PD 24-DEC-2003.
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND) DANA FARBER CANCER INST INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (USGO) US DEPT VETERANS AFFAIRS.
Query Match 3.9%; Score 50; DB 12; Length 191150;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 488
ID AED89391 standard; DNA; 207600 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 31.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 3.9%; Score 50; DB 14; Length 207600;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 489
ID ABD32868 standard; DNA; 238417 BP.
DE Human cancer-associated genomic DNA HD17-053.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.9%; Score 50; DB 13; Length 238417;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 490
ID ABD32694 standard; DNA; 252907 BP.
DE Human cancer-associated genomic DNA HD14-012.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.9%; Score 50; DB 13; Length 252907;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 491
ID ACN44042 standard; DNA; 338702 BP.
DE Human genomic sequence hCG323359.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.9%; Score 50; DB 11; Length 338702;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
RESULT 492
ID AAK75733 standard; DNA; 173 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30545.
PN WO2000157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 4; Length 173;
Best Local Similarity 100.0%; Pred. No. 4.4e-12;
RESULT 493
ID ABV57718 standard; cDNA; 432 BP.
DE Human prostate expression marker cDNA 57709.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.8%; Score 49; DB 5; Length 432;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
RESULT 494
ID ABN63722 standard; cDNA; 652 BP.
DE Human cancer related polynucleotide SEQ ID NO 3689.

PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.8%; Score 49; DB 6; Length 652;
Best Local Similarity 100.0%; Pred. No. 4.2e-12;
RESULT 495
ID AAK73494 standard; DNA; 1264 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28306.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 4; Length 1264;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
RESULT 496
ID AAK75760 standard; DNA; 1264 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30572.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 4; Length 1264;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
RESULT 497
ID AAZ27262 standard; cDNA; 1841 BP.
DE Human secreted protein cDNA encoding gene 30.
PN WO9946289-A1.
PD 16-SEP-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 2; Length 1841;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
RESULT 498
ID ADB61945 standard; cDNA; 3004 BP.
DE Human cDNA encoding clone BRACE20055560.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.8%; Score 49; DB 10; Length 3004;
Best Local Similarity 100.0%; Pred. No. 4e-12;
RESULT 499
ID AAK74676 standard; DNA; 7760 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29488.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 4; Length 7760;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
RESULT 500
ID ADU21193 standard; DNA; 25138 BP.
DE Human chromosomal DNA contig.
PN WO2004096016-A2.
PD 11-NOV-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.8%; Score 49; DB 13; Length 25138;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
RESULT 501
ID ADU48765 standard; DNA; 25138 BP.
DE Human glucagon receptor (GCGR) polynucleotide seqid 18.
PN WO2004096996-A2.
PD 11-NOV-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.8%; Score 49; DB 13; Length 25138;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
RESULT 502
ID ABA07406 standard; DNA; 32249 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 725.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 4; Length 32249;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
RESULT 503
ID AAK91137 standard; DNA; 32249 BP.

DE Human digestive system antigen genomic sequence SEQ ID NO: 4713.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 4; Length 32249;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
RESULT 504
ID ADA20005 standard; DNA; 32249 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12336.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 5; Length 32249;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
RESULT 505
ID AAK87551 standard; DNA; 50442 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42363.
PN WO200157182-A2.
PD 03-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 4; Length 50442;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
RESULT 506
ID AAK73083 standard; DNA; 50442 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27895.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.8%; Score 49; DB 4; Length 50442;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
RESULT 507
ID ADQ97207 standard; DNA; 56181 BP.
DE Human cancer associated sequence HD08-013, SEQ ID 183.
PN WO2004060304-A2.
PD 23-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.8%; Score 49; DB 12; Length 56181;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
RESULT 508
ID ADA02618 standard; DNA; 78313 BP.
DE Human FYN carcinoma associated gene, SEQ ID NO:1136.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.8%; Score 49; DB 9; Length 78313;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
RESULT 509
ID ADB72356 standard; DNA; 78313 BP.
DE Human FYN gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.8%; Score 49; DB 10; Length 78313;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
RESULT 510
ID ADE95866 standard; DNA; 78313 BP.
DE Human FYN gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.8%; Score 49; DB 10; Length 78313;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
RESULT 511
ID AAF30035 standard; DNA; 81001 BP.
DE Human apolipoprotein A-IV-related protein (AA4RP) gene.
PN WO200100803-A2.
PD 04-JAN-2001.
PA (GEST) GENSET.
Query Match 3.8%; Score 49; DB 4; Length 81001;
Best Local Similarity 100.0%; Pred. No. 3.6e-12;
RESULT 512
ID ACN44286 standard; DNA; 105219 BP.
DE Human genomic sequence hCG36856.

PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.8%; Score 49; DB 11; Length 105219;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
RESULT 513
ID ADC87336 standard; DNA; 108316 BP.
DE Human GPCR gene SEQ ID NO:1789.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.8%; Score 49; DB 10; Length 108316;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
RESULT 514
Query Match 3.8%; Score 49; DB 14; Length 110000;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
RESULT 515
ID ACN45206 standard; DNA; 139214 BP.
DE Human genomic sequence hCG23831.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.8%; Score 49; DB 11; Length 139214;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
RESULT 516
ID ADQ19389 standard; DNA; 155937 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2208.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.8%; Score 49; DB 12; Length 155937;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
RESULT 517
ID ADL08108 standard; DNA; 188971 BP.
DE Human gene associated with low HDL-C APOA1.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 3.8%; Score 49; DB 12; Length 188971;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
RESULT 518
ID AAX81786 standard; cDNA; 48 BP.
DE Probe used to isolate cDNA clones encoding PRO245.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 519
ID AAX37602 standard; DNA; 48 BP.
DE Human PRO245 hybridisation probe.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 520
ID AAX52313 standard; DNA; 48 BP.
DE Probe used to isolate a cDNA clone encoding PRO245.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 521
ID AAC56419 standard; DNA; 48 BP.
DE Human PRO245 (UNQ219) hybridisation probe SEQ ID NO:39.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;

RESULT 522
ID AA252211 standard; DNA; 48 BP.
DE Hybridisation probe to isolate cDNA clone encoding human PRO245.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 3; Length 48;
Pred. No. 1.3e-11;
RESULT 523
ID AA77565 standard; DNA; 48 BP.
DE Human PRO245 hybridisation probe SEQ ID NO:70.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 3; Length 48;
Pred. No. 1.3e-11;
RESULT 524
ID ADC78387 standard; DNA; 48 BP.
DE Human PRO protein-related probe SEQ ID 67.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 3; Length 48;
Pred. No. 1.3e-11;
RESULT 525
ID AAF72471 standard; DNA; 48 BP.
DE Human PRO polypeptide gene hybridisation probe SEQ ID NO: 67.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 4; Length 48;
Pred. No. 1.3e-11;
RESULT 526
ID AAS00166 standard; DNA; 48 BP.
DE Hybridisation probe for Human cDNA clone encoding PRO245 (UNQ219).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 4; Length 48;
Pred. No. 1.3e-11;
RESULT 527
ID AAC97440 standard; DNA; 48 BP.
DE Human PRO245 hybridisation probe, SEQ ID NO:94.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 4; Length 48;
Pred. No. 1.3e-11;
RESULT 528
ID AAC91499 standard; DNA; 48 BP.
DE Human PRO cDNA PCR primer, SEQ ID NO: 12.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 5; Length 48;
Pred. No. 1.3e-11;
RESULT 529
ID ACA60055 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein PRO245 probe.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 8; Length 48;
Pred. No. 1.3e-11;
RESULT 530
ID ACD07455 standard; DNA; 48 BP.
DE Novel human secreted and transmembrane protein PCR probe #9.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 8; Length 48;
Pred. No. 1.3e-11;
RESULT 531

ID ABX71503 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein PRO245 probe.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 8; Length 48;
Pred. No. 1.3e-11;
RESULT 532
ID ACH06835 standard; DNA; 48 BP.
DE Human secreted/transmembrane polypeptide PRO245 probe.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 8; Length 48;
Pred. No. 1.3e-11;
RESULT 533
ID AEX96072 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein cDNA, #13, probe.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 8; Length 48;
Pred. No. 1.3e-11;
RESULT 534
ID ACA05393 standard; DNA; 48 BP.
DE Human secreted protein PRO245 probe.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 8; Length 48;
Pred. No. 1.3e-11;
RESULT 535
ID ACD20060 standard; DNA; 48 BP.
DE Human secreted / transmembrane polypeptide PRO245 probe.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 8; Length 48;
Pred. No. 1.3e-11;
RESULT 536
ID ABX93492 standard; DNA; 48 BP.
DE Human DNA35638 hybridisation probe.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 8; Length 48;
Pred. No. 1.3e-11;
RESULT 537
ID ACA54863 standard; DNA; 48 BP.
DE Novel secreted and transmembrane protein associated probe #9.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 8; Length 48;
Pred. No. 1.3e-11;
RESULT 538
ID ACD19698 standard; DNA; 48 BP.
DE Human secreted / transmembrane polypeptide PRO245 probe.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 9; Length 48;
Pred. No. 1.3e-11;
RESULT 539
ID ADB29272 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 9; Length 48;
Pred. No. 1.3e-11;
RESULT 540
ID ADA18128 standard; DNA; 48 BP.

DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 541
ID ACD66845 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein PRO245 probe.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 542
ID ACD83006 standard; DNA; 48 BP.
DE Human PRO probe #14.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 543
ID ADA16103 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 544
ID ADA42248 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 545
ID ACD23184 standard; DNA; 48 BP.
DE Human PRO probe #11.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 546
ID ADA16527 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 547
ID ADA12956 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 548
ID ADA41824 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 549
ID ADA17171 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.

PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 550
ID ADA42674 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 551
ID ACD23546 standard; DNA; 48 BP.
DE Human PRO probe #11.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 552
ID ADB77593 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 553
ID ADB74729 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 554
ID ADC28375 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 555
ID ADC39575 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 556
ID ADC40089 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 557
ID ADC18917 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 558
ID ADC34213 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003036094-A1.

PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 559
ID ADC29268 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 560
ID ADC28799 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 561
ID ADC40684 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 562
ID ADC19341 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 563
ID ADC33789 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 564
ID ADC12859 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 565
ID ADC12311 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 566
ID ADD04866 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 567
ID ADD03872 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003104381-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 568
ID ADD03448 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 569
ID ADE34700 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 570
ID ADH62557 standard; DNA; 48 BP.
DE Human DNA30954 consensus DNA specific hybridisation probe.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 571
ID ADH59183 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 572
ID ADI37962 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 573
ID ACA58951 standard; DNA; 48 BP.
DE Human PRO probe #11.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 574
ID ACA58348 standard; DNA; 48 BP.
DE Probe #12 used to isolate cDNA encoding a human PRO polypeptide.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 575
ID ADJ26230 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;


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RESULT 576
ID ADE79145 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 577
ID ADE79569 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 578
ID ADE73245 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 579
ID ADE73780 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US20031148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 580
ID ADE99334 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 581
ID ADE98453 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 582
ID ADE98880 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 583
ID ADG40350 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 584
ID ADF73744 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 585
ID ADF73320 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 586
ID ADG92163 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 587
ID ADG92590 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 588
ID ADH20379 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 589
ID ADH07234 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 590
ID ADH59779 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 591
ID ADH06807 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
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RESULT 592
ID AD118549 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 593
ID AD165269 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 594
ID AD137532 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 595
ID ADH97336 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 596
ID AD165696 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 597
ID ADH60439 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN ) DESNOYERS L.
PA (GODD ) GODDARD A.
PA (GODO ) GODOWSKI P J.
PA (GURN ) GURNEY A L.
PA (MATH ) MATHER J P.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 598
ID ADJ99496 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 599
ID ADL08689 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 600
ID ADM25034 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 601
ID ADM29780 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 602
ID ADO06102 standard; DNA; 48 BP.
DE Human PRO probe #11.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 603
ID ADN35309 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 604
ID ADR10954 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 3.7%; Score 48; DB 12; Length 48;
Pred. No. 1.3e-11;
RESULT 605
ID ADR17863 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK ) ASHKENAZI A.
PA (BOTS ) BOTSTEIN D.
PA (DESN ) DESNOYERS L.
PA (EATO ) EATON D L.
PA (FERR ) FERRARA N.
PA (FILV ) FILVAROFF E.
PA (FONG ) FONG S.
PA (GAOW ) GAO W.
PA (GERB ) GERBER H.
PA (GERR ) GERRITSEN M E.
PA (GODD ) GODDARD A.
PA (GODO ) GODOWSKI P J.
PA (GRIM ) GRIMALDI C J.
PA (GURN ) GURNEY A L.
PA (HILL ) HILLAN K J.
PA (KLJA ) KLJAVIN I J.
PA (MATH ) MATHER J P.
PA (PANJ ) PAN J.
PA (PAON ) PAONI N F.
PA (ROYM ) ROY M A.
PA (STEW ) STEWART T A.
PA (TUMA ) TUMAS D.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
Query Match
Best Local Similarity 3.7%; Score 48; DB 13; Length 48;
Pred. No. 1.3e-11;
RESULT 606
ID ADT94240 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN AU2003259607-A1.
PD 27-NOV-2003.

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PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 13; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 607
ID ADS74502 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF B.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 3.7%; Score 48; DB 13; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 608
ID ADT03539 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 13; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 609
ID AEA37777 standard; DNA; 48 BP.
DE Human secreted/transmembrane protein, #13, DNA probe #1.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 14; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 610
ID AED23811 standard; DNA; 48 BP.
DE Human secreted protein PRO 245 hybridization probe, SEQ ID 67.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 14; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 611
ID AEE68980 standard; DNA; 48 BP.
DE Tyrosine kinase homologous PRO245 PCR primer/probe, SEQ ID 67.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Query Match 3.7%; Score 48; DB 15; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 612
ID AAI69074 standard; DNA; 234 BP.
DE Activated T-cell derived DNA fragment #210.
PN DE10021834-A1.
PD 15-NOV-2001.
PA (LYNX-) LYNX THERAPEUTICS GMBH.
Query Match 3.7%; Score 48; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 613
ID AAQ5959 standard; cDNA; 286 BP.
DE Human brain Expressed Sequence Tag EST01930.
PN WO9316178-A2.
PD 19-AUG-1993.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match 3.7%; Score 48; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
RESULT 614
ID AAI82362 standard; cDNA; 394 BP.
DE Human polynucleotide SEQ ID NO 2422.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.7%; Score 48; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
RESULT 615
ID ABN61483 standard; cDNA; 433 BP.
DE Human cancer related polynucleotide SEQ ID NO 1450.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.7%; Score 48; DB 6; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
RESULT 616
ID ACL60086 standard; cDNA; 433 BP.
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:6221.
PN WO2005000087-A2.
PD 06-JAN-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.7%; Score 48; DB 14; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
RESULT 617
ID ABK42295 standard; DNA; 10256 BP.
DE Genomic sequence #194 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 48; DB 4; Length 10256;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 618
ID ADB60451 standard; DNA; 10256 BP.
DE Connective tissue related genomic DNA #194.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 48; DB 9; Length 10256;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 619
ID AAL04059 standard; DNA; 10339 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6747.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 48; DB 4; Length 10339;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 620
ID AAS40445 standard; DNA; 10339 BP.
DE DNA encoding human prostate cancer antigen, Seq ID No 597.
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 48; DB 5; Length 10339;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 621
ID ADJ09651 standard; DNA; 10339 BP.
DE Human prostate cancer associated gene-related DNA SeqID597.
PN US2003054373-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 48; DB 11; Length 10339;


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Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 622
ID ABK13086 standard; DNA; 10500 BP.
DE DNA encoding immunoglobulin superfamily member GP286.
PN WO200200727-A2.
PD 03-JAN-2002.
PA (BIOJ-) BIOGEN INC.
Query Match 3.7%; Score 48; DB 6; Length 10500;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 623
ID ACD13393 standard; cDNA; 15382 BP.
DE Human DNA encoding a p53 modifier, SEQ ID 64.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 3.7%; Score 48; DB 8; Length 15382;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 624
ID ACN37222 standard; DNA; 20001 BP.
DE Human periodontal disease related gene TIMP3 SEQ ID NO:132.
PN WO2004042054-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (KAMO/) KAMO I K.
Query Match 3.7%; Score 48; DB 13; Length 20001;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 625
ID AAK77045 standard; DNA; 23130 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31857.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 48; DB 4; Length 23130;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 626
ID ABX11387 standard; DNA; 29921 BP.
DE DNA encoding human growth factor A.ctg12831-000000.10.0.
PN US2002164709-A1.
PD 07-NOV-2002.
PA (AFFY-) AFFYMETRIX INC.
Query Match 3.7%; Score 48; DB 8; Length 29921;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 627
ID ABA18857 standard; DNA; 32196 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11188.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.7%; Score 48; DB 5; Length 32196;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
RESULT 628
ID ACN43958 standard; DNA; 75839 BP.
DE Human genomic sequence hCG1640505.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.7%; Score 48; DB 11; Length 75839;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 629
ID ADQ94674 standard; DNA; 77777 BP.
DE Human chromosome 15 nucleotides 362825-440601.
PN US2004121328-A1.
PD 24-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.7%; Score 48; DB 12; Length 77777;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 630
ID ADP03055 standard; cDNA; 124987 BP.
DE Human housekeeping gene cDNA #96.
PN JP2004135552-A.
PD 13-MAY-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 3.7%; Score 48; DB 12; Length 124987;

Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 631
ID ADS8553 standard; cDNA; 124990 BP.
DE Human housekeeping gene cDNA sequence SEQ ID NO:96.
PN WO2004035785-A1.
PD 29-APR-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 3.7%; Score 48; DB 13; Length 124990;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 632
ID ADU60195 standard; cDNA; 124990 BP.
DE Housekeeping gene cDNA, SEQ ID 156.
PN US2004229233-A1.
PD 18-NOV-2004.
PA (NIGA) NGK INSULATORS LTD.
Query Match 3.7%; Score 48; DB 13; Length 124990;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 633
ID ABL68122 standard; DNA; 174424 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6459.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.7%; Score 48; DB 6; Length 174424;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 634
ID ADQ19573 standard; DNA; 181343 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.7%; Score 48; DB 12; Length 181343;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 635
ID ABK83564 standard; cDNA; 198161 BP.
DE Human cDNA differentially expressed in granulocytic cells #135.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.7%; Score 48; DB 6; Length 198161;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 636
ID ADQ17348 standard; DNA; 198161 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 165.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.7%; Score 48; DB 12; Length 198161;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 637
ID ADR52701 standard; DNA; 198161 BP.
DE Drug therapy altered expressed gene #52.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 3.7%; Score 48; DB 13; Length 198161;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 638
ID ABK84798 standard; cDNA; 220895 BP.
DE Human cDNA differentially expressed in granulocytic cells #1369.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.7%; Score 48; DB 6; Length 220895;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 639
ID ADR52737 standard; DNA; 220895 BP.
DE Drug therapy altered expressed gene #88.
PN WO2004072265-A2.

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ID 26-AUG-2004.
PA (AMHP) WIETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 3.7%; Score 48; DB 13; Length 220895;
Best Local Similarity 100.0%; Pred. No. 1e-11;
RESULT 640
ID ACN45174 standard; DNA; 235070 BP.
DE Human genomic sequence hCG15927.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.7%; Score 48; DB 11; Length 235070;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
RESULT 641
ID ACN45182 standard; DNA; 261817 BP.
DE Human genomic sequence hCG14925.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.7%; Score 48; DB 11; Length 261817;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
RESULT 642
ID AQO97433 standard; DNA; 295772 BP.
DE Human cancer associated sequence HD08-047, SEQ ID 410.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.7%; Score 48; DB 12; Length 295772;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
RESULT 643
ID AAK76146 standard; DNA; 109 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30958.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
RESULT 644
ID ABV49815 standard; cDNA; 325 BP.
DE Human prostate expression marker cDNA 49806.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 47; DB 5; Length 325;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
RESULT 645
ID ABV49728 standard; cDNA; 352 BP.
DE Human prostate expression marker cDNA 49719.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 47; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
RESULT 646
ID ABV19967 standard; cDNA; 421 BP.
DE Human prostate expression marker cDNA 19958.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 47; DB 5; Length 421;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
RESULT 647
ID ASV20056 standard; cDNA; 531 BP.
DE Human prostate expression marker cDNA 20047.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 47; DB 5; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
RESULT 648

ID AAC79899 standard; cDNA; 1154 BP.
DE Human secreted protein encoding cDNA for gene 2.
PN WO200055200-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 3; Length 1154;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
RESULT 649
ID ADQ38623 standard; DNA; 1690 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 286.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.6%; Score 47; DB 13; Length 1690;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
RESULT 650
ID AAK78365 standard; DNA; 1693 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33177.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 4; Length 1693;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
RESULT 651
ID AAK78362 standard; DNA; 1693 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33174.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 4; Length 1693;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
RESULT 652
ID ABD01719 standard; cDNA; 1715 BP.
DE Human solid cancer antigen polypeptide cDNA SEQ ID NO 68.
PN WO2005093063-A1.
PD 06-OCT-2005.
PA (MEDI-) MEDICAL BIOLOGICAL LAB CO LTD.
PA (SHIM/) SHIMADA H.
Query Match 3.6%; Score 47; DB 14; Length 1715;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
RESULT 653
ID ADQ63400 standard; cDNA; 1967 BP.
DE Novel human cDNA sequence #561.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 47; DB 12; Length 1967;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
RESULT 654
ID ADR08388 standard; cDNA; 2301 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1894.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 47; DB 13; Length 2301;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
RESULT 655
ID AAK91340 standard; DNA; 5780 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4916.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 4; Length 5780;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
RESULT 656
ID AAK79810 standard; DNA; 5780 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34622.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 4; Length 5780;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
RESULT 657

RESULT 666
ID ADZ42275 standard; DNA; 5287 BP.
DE Human thiadze sensitivity NaCl symporter gene with C4784T SNP Seq 2.
PN JP2005110606-A.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 4; Length 5780;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
RESULT 667
ID ABL98579 standard; DNA; 5780 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3231.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 4; Length 5780;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
RESULT 668
ID ADR05177 standard; DNA; 6518 BP.
DE Human serine/threonine kinase 6 (STK6) DNA.
PN WO2004065959-A2.
PD 05-AUG-2004.
PA (ETRX-) ETRX THERAPEUTICS LTD.
Query Match 3.6%; Score 47; DB 13; Length 6518;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
RESULT 669
ID ADR05177 standard; DNA; 6518 BP.
DE Human serine/threonine kinase 6 (STK6) DNA.
PN WO2004065959-A2.
PD 05-AUG-2004.
PA (ETRX-) ETRX THERAPEUTICS LTD.
Query Match 3.6%; Score 47; DB 13; Length 6518;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
RESULT 670
ID ADP23812 standard; cDNA; 6906 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:990.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 3.6%; Score 47; DB 13; Length 6906;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
RESULT 671
ID AAK7961 standard; DNA; 10468 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32773.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 4; Length 10468;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
RESULT 672
ID AAL53468 standard; DNA; 20951 BP.
DE Genomic DNA encoding human Ras-like protein.
PN WO200272765-A2.
PD 19-SEP-2002.
PA (PEKE) PE CORP NY.
Query Match 3.6%; Score 47; DB 6; Length 20951;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
RESULT 673
ID ADQ59374 standard; DNA; 25899 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:10.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 47; DB 12; Length 25899;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
RESULT 674
ID AOC87242 standard; DNA; 38918 BP.
DE Human GPCR gene SEQ ID NO:1695.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.6%; Score 47; DB 10; Length 38918;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
RESULT 675
ID ADU50859 standard; DNA; 48208 BP.
DE Human thiadze sensitive Na-Cl cotransporter gene - SEQ ID 1.
PN JP2004313168-A.
PD 11-NOV-2004.
PA (KOKU-) KOKURITSU JUNKANKI BYO CENT SOCHO.
PA (DOKU-) DOKURITSU GYOSHI HOJIN IYAKUJIN IRYO KIK.
Query Match 3.6%; Score 47; DB 13; Length 48208;
Best Local Similarity 100.0%; Pred. No. 3e-11;

RESULT 666
ID ADZ42275 standard; DNA; 5287 BP.
DE Human thiadze sensitivity NaCl symporter gene with C4784T SNP Seq 2.
PN JP2005110606-A.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 47; DB 4; Length 5287;
Best Local Similarity 100.0%; Pred. No. 3e-11;
RESULT 667
ID ACN43886 standard; DNA; 61103 BP.
DE Human genomic sequence hCG1784975.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 47; DB 11; Length 61103;
Best Local Similarity 100.0%; Pred. No. 3e-11;
RESULT 668
ID ADZ13418 standard; DNA; 85920 BP.
DE Human cancer-associated genomic DNA #80.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.6%; Score 47; DB 14; Length 85920;
Best Local Similarity 100.0%; Pred. No. 3e-11;
RESULT 669
ID ADL13678 standard; DNA; 97700 BP.
DE Osteoarthritis-associated polymorphic nucleotide #210.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 47; DB 10; Length 97700;
Best Local Similarity 100.0%; Pred. No. 3e-11;
RESULT 670
ID ADO32260 standard; DNA; 106707 BP.
DE Human chromosome 20 region containing type 2 diabetes mellitus genes.
PN WO2004039954-A2.
PD 13-MAY-2004.
PA (JOSL-) JOSLIN DIABETES CENT INC.
Query Match 3.6%; Score 47; DB 12; Length 106707;
Best Local Similarity 100.0%; Pred. No. 3e-11;
RESULT 671
ID ADZ12617 standard; DNA; 575899 BP.
DE Human cancer-associated genomic DNA #12.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.6%; Score 47; DB 14; Length 110000;
Best Local Similarity 100.0%; Pred. No. 3e-11;
RESULT 672
ID ADQ18153 standard; DNA; 112604 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 970.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.6%; Score 47; DB 12; Length 112604;
Best Local Similarity 100.0%; Pred. No. 3e-11;
RESULT 673
ID ADL13941 standard; DNA; 125515 BP.
DE Osteoarthritis-associated polymorphic nucleotide #473.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.6%; Score 47; DB 10; Length 125515;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
RESULT 675
ID ABK84798 standard; cDNA; 220895 BP.
DE Human cDNA differentially expressed in granulocytic cells #1369.
PN WO200228999-A2.
PD 11-APR-2002.

PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 47; DB 6; Length 220895;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
RESULT 676
ID ADR52737 standard; DNA; 220895 BP.
DE Drug therapy altered expressed gene #88.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 3.6%; Score 47; DB 13; Length 220895;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
RESULT 677
ID AD213715 standard; DNA; 234882 BP.
DE Human cancer-associated genomic DNA #106.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.6%; Score 47; DB 14; Length 234882;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
RESULT 678
ID ADQ59422 standard; DNA; 246940 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:58.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 47; DB 12; Length 246940;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
RESULT 679
ID ACH26529 standard; cDNA; 496 BP.
DE Human adult ovary cDNA #4909.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.6%; Score 46; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 680
ID ABV48210 standard; cDNA; 551 BP.
DE Human prostate expression marker cDNA 48201.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 46; DB 5; Length 551;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 681
ID ABV18425 standard; cDNA; 613 BP.
DE Human prostate expression marker cDNA 18416.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.6%; Score 46; DB 5; Length 613;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 682
ID AAL02996 standard; DNA; 1160 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5684.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 46; DB 4; Length 1160;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 683
ID ABL97343 standard; DNA; 1160 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 1995.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.6%; Score 46; DB 4; Length 1160;
Best Local Similarity 100.0%; Pred. No. 1e-10;
RESULT 684
ID AAH17845 standard; cDNA; 2566 BP.
DE Human cDNA sequence SEQ ID NO:17535.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.6%; Score 46; DB 4; Length 2566;
Best Local Similarity 100.0%; Pred. No. 9.8e-11;
RESULT 685
ID AED22705 standard; cDNA; 2566 BP.
DE Human TRRF1 (TRF1)-interacting nuclear factor 2 (TINF2), cDNA SEQ ID 597.
PN WO2005057189-A1.
PD 20-OCT-2005.
PA (GENE-) GENE CARE RES INST CO LTD.
Query Match 3.6%; Score 46; DB 14; Length 2566;
Best Local Similarity 100.0%; Pred. No. 9.8e-11;
RESULT 686
ID ADQ83826 standard; cDNA; 2824 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #640.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.6%; Score 46; DB 13; Length 2824;
Best Local Similarity 100.0%; Pred. No. 9.7e-11;
RESULT 687
ID ACN38463 standard; cDNA; 2824 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA324787, SEQ ID NO:1994.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.6%; Score 46; DB 13; Length 2824;
Best Local Similarity 100.0%; Pred. No. 9.7e-11;
RESULT 688
ID ADA53590 standard; cDNA; 2841 BP.
DE Human coding sequence, SEQ ID 1158.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 46; DB 10; Length 2841;
Best Local Similarity 100.0%; Pred. No. 9.7e-11;
RESULT 689
ID AAS41928 standard; DNA; 3011 BP.
DE Genomic sequence #244 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 46; DB 4; Length 3011;
Best Local Similarity 100.0%; Pred. No. 9.7e-11;
RESULT 690
ID AAS35102 standard; DNA; 3011 BP.
DE DNA #52 encoding human neoplastic disease associated polypeptide.
PN WO200155163-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 46; DB 4; Length 3011;
Best Local Similarity 100.0%; Pred. No. 9.7e-11;
RESULT 691
ID ADC46544 standard; DNA; 3011 BP.
DE Human neoplastic disease-associated gene 96 DNA #2.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 46; DB 10; Length 3011;
Best Local Similarity 100.0%; Pred. No. 9.7e-11;
RESULT 692
ID ADR08002 standard; cDNA; 4234 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1508.
PN EP1447413-A2.

PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.6%; Score 46; DB 13; Length 4234;
Best Local Similarity 100.0%; Pred. No. 9.6e-11;
RESULT 693
ID ADO80844 standard; DNA; 4551 BP.
DE Human SPARC gene SEQ ID NO:13.
PD 05-AUG-2004.
PA (DAND) DANA FARBER CANCER INST.
Query Match 3.6%; Score 46; DB 13; Length 4651;
Best Local Similarity 100.0%; Pred. No. 9.8e-11;
RESULT 694
ID ABE39819 standard; DNA; 6209 BP.
DE Human TCF19 gene.
PD 02-DEC-2005.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 3.6%; Score 46; DB 15; Length 6209;
Best Local Similarity 100.0%; Pred. No. 9.5e-11;
RESULT 695
ID AEA61128 standard; DNA; 6798 BP.
DE Human FLJ20132 gene genomic sequence SEQ ID NO:38.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 3.6%; Score 46; DB 14; Length 6798;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 696
ID AAS27657 standard; DNA; 7734 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1317.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 46; DB 4; Length 7734;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 697
ID AAK72311 standard; DNA; 7734 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27123.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 46; DB 4; Length 7734;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 698
ID ABE94460 standard; DNA; 7734 BP.
DE Novel human protein DNA #69.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.6%; Score 46; DB 10; Length 7734;
Best Local Similarity 100.0%; Pred. No. 9.4e-11;
RESULT 699
ID AAK83897 standard; DNA; 17245 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38709.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.6%; Score 46; DB 4; Length 17245;
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
RESULT 700
ID AA232184 standard; cDNA; 26928 BP.
DE Human prothrombin nucleotide sequence.
PD 07-OCT-1999.
PA (WHEH) WHITEHEAD INST BIOMEDICAL RES.
Query Match 3.6%; Score 46; DB 2; Length 26928;
Best Local Similarity 100.0%; Pred. No. 9e-11;
RESULT 701
ID ABN95780 standard; DNA; 26928 BP.
DE Gene #2278 used to diagnose liver cancer.

PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.6%; Score 46; DB 6; Length 26928;
Best Local Similarity 100.0%; Pred. No. 9e-11;
RESULT 702
ID ABQ77403 standard; DNA; 26928 BP.
DE Human F2 DNA.
PD 27-FEB-2003.
PA (VITI-) VITIVITY INC.
Query Match 3.6%; Score 46; DB 8; Length 26928;
Best Local Similarity 100.0%; Pred. No. 9e-11;
RESULT 703
ID ADB88550 standard; DNA; 26928 BP.
DE Human Factor 2, F2, gene, SEQ ID 1.
PD 10-APR-2003.
PA (VITI-) VITIVITY INC.
Query Match 3.6%; Score 46; DB 10; Length 26928;
Best Local Similarity 100.0%; Pred. No. 9e-11;
RESULT 704
ID ADL08115 standard; DNA; 26928 BP.
DE Human gene associated with low HDL-C F2 #2.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 3.6%; Score 46; DB 12; Length 26928;
Best Local Similarity 100.0%; Pred. No. 9e-11;
RESULT 705
ID ACN44590 standard; DNA; 33037 BP.
DE Human genomic sequence hCG40203.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 46; DB 11; Length 33037;
Best Local Similarity 100.0%; Pred. No. 8.9e-11;
RESULT 706
ID AAF97846 standard; DNA; 51474 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:60.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 3.6%; Score 46; DB 5; Length 51474;
Best Local Similarity 100.0%; Pred. No. 8.8e-11;
RESULT 707
ID ACN43926 standard; DNA; 53242 BP.
DE Human genomic sequence hCG1782215.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 46; DB 11; Length 53242;
Best Local Similarity 100.0%; Pred. No. 8.8e-11;
RESULT 708
ID ABQ75680 standard; DNA; 55050 BP.
DE Human SEEK1 consensus genomic DNA.
PD 22-AUG-2002.
PA (OXAG-) OXAGEN LTD.
Query Match 3.6%; Score 46; DB 6; Length 55050;
Best Local Similarity 100.0%; Pred. No. 8.8e-11;
RESULT 709
ID ACN44190 standard; DNA; 74183 BP.
DE Human genomic sequence hCG27588.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.6%; Score 46; DB 11; Length 74183;
Best Local Similarity 100.0%; Pred. No. 8.7e-11;
RESULT 710
ID ABD33303 standard; DNA; 122336 BP.
DE Human cancer-associated (CA) gene HD07-054.

PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 46; DB 13; Length 122336;
Best Local Similarity 100.0%; Pred. No. 8.6e-11;
RESULT 711
ID ADE43582 standard; DNA; 128034 BP.
DE Polymorphic human IDE genomic sequence, SEQ ID 187.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 46; DB 10; Length 128034;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
RESULT 712
ID ADE43581 standard; DNA; 128034 BP.
DE Human IDE genomic sequence, SEQ ID 186.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 46; DB 10; Length 128034;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
RESULT 713
ID ADH54059 standard; DNA; 128034 BP.
DE Human IDE gene DNA sequence SeqID186.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 46; DB 12; Length 128034;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
RESULT 714
ID ADH54060 standard; DNA; 128034 BP.
DE Human IDE gene variant DNA sequence SeqID187.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 46; DB 12; Length 128034;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
RESULT 715
ID ADQ97721 standard; DNA; 178024 BP.
DE Human cancer associated sequence HD10-033, SEQ ID 698.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.6%; Score 46; DB 12; Length 178024;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
RESULT 716
ID ADE43315 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 46; DB 10; Length 202100;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
RESULT 717
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.6%; Score 46; DB 12; Length 202100;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
RESULT 718
ID AAI85695 standard; cDNA; 391 BP.
DE Human polynucleotide SEQ ID NO 5755.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.5%; Score 45; DB 4; Length 391;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 719

ID AAH09032 standard; cDNA; 572 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:5867.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.5%; Score 45; DB 4; Length 572;
Best Local Similarity 100.0%; Pred. No. 3e-10;
RESULT 720
ID ADB62629 standard; cDNA; 2275 BP.
DE Human cDNA encoding clone KIDNE20137310.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.5%; Score 45; DB 10; Length 2275;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 721
ID AAH18196 standard; cDNA; 5509 BP.
DE Human cDNA sequence SEQ ID NO:18110.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.5%; Score 45; DB 4; Length 5509;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
RESULT 722
ID AAF97863 standard; DNA; 11967 BP.
DE Human neuroblastoma cell line NB-1 lp36 nucleotide sequence SEQ ID NO:77.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 3.5%; Score 45; DB 5; Length 11967;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
RESULT 723
ID AAA60207 standard; DNA; 26664 BP.
DE Human prostate cancer predisposing gene HPC2 genomic sequence.
PN WO200027864-A1.
PD 18-MAY-2000.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 3.5%; Score 45; DB 3; Length 26664;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 724
ID AAS98942 standard; DNA; 26664 BP.
DE Human prostate cancer predisposing gene (HPC2) genomic DNA.
PN WO200185911-A2.
PD 15-NOV-2001.
PA (MYRI-) MYRIAD GENETICS INC.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
Query Match 3.5%; Score 45; DB 6; Length 26664;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 725
ID AAK90698 standard; DNA; 31804 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4274.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 45; DB 4; Length 31804;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 726
ID AAK81763 standard; DNA; 37959 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36575.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 45; DB 4; Length 37959;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 727
ID AAK69848 standard; DNA; 38894 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24660.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 45; DB 4; Length 38894;

Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 728
ID A8Q88150 standard; cDNA; 40668 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 57.
PN W0200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 3.5%; Score 45; DB 6; Length 40668;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 729
ID AAA75080 standard; DNA; 44848 BP.
DE Nucleotide sequence of the human heparanase gene.
PN W0200052178-A1.
PD 08-SEP-2000.
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
Query Match 3.5%; Score 45; DB 3; Length 44848;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 730
ID ADG88032 standard; DNA; 44848 BP.
DE Human hpa genomic DNA.
PN U2003161823-A1.
PD 28-AUG-2003.
PA (ILAN/) ILAN N.
PA (VLOD/) VLODAVSKY I.
PA (YACO/) YACOBY-ZEERY O.
PA (PECK/) PECKER I.
PA (FEIN/) FEINSTEIN E.
Query Match 3.5%; Score 45; DB 10; Length 44848;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 731
ID ADL16411 standard; DNA; 44848 BP.
DE Human heparanase genomic DNA.
PN U2003236215-A1.
PD 25-DEC-2003.
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
Query Match 3.5%; Score 45; DB 12; Length 44848;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 732
ID ADM48748 standard; DNA; 44848 BP.
DE Human hpa genomic DNA.
PN U2003217375-A1.
PD 20-NOV-2003.
PA (ZCHA/) ZCHARIA E.
PA (VLOD/) VLODAVSKY I.
PA (METZ/) METZGER S.
PA (PECK/) PECKER I.
PA (ILAN/) ILAN N.
PA (CHAJ/) CHAJEK-SHAUL T.
PA (GOLD/) GOLDSHMIDT O.
Query Match 3.5%; Score 45; DB 12; Length 44848;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 733
ID AAK78813 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33625.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 45; DB 4; Length 51469;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 734
ID AAK70270 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25082.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 45; DB 4; Length 51469;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 735
ID AAK69322 standard; DNA; 51469 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24134.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.5%; Score 45; DB 4; Length 51469;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 736
ID ADA02666 standard; DNA; 52242 BP.
DE Human MDM2 carcinoma associated gene, SEQ ID NO:1184.
PN W02003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 45; DB 9; Length 52242;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 737
ID ADB72404 standard; DNA; 52242 BP.
DE Human MDM2 gene.
PN W02003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 45; DB 10; Length 52242;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 738
ID ADE95914 standard; DNA; 52242 BP.
DE Human MDM2 gene genomic DNA sequence.
PN W02003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 45; DB 10; Length 52242;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
RESULT 739
ID ADZ13482 standard; DNA; 57501 BP.
DE Human cancer-associated genomic DNA #85.
PN W02005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.5%; Score 45; DB 14; Length 57501;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 740
ID AEC32873 standard; DNA; 57759 BP.
DE Breast cancer detection estrogen receptor negative gene, SEQ ID 108.
PN U2005186577-A1.
PD 25-AUG-2005.
PA (WANG/) WANG Y.
Query Match 3.5%; Score 45; DB 14; Length 57759;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 741
ID AEC82540 standard; cDNA; 57759 BP.
DE Breast cancer associated cDNA SEQ ID NO 108.
PN W02005083429-A2.
PD 09-SEP-2005.
PA (VERI-) VERIDEX LLC.
Query Match 3.5%; Score 45; DB 14; Length 57759;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 742
ID ADZ10962 standard; DNA; 74424 BP.
DE Human STAT3 DNA sequence - SEQ ID 153.
PN U2005074879-A1.
PD 07-APR-2005.
PA (KARR/) KARRAS J G.
Query Match 3.5%; Score 45; DB 14; Length 74424;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 743
ID ACN44694 standard; DNA; 101505 BP.
DE Human genomic sequence hCG16728.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 45; DB 11; Length 101505;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 744
ID ACN44014 standard; DNA; 370469 BP.
DE Human genomic sequence hCG33130.

PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.5%; Score 45; DB 11; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 745
ID ADQ21090 standard; DNA; 114411 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3910.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.5%; Score 45; DB 12; Length 114411;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 746
ID ADP80536 standard; DNA; 118788 BP.
DE Human HPC2/ELAC2 gene SeqID1.
PN JP2004166565-A.
PD 17-JUN-2004.
PA (TAKA/) TAKAHASHI H.
PA (WATA/) WATANABE M.
PA (FURU/) FURUSATO M.
PA (HONS) YAKULT HONSHA KK.
Query Match 3.5%; Score 45; DB 12; Length 118788;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 747
ID ADZ12801 standard; DNA; 120502 BP.
DE Human cancer-associated genomic DNA #28.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.5%; Score 45; DB 14; Length 120502;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 748
ID ABC83035 standard; cDNA; 139378 BP.
DE Breast cancer associated cDNA SEQ ID NO 603.
PN WO2005083429-A2.
PD 09-SEP-2005.
PA (VERI-) VERIDEX LLC.
Query Match 3.5%; Score 45; DB 14; Length 139378;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 749
ID AEF75355 standard; DNA; 139378 BP.
DE Human polynucleotide #869.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 3.5%; Score 45; DB 15; Length 139378;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
RESULT 750
ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.5%; Score 45; DB 11; Length 304905;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
RESULT 751
ID AAS43104 standard; DNA; 325791 BP.
DE Human Oestrogen receptor beta gene.
PN WO200162793-A2.
PD 30-AUG-2001.
PA (PEKE) PE CORP NY.
Query Match 3.5%; Score 45; DB 4; Length 325791;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
RESULT 752
ID AAK84121 standard; DNA; 428 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38933.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 8.7e-10;

RESULT 753
ID AAL37637 standard; DNA; 428 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 4002.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 8.7e-10;
RESULT 754
ID AAL06685 standard; DNA; 428 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9373.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 8.7e-10;
RESULT 755
ID ABA08024 standard; DNA; 428 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 819.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 8.7e-10;
RESULT 756
ID ABX60625 standard; cDNA; 428 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2969.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.4%; Score 44; DB 8; Length 428;
Best Local Similarity 100.0%; Pred. No. 8.7e-10;
RESULT 757
ID ADJ31375 standard; DNA; 428 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 4002.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 12; Length 428;
Best Local Similarity 100.0%; Pred. No. 8.7e-10;
RESULT 758
ID AAH09816 standard; cDNA; 519 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:6651.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.4%; Score 44; DB 4; Length 519;
Best Local Similarity 100.0%; Pred. No. 8.7e-10;
RESULT 759
ID AAK82363 standard; DNA; 1311 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37175.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 1311;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
RESULT 760
ID AAK82362 standard; DNA; 1311 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37174.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 1311;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
RESULT 761
ID AAH17269 standard; cDNA; 1615 BP.
DE Human cDNA sequence SEQ ID NO:16661.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.4%; Score 44; DB 4; Length 1615;

Best Local Similarity 100.0%; Pred. No. 8.3e-10;
RESULT 762
ID AAK84877 standard; DNA; 1641 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39689.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 1641;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
RESULT 763
ID AAK66421 standard; DNA; 5701 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21233.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 5701;
Best Local Similarity 100.0%; Pred. No. 8e-10;
RESULT 764
ID AAK95944 standard; DNA; 11820 BP.
DE Human KLK-L5 gene.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 3.4%; Score 44; DB 3; Length 11820;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
RESULT 765
ID ADN10929 standard; DNA; 11820 BP.
DE Human kallikrein 12 gene, marker of endocrine cancer.
PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 3.4%; Score 44; DB 12; Length 11820;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
RESULT 766
ID ADS36476 standard; DNA; 17804 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1690.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.4%; Score 44; DB 13; Length 17804;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
RESULT 767
ID ADS36457 standard; DNA; 17809 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1671.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.4%; Score 44; DB 13; Length 17809;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
RESULT 768
ID ASK12674 standard; DNA; 27780 BP.
DE Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene.
PN WO200216654-A1.
PD 28-FEB-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 3.4%; Score 44; DB 6; Length 27780;
Best Local Similarity 100.0%; Pred. No. 7.6e-10;
RESULT 769
ID AAK89230 standard; DNA; 30110 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2806.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 30110;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
RESULT 770
ID AAK82215 standard; DNA; 31934 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37027.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.4%; Score 44; DB 4; Length 31934;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;

RESULT 771
ID ADO59404 standard; DNA; 32351 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:40.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 44; DB 12; Length 32351;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
RESULT 772
ID ABD32744 standard; DNA; 39533 BP.
DE Human cancer-associated genomic DNA HD15-022.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 44; DB 13; Length 39533;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
RESULT 773
ID ADC85349 standard; DNA; 40954 BP.
DE Mouse Sell coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.4%; Score 44; DB 10; Length 40954;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
RESULT 774
ID ADA02870 standard; DNA; 40955 BP.
DE Human SELL carcinoma associated gene, SEQ ID NO:1388.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.4%; Score 44; DB 9; Length 40955;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
RESULT 775
ID ADB72608 standard; DNA; 40955 BP.
DE Human SELL gene.
PN WO200308583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.4%; Score 44; DB 10; Length 40955;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
RESULT 776
ID ADM74465 standard; DNA; 40955 BP.
DE Human carcinoma associated (CA) nucleic acid #67.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 3.4%; Score 44; DB 12; Length 40955;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
RESULT 777
ID ADZ12689 standard; DNA; 41042 BP.
DE Human cancer-associated genomic DNA #16.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.4%; Score 44; DB 14; Length 41042;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
RESULT 778
ID ABD33486 standard; DNA; 51289 BP.
DE Human cancer-associated (CA) gene HD07-094.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 44; DB 13; Length 51289;
Best Local Similarity 100.0%; Pred. No. 7.4e-10;
RESULT 779
ID ADZ13673 standard; DNA; 63810 BP.
DE Human cancer-associated genomic DNA #103.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.4%; Score 44; DB 14; Length 63810;
Best Local Similarity 100.0%; Pred. No. 7.4e-10;


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RESULT 780
ID ABE04935 standard; DNA; 70803 BP.
DE Cancer-associated gene SEQ ID NO:153.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR ) CHIRON CORP.
Query Match 3.4%; Score 44; DB 14; Length 70803;
Best Local Similarity 100.0%; Pred. No. 7.3e-10;
RESULT 781
ID ADY70791 standard; DNA; 104424 BP.
DE Human soluble adenylyl cyclase (SAC) gene SEQ ID NO:21.
PN CN1548557-A.
PD 24-NOV-2004.
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
Query Match 3.4%; Score 44; DB 14; Length 104424;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 782
ID ADZ46659 standard; DNA; 104424 BP.
DE Type-II diabetes susceptibility gene SAC, SEQ ID 27.
PN CN1548553-A.
PD 24-NOV-2004.
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
Query Match 3.4%; Score 44; DB 14; Length 104424;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 783
ID ASA61123 standard; DNA; 122673 BP.
DE Human PDE9A gene genomic sequence SEQ ID NO:33.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB ) BAYER CORP.
Query Match 3.4%; Score 44; DB 14; Length 122673;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 784
ID AAA34791 standard; DNA; 138169 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2480.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 3.4%; Score 44; DB 3; Length 138169;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 785
ID ASD20695 standard; DNA; 141589 BP.
DE Human pulmonary and inflammatory target DNA #306.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.4%; Score 44; DB 11; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 786
ID AAA35005 standard; DNA; 141589 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2694.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 3.4%; Score 44; DB 3; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 787
ID AAA35030 standard; DNA; 141589 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2719.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 3.4%; Score 44; DB 3; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 788
ID AAF21152 standard; DNA; 141589 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2719.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 3.4%; Score 44; DB 3; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 789
ID AAF20913 standard; DNA; 141589 BP.
DE Human ELAM-1 polynucleotide fragment #2480.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 3.4%; Score 44; DB 3; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 790
ID AAF21127 standard; DNA; 141589 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2694.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 3.4%; Score 44; DB 3; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 791
ID ABZ96821 standard; DNA; 141589 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.4%; Score 44; DB 10; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 792
ID ABZ96607 standard; DNA; 141589 BP.
DE Human ELAM-1 nucleic acid.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.4%; Score 44; DB 10; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 793
ID ABZ96846 standard; DNA; 141589 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.4%; Score 44; DB 10; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 794
ID ABD20670 standard; DNA; 141589 BP.
DE Human pulmonary and inflammatory target DNA #281.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.4%; Score 44; DB 11; Length 141589;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 795
ID ABD19162 standard; DNA; 141601 BP.
DE Human ELAM-1 DNA fragment #2.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.4%; Score 44; DB 11; Length 141601;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
RESULT 796
ID RAP21442 standard; DNA; 146981 BP.
DE Human ELAM-1 polynucleotide fragment #3009.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 3.4%; Score 44; DB 3; Length 146981;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 797
ID ABZ97136 standard; DNA; 146982 BP.
DE Human ELAM-1 antisense fragment no.1738.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
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Query Match 3.4%; Score 44; DB 10; Length 146982;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 798
ID ABD19160 standard; DNA; 146984 BP.
DE Human ELAM-1 DNA fragment 1738.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.4%; Score 44; DB 11; Length 146984;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 799
ID AED89411 standard; DNA; 157224 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 51.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 3.4%; Score 44; DB 14; Length 157224;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 800
ID ADN01278 standard; DNA; 166910 BP.
DE Human endothelial differentiation gene 2 related DNA #1.
PN US2004092462-A1.
PD 13-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.4%; Score 44; DB 12; Length 166910;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 801
ID AED89410 standard; DNA; 170189 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 50.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 3.4%; Score 44; DB 14; Length 170189;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 802
ID AAD55694 standard; DNA; 175561 BP.
DE Human THBS4 reference gene (GI 14916146).
PN WO2003020120-A2.
PD 13-MAR-2003.
PA (VITI-) VITIVITY INC.
Query Match 3.4%; Score 44; DB 8; Length 175561;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 803
ID ADL08129 standard; DNA; 175561 BP.
DE Human gene associated with low HDL-C THBS4.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 3.4%; Score 44; DB 12; Length 175561;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 804
ID ADZ13037 standard; DNA; 188267 BP.
DE Human cancer-associated genomic DNA #115.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.4%; Score 44; DB 14; Length 188267;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 805
ID ADQ59476 standard; DNA; 188794 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:112.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.4%; Score 44; DB 12; Length 188794;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 806
ID AAF21437 standard; DNA; 209273 BP.
DE Human factor-related antisense polynucleotide #3004.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.
Query Match 3.4%; Score 44; DB 3; Length 209273;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 807
ID ABZ97131 standard; DNA; 209274 BP.
DE Human enzyme-related antisense polynucleotide.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.4%; Score 44; DB 10; Length 209274;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 808
ID ABD17970 standard; DNA; 209284 BP.
DE Human factor-related antisense polynucleotide.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.4%; Score 44; DB 11; Length 209284;
Best Local Similarity 100.0%; Pred. No. 7.1e-10;
RESULT 809
ID ABA14706 standard; DNA; 102 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7037.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
RESULT 810
ID AAS36217 standard; DNA; 114 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1717.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
RESULT 811
ID ADE46911 standard; DNA; 114 BP.
DE Human cardiovascular system related genomic DNA #477.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 10; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
RESULT 812
ID ADJ08329 standard; DNA; 114 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1717.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
RESULT 813
ID AAK79793 standard; DNA; 127 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34605.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 814
ID AAS27830 standard; DNA; 134 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1490.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 815
ID AAS27828 standard; DNA; 134 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1488.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.3%; Score 43; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 816
ID ADB94633 standard; DNA; 134 BP.
DE Novel human protein DNA #242.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.3%; Score 43; DB 10; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 817
ID ADB94631 standard; DNA; 134 BP.
DE Novel human protein DNA #240.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.3%; Score 43; DB 10; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 818
ID AAK73573 standard; DNA; 165 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28385.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 819
ID AAS30391 standard; DNA; 167 BP.
DE DNA encoding novel prostate gland antigen, Seq ID No 249.
PN WO200155447-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 820
ID AAS30390 standard; DNA; 167 BP.
DE DNA encoding novel prostate gland antigen, Seq ID No 248.
PN WO200155447-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 821
ID AAL03506 standard; DNA; 167 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6594.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 822
ID AAL03905 standard; DNA; 167 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6593.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 823
ID AAC21088 standard; cDNA; 198 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 25163.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.3%; Score 43; DB 3; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 824
ID AAC14894 standard; cDNA; 251 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 18969.

PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.3%; Score 43; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 825
ID ABV20082 standard; cDNA; 267 BP.
DE Human prostate expression marker cDNA 20073.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 826
ID AAC04965 standard; cDNA; 278 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 9040.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.3%; Score 43; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 827
ID ABV11145 standard; cDNA; 284 BP.
DE Human prostate expression marker cDNA 11136.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 284;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 828
ID AAC15814 standard; cDNA; 298 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 19889.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.3%; Score 43; DB 3; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 829
ID ABK45452 standard; cDNA; 323 BP.
DE cDNA encoding colon tumour protein, SEQ ID No 1003.
PN WO200212328-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.3%; Score 43; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 830
ID ABV48569 standard; cDNA; 329 BP.
DE Human prostate expression marker cDNA 48560.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
RESULT 831
ID ACL59792 standard; cDNA; 361 BP.
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:5927.
PN WO200500087-A2.
PD 06-JAN-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 832
ID AAQ59423 standard; cDNA; 364 BP.
DE Human brain Expressed Sequence Tag EST01442.
PN WO9316178-A2.
PD 19-AUG-1993.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match 3.3%; Score 43; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 833
ID ACH29419 standard; cDNA; 369 BP.
DE Human adult spleen cDNA #438.
PN US2003073623-A1.

PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 3.3%; Score 43; DB 9; Length 369;
100.0%; Pred. No. 2.5e-09;
RESULT 834
ID ABL85369 standard; cDNA; 400 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:8347.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 3.3%; Score 43; DB 6; Length 400;
100.0%; Pred. No. 2.5e-09;
RESULT 835
ID AAK95930 standard; DNA; 401 BP.
DE Human neuroregulin gene single nucleotide polymorphism SNP8RG847327.
PN WO200164876-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHP.
Query Match
Best Local Similarity 3.3%; Score 43; DB 4; Length 401;
100.0%; Pred. No. 2.5e-09;
RESULT 836
ID AAK97423 standard; DNA; 401 BP.
DE Human neuroregulin gene single nucleotide polymorphism SNP8RG847327.
PN WO200164877-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHP.
Query Match
Best Local Similarity 3.3%; Score 43; DB 4; Length 401;
100.0%; Pred. No. 2.5e-09;
RESULT 837
ID ABT00700 standard; DNA; 401 BP.
DE Human neuroregulin-1-associated gene 1 fragment SEQ ID NO: 729.
PN US2002045577-A1.
PD 18-APR-2002.
PA (DECO-) DECODE GENETICS EHP.
Query Match
Best Local Similarity 3.3%; Score 43; DB 6; Length 401;
100.0%; Pred. No. 2.5e-09;
RESULT 838
ID ABT02193 standard; DNA; 401 BP.
DE Human neuroregulin-1-associated gene 1 fragment SEQ ID NO: 729.
PN US2002094954-A1.
PD 18-JUL-2002.
PA (DECO-) DECODE GENETICS EHP.
Query Match
Best Local Similarity 3.3%; Score 43; DB 6; Length 401;
100.0%; Pred. No. 2.5e-09;
RESULT 839
ID ACH21579 standard; cDNA; 406 BP.
DE Human adult liver cDNA #1191.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 3.3%; Score 43; DB 9; Length 406;
100.0%; Pred. No. 2.5e-09;
RESULT 840
ID ABV41222 standard; cDNA; 414 BP.
DE Human prostate expression marker cDNA 41213.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 5; Length 414;
100.0%; Pred. No. 2.5e-09;
RESULT 841
ID AAF66195 standard; cDNA; 422 BP.
DE Novel human polynucleotide, SEQ ID NO: 1951.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (STAC/) STACHE-CRAIN B.
PA (LABA/) LABAT I.
PA (DRMA/) DRMANAC R T.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 3.3%; Score 43; DB 9; Length 487;
100.0%; Pred. No. 2.5e-09;
RESULT 842
ID AEN63947 standard; cDNA; 441 BP.
DE Human cancer related polynucleotide SEQ ID NO 3914.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 6; Length 441;
100.0%; Pred. No. 2.5e-09;
RESULT 843
ID ABV32291 standard; cDNA; 444 BP.
DE Human prostate expression marker cDNA 32282.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 5; Length 444;
100.0%; Pred. No. 2.5e-09;
RESULT 844
ID AAH10091 standard; cDNA; 470 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:6926.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 3.3%; Score 43; DB 4; Length 470;
100.0%; Pred. No. 2.5e-09;
RESULT 845
ID ABV49840 standard; cDNA; 486 BP.
DE Human prostate expression marker cDNA 49831.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 5; Length 486;
100.0%; Pred. No. 2.5e-09;
RESULT 846
ID ABV95412 standard; cDNA; 487 BP.
DE Human pancreatic cancer expressed cDNA SEQ ID NO 820.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 3.3%; Score 43; DB 6; Length 487;
100.0%; Pred. No. 2.5e-09;
RESULT 847
ID ACH39583 standard; cDNA; 487 BP.
DE Human foetal brain cDNA #950.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 3.3%; Score 43; DB 9; Length 487;
100.0%; Pred. No. 2.5e-09;
RESULT 848
ID AAH09995 standard; cDNA; 498 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:6830.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 3.3%; Score 43; DB 4; Length 498;
100.0%; Pred. No. 2.5e-09;
RESULT 849
ID ACH39071 standard; cDNA; 507 BP.
DE Human foetal brain cDNA #438.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.


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PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
  Query Match 3.3%; Score 43; DB 9; Length 507;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 850
ID ABL37264 standard; cDNA; 529 BP.
DE Human colon tumour antigen polynucleotide SEQ ID NO:853.
PN WO200196388-A2.
PD 20-DEC-2001.
PA (CORI-) CORIXA CORP.
  Query Match 3.3%; Score 43; DB 6; Length 529;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 851
ID AAK73475 standard; DNA; 589 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28287.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 3.3%; Score 43; DB 4; Length 589;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 852
ID AEB33893 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1473.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
  Query Match 3.3%; Score 43; DB 14; Length 601;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 853
ID AEB33968 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1548.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
  Query Match 3.3%; Score 43; DB 14; Length 601;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 854
ID AEB33933 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1513.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
  Query Match 3.3%; Score 43; DB 14; Length 601;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 855
ID AEB33974 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1554.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
  Query Match 3.3%; Score 43; DB 14; Length 601;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 856
ID AEB33995 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1475.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
  Query Match 3.3%; Score 43; DB 14; Length 601;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 857
ID AEB33932 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1512.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
  Query Match 3.3%; Score 43; DB 14; Length 601;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 858
ID AEB33934 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1514.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
  Query Match 3.3%; Score 43; DB 14; Length 601;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 859
ID AEB33894 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1474.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
  Query Match 3.3%; Score 43; DB 14; Length 601;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 860
ID AAL16199 standard; DNA; 629 BP.
DE Human colon cancer differentially expressed nucleotide sequence #204.
PN WO200012702-A2.
PD 09-MAR-2000.
PA (FARB) BAYER CORP.
  Query Match 3.3%; Score 43; DB 3; Length 629;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 861
ID AAF64996 standard; cDNA; 634 BP.
DE Novel human polynucleotide, SEQ ID NO: 752.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
  Query Match 3.3%; Score 43; DB 5; Length 634;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 862
ID AAH92469 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR1169a.
PN WO200142511-A2.
PD 14-JUN-2001.
PA (WHEI) WHITEHEAD INST BIOMEDICAL RES.
  Query Match 3.3%; Score 43; DB 4; Length 700;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 863
ID ADB83255 standard; cDNA; 786 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID 1468).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
  Query Match 3.3%; Score 43; DB 9; Length 786;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 864
ID AAK73190 standard; DNA; 864 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28002.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 3.3%; Score 43; DB 4; Length 864;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 865
ID AAK80191 standard; DNA; 1074 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35003.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 3.3%; Score 43; DB 4; Length 1074;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 866
ID AAK80190 standard; DNA; 1074 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35002.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 3.3%; Score 43; DB 4; Length 1074;
  Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 867
ID ABV28234 standard; cDNA; 1116 BP.
DE Human prostate expression marker cDNA 28225.
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PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 1116;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 868
ID ABV22420 standard; cDNA; 1116 BP.
DE Human prostate expression marker cDNA 22411.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 1116;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
RESULT 869
ID AD182480 standard; DNA; 1423 BP.
DE Human modifier of p21 (MP21) gene sequence SeqID46.
PN WO2004005486-A2.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 3.3%; Score 43; DB 12; Length 1423;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 870
ID AD182481 standard; DNA; 1423 BP.
DE Human modifier of p21 (MP21) gene sequence SeqID47.
PN WO2004005486-A2.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 3.3%; Score 43; DB 12; Length 1423;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 871
ID AQ085730 standard; cDNA; 1455 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2544.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.3%; Score 43; DB 13; Length 1455;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 872
ID ABK35076 standard; cDNA; 1504 BP.
DE Human cDNA encoding secreted protein #214.
PN WO200177288-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 3.3%; Score 43; DB 6; Length 1504;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 873
ID AAH17341 standard; cDNA; 1554 BP.
DE Human cDNA sequence SEQ ID NO:16757.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.3%; Score 43; DB 4; Length 1554;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 874
ID ADU45647 standard; DNA; 1578 BP.
DE Human ovarian cancer DNA marker #19537.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 1578;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 875
ID AAK73699 standard; DNA; 1819 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28511.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 1819;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 876
ID AAH17398 standard; cDNA; 1956 BP.

DE Human cDNA sequence SEQ ID NO:16836.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.3%; Score 43; DB 4; Length 1956;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 877
ID ADO15897 standard; DNA; 1989 BP.
DE 4 synthesis-period of neuroblastoma related DNA, SEQ ID 159.
PN WO2004039975-A1.
PD 13-MAY-2004.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 3.3%; Score 43; DB 12; Length 1989;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 878
ID ACS57389 standard; cDNA; 2013 BP.
DE Human macroprotein 1503-8.8 encoding cDNA.
PN CN1359929-A.
PD 24-JUL-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 3.3%; Score 43; DB 6; Length 2013;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 879
ID AAD04177 standard; cDNA; 2214 BP.
DE Human Her-2/neu over expression modulated protein (HOMPS) H14 cDNA.
PN WO200125250-A1.
PD 12-APR-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 3.3%; Score 43; DB 4; Length 2214;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 880
ID AAA49881 standard; cDNA; 2375 BP.
DE Human pancreatic polypeptide zsig66 cDNA.
PN WO200036104-A1.
PD 22-JUN-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 3.3%; Score 43; DB 3; Length 2375;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 881
ID ADQ23263 standard; DNA; 2377 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6083.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.3%; Score 43; DB 12; Length 2377;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 882
ID ABL41330 standard; cDNA; 2425 BP.
DE Human mitochondrial ATPase coupling factor F69.35 encoding cDNA.
PN CN1326954-A.
PD 19-DEC-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 3.3%; Score 43; DB 6; Length 2425;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 883
ID AAK68027 standard; DNA; 2664 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22839.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 2664;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 884
ID ABV28548 standard; cDNA; 2685 BP.
DE Human prostate expression marker cDNA 28539.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 2685;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 885
ID ABV22723 standard; cDNA; 2685 BP.

DE Human prostate expression marker cDNA 22714.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 2685;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 886
ID ADQ64778 standard; cDNA; 2913 BP.
DE Novel human cDNA sequence #1939.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.3%; Score 43; DB 12; Length 2913;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 887
ID ADM03126 standard; cDNA; 3291 BP.
DE Human cDNA of the invention SEQ ID NO:1811.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.3%; Score 43; DB 11; Length 3291;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 888
ID ASC86056 standard; cDNA; 3291 BP.
DE Human cDNA clone STOMA20032890, SEQ ID 1811.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.3%; Score 43; DB 14; Length 3291;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 889
ID ADR08359 standard; cDNA; 3597 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1865.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.3%; Score 43; DB 13; Length 3597;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 890
ID AA161061 standard; cDNA; 3775 BP.
DE Human polynucleotide SEQ ID NO 5050.
PN WO200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.3%; Score 43; DB 4; Length 3775;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
RESULT 891
ID AAP28781 standard; DNA; 3903 BP.
DE Human GABA(b) receptor 1 promoter Pla.
PN WO20068268-A1.
PD 16-NOV-2000.
PA (ASTR) ASTRAZENECA AB.
Query Match 3.3%; Score 43; DB 4; Length 3903;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 892
ID AAS22674 standard; cDNA; 4385 BP.
DE Human cDNA encoding a novel human protein #240.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.3%; Score 43; DB 4; Length 4385;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 893
ID AEE23807 standard; DNA; 4385 BP.
DE Novel human protein coding sequence (contig) - SEQ ID 476.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NOVE-) NUVELO INC.
Query Match 3.3%; Score 43; DB 15; Length 4385;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 894
ID ADB99093 standard; cDNA; 4421 BP.
DE Human retinal pigment epithelial-derived factor (PEDF) genomic DNA #3.
PN US2003096750-A1.
PD 22-MAY-2003.
PA (TOMB/) TOMBRAN-TINK J.
PA (STEE/) STEELE F R.
PA (CHAD/) CHADER G J.
PA (BECE/) BECERRA S P.
PA (JOHN/) JOHNSON L V.
PA (RODR/) RODRIGUEZ I R.
Query Match 3.3%; Score 43; DB 10; Length 4421;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 895
ID ABS57269 standard; DNA; 4421 BP.
DE Partial sequence #3 of genomic DNA encoding human PEDF.
PN US6451763-B1.
PD 17-SEP-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 3.3%; Score 43; DB 10; Length 4421;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 896
ID ABV25420 standard; cDNA; 4489 BP.
DE Human prostate expression marker cDNA 25411.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 4489;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 897
ID ABV23415 standard; cDNA; 4489 BP.
DE Human prostate expression marker cDNA 23406.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 4489;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 898
ID ABV29272 standard; cDNA; 4489 BP.
DE Human prostate expression marker cDNA 29263.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 43; DB 5; Length 4489;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 899
ID ACN282859 standard; DNA; 4733 BP.
DE Breast cancer related marker, seq id 14009.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.3%; Score 43; DB 11; Length 4733;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 900
ID AAS32799 standard; DNA; 4957 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 753.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 4957;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 901
ID AAS32798 standard; DNA; 4961 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 752.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 4961;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 902
ID AAH18645 standard; cDNA; 4964 BP.
DE Human cDNA sequence SEQ ID NO:18873.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.3%; Score 43; DB 4; Length 4964;

Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 903
ID ACG33000 standard; DNA; 5207 BP.
DE Human DNA differentially expressed in patients with SLE SeqID324.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 3.3%; Score 43; DB 10; Length 5207;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 904
ID ADP56079 standard; cDNA; 5207 BP.
DE Human PRO cDNA sequence SEQ ID NO:2055.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 3.3%; Score 43; DB 13; Length 5207;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 905
ID ADF69151 standard; cDNA; 5223 BP.
DE Human MP53 nucleotide sequence SEQ ID NO:9.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 3.3%; Score 43; DB 10; Length 5223;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 906
ID AAC62160 standard; DNA; 5375 BP.
DE Nucleotide sequence of human apolipoprotein C.
PN US6136530-A.
PD 24-OCT-2000.
PA (UYTE-) UNIV TEXAS TECH HEALTH SCI CENT.
Query Match 3.3%; Score 43; DB 4; Length 5375;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 907
ID AAN95794 standard; DNA; 5375 BP.
DE Gene #2292 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 43; DB 6; Length 5375;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 908
ID AAS16182 standard; DNA; 5375 BP.
DE Human apolipoprotein C1 (APOC1) DNA.
PN WO200177129-A2.
PD 18-OCT-2001.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 3.3%; Score 43; DB 6; Length 5375;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 909
ID AEB63802 standard; DNA; 5375 BP.
DE Human apolipoprotein C-1 (APOC1) gene.
PN WO2005072152-A2.
PD 11-AUG-2005.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 3.3%; Score 43; DB 14; Length 5375;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 910
ID AAS32797 standard; DNA; 5668 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 751.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 5668;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 911
ID AAL03708 standard; DNA; 5932 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6396.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 5932;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;

RESULT 912
ID ABA07891 standard; DNA; 5932 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 686.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 5932;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 913
ID AAL03707 standard; DNA; 5966 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6395.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 5966;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 914
ID ABA07890 standard; DNA; 5966 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 685.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 5966;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 915
ID AAK84334 standard; DNA; 6052 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39146.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 6052;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 916
ID AAH57456 standard; cDNA; 6138 BP.
DE Human liver cell specific cDNA sequence SEQ ID NO:296.
PN WO200132927-A2.
PD 10-MAY-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.3%; Score 43; DB 4; Length 6138;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 917
ID AAQ95493 standard; DNA; 6511 BP.
DE Human Cdn-2 DNA.
PN WO9515084-A1.
PD 08-JUN-1995.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
Query Match 3.3%; Score 43; DB 2; Length 6511;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 918
ID AAD04467 standard; DNA; 7240 BP.
DE Human insulin receptor DNA (from exons 14 to 17).
PN WO200128540-A2.
PD 26-APR-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 3.3%; Score 43; DB 4; Length 7240;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 919
ID AAH31267 standard; DNA; 7240 BP.
DE Human insulin receptor gene from exon 14 to 17.
PN WO200129256-A2.
PD 26-APR-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 3.3%; Score 43; DB 4; Length 7240;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 920
ID AAH31170 standard; DNA; 7240 BP.
DE Human insulin receptor gene, exons 14 to 17.
PN WO200129255-A2.
PD 26-APR-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 3.3%; Score 43; DB 4; Length 7240;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 921
ID AAH31170 standard; DNA; 7240 BP.
DE Human insulin receptor gene, exons 14 to 17.
PN WO200129255-A2.
PD 26-APR-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 3.3%; Score 43; DB 4; Length 7240;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;

ID AAK50570 standard; DNA; 7240 BP.
DE Insulin receptor gene exons 14-17 including introns SEQ ID NO:25.
PN WO200128539-A2.
PD 26-APR-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 3.3%; Score 43; DB 5; Length 7240;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 922
ID AAK72725 standard; DNA; 7240 BP.
DE Human insulin receptor gene.
PN WO200233121-A2.
PD 25-APR-2002.
PA (GLAX) GLAXO GROUP LTD.
Query Match 3.3%; Score 43; DB 6; Length 7240;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 923
ID AAL62772 standard; DNA; 7240 BP.
DE Human insulin receptor gene fragment DNA.
PN WO2003056328-A1.
PD 10-JUL-2003.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 3.3%; Score 43; DB 9; Length 7240;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 924
ID AAK85594 standard; DNA; 7452 BP.
DE Human glycoprotein V gene.
PN WO9502054-A2.
PD 19-JAN-1995.
PA (CORT-) COR THERAPEUTICS INC.
Query Match 3.3%; Score 43; DB 2; Length 7452;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 925
ID AAZ61217 standard; DNA; 7452 BP.
DE DNA encoding human glycoprotein V (GP V).
PN WO200008137-A2.
PD 17-FEB-2000.
PA (CORT-) COR THERAPEUTICS INC.
Query Match 3.3%; Score 43; DB 3; Length 7452;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 926
ID AAF90646 standard; DNA; 7452 BP.
DE Human secreted protein encoding DNA, SEQ ID NO:92.
PN WO200109162-A2.
PD 08-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.3%; Score 43; DB 4; Length 7452;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 927
ID ABK48275 standard; DNA; 7452 BP.
DE DNA encoding human endothelial cell specific glycoprotein GP V.
PN WO200217711-A2.
PD 07-MAR-2002.
PA (CORT-) COR THERAPEUTICS INC.
Query Match 3.3%; Score 43; DB 6; Length 7452;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 928
ID ADS89083 standard; DNA; 8172 BP.
DE Human MSMB gene SEQ ID NO:99.
PN WO2004035803-A2.
PD 23-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43; DB 13; Length 8172;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 929
ID AAK79591 standard; DNA; 8965 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34403.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 8965;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 930
ID AAK67429 standard; DNA; 9840 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22241.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 9840;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
RESULT 931
ID AAL37152 standard; DNA; 14171 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3517.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 14171;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 932
ID ABX60140 standard; cDNA; 14171 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2484.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.3%; Score 43; DB 8; Length 14171;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 933
ID ADJ30890 standard; DNA; 14171 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3517.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 12; Length 14171;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 934
ID ABS52512 standard; DNA; 14485 BP.
DE Human dehydrogenase protein genomic DNA.
PN US2002081689-A1.
PD 27-JUN-2002.
PA (YANC/) YAN C.
PA (LIEZ/) LI Z.
PA (MERK/) MERKULOV G V.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E.
Query Match 3.3%; Score 43; DB 6; Length 14485;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 935
ID AAD47902 standard; DNA; 14485 BP.
DE Human retinol dehydrogenase-related enzyme encoding genomic DNA.
PN US2003138930-A1.
PD 24-JUL-2003.
PA (APPL-) APPLERA CORP.
Query Match 3.3%; Score 43; DB 10; Length 14485;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 936
ID AEB48324 standard; DNA; 14485 BP.
DE Human dehydrogenase gene, SEQ ID NO: 3.
PN US2005158776-A1.
PD 21-JUL-2005.
PA (APPL-) APPLERA CORP.
Query Match 3.3%; Score 43; DB 14; Length 14485;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 937
ID AAN50107 standard; DNA; 15155 BP.
DE DNA encoding Factor-VIIIC.
PN EP150735-A.
PD 07-AUG-1985.
PA (CHIR) CHIRON CORP.
PA (NORD-) NORDISK GENTOFTE AS.
Query Match 3.3%; Score 43; DB 1; Length 15155;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 938
ID AAA58442 standard; DNA; 15155 BP.
DE Human Factor VIIIC clone 23D sequence.
PN EP1006182-A2.

PD 07-JUN-2000.
PA (CHIR) CHIRON CORP.
PA (NOVO) NOVO-NORDISK AS.
Query Match 3.3%; Score 43; DB 3; Length 15155;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 939
ID AAL37153 standard; DNA; 15998 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3518.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 15998;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 940
ID AXK60141 standard; cDNA; 15998 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2485.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.3%; Score 43; DB 8; Length 15998;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 941
ID ADJ30891 standard; DNA; 15998 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3518.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 12; Length 15998;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 942
ID ADC86818 standard; DNA; 16256 BP.
DE Human GPCR gene SEQ ID NO:1271.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.3%; Score 43; DB 10; Length 16256;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 943
ID AAX58060 standard; DNA; 16862 BP.
DE Genomic DNA for Human GABAB receptors.
PN WO9921890-A1.
PD 06-MAY-1999.
PA (ASTR) ASTRA AB.
Query Match 3.3%; Score 43; DB 2; Length 16862;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 944
ID ADC87692 standard; DNA; 16976 BP.
DE Human mammalian target of rapamycin genomic fragment #37.
PN WO2003048360-A1.
PD 12-JUN-2003.
PA (NEWI-) NEW IND RES ORG.
Query Match 3.3%; Score 43; DB 10; Length 16976;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 945
ID ADS89105 standard; DNA; 17203 BP.
DE Human PRKCD gene SEQ ID NO:121.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 43; DB 13; Length 17203;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 946
ID ADC86824 standard; DNA; 17588 BP.
DE Human GPCR gene SEQ ID NO:1277.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.3%; Score 43; DB 10; Length 17588;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;

RESULT 947
ID AAS30396 standard; DNA; 17601 BP.
DE DNA encoding novel prostate gland antigen, Seq ID No 254.
PN WO200155447-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 17601;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 948
ID AAK70280 standard; DNA; 17601 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25092.
PN WO200157182-A2.
PD 03-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 17601;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 949
ID AAL04423 standard; DNA; 17601 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7111.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 17601;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 950
ID AAS36099 standard; DNA; 17792 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1599.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 17792;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 951
ID AAS32727 standard; DNA; 17792 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 681.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 17792;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 952
ID ADE46793 standard; DNA; 17792 BP.
DE Human cardiovascular system related genomic DNA #359.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 10; Length 17792;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 953
ID ADJ08211 standard; DNA; 17792 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1599.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 13; Length 17792;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 954
ID AAK77679 standard; DNA; 17947 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32491.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 17947;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 955
ID ABA81553 standard; DNA; 18925 BP.
DE Human phospholipid transfer protein gene.
PN WO200172761-A2.
PD 04-OCT-2001.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 3.3%; Score 43; DB 4; Length 18925;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 956

ID AAS94692 standard; DNA; 18925 BP.
DE Human phospholipid transfer protein (PLTP) generic genomic DNA.
PN WO200172966-A2.
PD 04-OCT-2001.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 3.3%; Score 43; DB 6; Length 18925;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 957
ID AAS94565 standard; DNA; 18925 BP.
DE Human phospholipid transfer protein (PLTP) genomic DNA.
PN WO200172966-A2.
PD 04-OCT-2001.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 3.3%; Score 43; DB 6; Length 18925;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 958
ID ADY31049 standard; DNA; 19858 BP.
DE Human solute carrier family 6 member 7, SLC6A7, gene.
PN WO2005019474-A2.
PD 03-MAR-2005.
PA (INTE-) INTEGRAGEN.
Query Match 3.3%; Score 43; DB 14; Length 19858;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 959
ID ADQ59165 standard; DNA; 19913 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:2.
PN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
Query Match 3.3%; Score 43; DB 12; Length 19913;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 960
ID AAK87416 standard; DNA; 19942 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42228.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 19942;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 961
ID AAK79930 standard; DNA; 21693 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34742.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 21693;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 962
ID AAK71708 standard; DNA; 23118 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26520.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 23118;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 963
ID AD33393 standard; DNA; 24318 BP.
DE Human cancer-associated (CA) gene HD07-073.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 13; Length 24318;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 964
ID ABD33080 standard; DNA; 24976 BP.
DE Human cancer-associated (CA) gene HD07-003.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 13; Length 24976;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 965
ID ADC87256 standard; DNA; 25001 BP.
DE Human GPCR gene SEQ ID NO:1709.
PN RP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.3%; Score 43; DB 10; Length 25001;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 966
ID ADZ13568 standard; DNA; 25261 BP.
DE Human cancer-associated genomic DNA #93.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 25261;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 967
ID ADQ97243 standard; DNA; 25988 BP.
DE Human cancer associated sequence HD08-019, SEQ ID 219.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 12; Length 25988;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 968
ID AEB32399 standard; DNA; 28253 BP.
DE Human genomic DNA #40.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 3.3%; Score 43; DB 14; Length 28253;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 969
ID AEB32400 standard; DNA; 28253 BP.
DE Human genomic DNA #41.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 3.3%; Score 43; DB 14; Length 28253;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 970
ID AEB32402 standard; DNA; 28316 BP.
DE Human genomic DNA #43.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 3.3%; Score 43; DB 14; Length 28316;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 971
ID AEB32403 standard; DNA; 28316 BP.
DE Human genomic DNA #44.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 3.3%; Score 43; DB 14; Length 28316;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 972
ID RAK91264 standard; DNA; 28563 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4840.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 28563;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 973
ID ABK83555 standard; cDNA; 28772 BP.
DE Human cDNA differentially expressed in granulocytic cells #126.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 43; DB 6; Length 28772;

Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 974
ID ADQ19885 standard; DNA; 28772 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2704.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.3%; Score 43; DB 12; Length 28772;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 975
ID AAK81054 standard; DNA; 31584 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35866.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 31584;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 976
ID AAL36806 standard; DNA; 32185 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3171.
FN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 32185;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 977
ID ABX59794 standard; cDNA; 32185 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2138.
FN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.3%; Score 43; DB 8; Length 32185;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 978
ID ADJ30544 standard; DNA; 32185 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3171.
FN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 12; Length 32185;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 979
ID AAK89689 standard; DNA; 32190 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3265.
FN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 32190;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 980
ID AAS36517 standard; DNA; 32195 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2017.
FN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 32195;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 981
ID ADE47211 standard; DNA; 32195 BP.
DE Human cardiovascular system related genomic DNA #777.
FN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 10; Length 32195;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 982
ID ADJ08629 standard; DNA; 32195 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2017.
FN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.3%; Score 43; DB 13; Length 32195;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 983
ID AAS36516 standard; DNA; 32219 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2016.
FN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 32219;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 984
ID ADE47210 standard; DNA; 32219 BP.
DE Human cardiovascular system related genomic DNA #776.
FN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 10; Length 32219;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 985
ID ADJ08628 standard; DNA; 32219 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2016.
FN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 13; Length 32219;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 986
ID ACN44482 standard; DNA; 34096 BP.
DE Human genomic sequence hCG26017.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 34096;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 987
ID AAF97854 standard; DNA; 34488 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:68.
FN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 3.3%; Score 43; DB 5; Length 34488;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 988
ID ABK13324 standard; DNA; 34863 BP.
DE DNA encoding paraoxonase 2 (PON2).
FN WO200188202-A1.
PD 22-NOV-2001.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 3.3%; Score 43; DB 6; Length 34863;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 989
ID ACN45038 standard; DNA; 35548 BP.
DE Human genomic sequence hCG1781938.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 35548;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 990
ID ABE04707 standard; DNA; 38019 BP.
DE Cancer-associated gene SEQ ID NO:25.
FN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 38019;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 991
ID ABZ74034 standard; DNA; 39119 BP.
DE Secreted protein gene 163 genomic fragment HJFCH08, SEQ ID NO:1181.
FN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.3%; Score 43; DB 8; Length 39119;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 992
ID ADA98641 standard; DNA; 39119 BP.
DE Human secreted protein-related DNA sequence #234.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 8; Length 39119;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 993
ID ADC20764 standard; DNA; 39119 BP.
DE Human secreted protein-related DNA sequence #182.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 10; Length 39119;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 994
ID ABZ67621 standard; DNA; 39119 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1144.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 10; Length 39119;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 995
ID AAL57448 standard; DNA; 39726 BP.
DE Human NSD1 genomic DNA sequence.
PN EP1321533-A2.
PD 25-JUN-2003.
PA (UYNA-) UNIV NAGASAKI.
Query Match 3.3%; Score 43; DB 9; Length 39726;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 996
ID AAK81263 standard; DNA; 39887 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36075.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 39887;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 997
ID AAK79153 standard; DNA; 39887 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33965.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 39887;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 998
ID ADL13819 standard; DNA; 41150 BP.
DE Osteoarthritis-associated polymorphic nucleotide #351.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.3%; Score 43; DB 10; Length 41150;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 999
ID AED18343 standard; DNA; 41150 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 594.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 3.3%; Score 43; DB 14; Length 41150;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1000
ID ADA02588 standard; DNA; 42334 BP.
DE Human ICSBP1 carcinoma associated gene, SEQ ID NO:1106.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 9; Length 42334;

Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1001
ID ADB72326 standard; DNA; 42334 BP.
DE Human ICSBP1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 10; Length 42334;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1002
ID ADE95836 standard; DNA; 42334 BP.
DE Human ICSBP1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 10; Length 42334;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1003
ID ADA02774 standard; DNA; 44075 BP.
DE Human ARHGEF1 carcinoma associated gene, SEQ ID NO:1292.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 9; Length 44075;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1004
ID ADB72512 standard; DNA; 44075 BP.
DE Human ARHGEF1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 10; Length 44075;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1005
ID ADC85254 standard; DNA; 44075 BP.
DE Human Arhgef1 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 10; Length 44075;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1006
ID ADM74369 standard; DNA; 44075 BP.
DE Human carcinoma associated (CA) nucleic acid #19.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENG/) ENGELHARD E K.
Query Match 3.3%; Score 43; DB 12; Length 44075;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1007
ID AAK77458 standard; DNA; 44196 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32270.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 44196;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1008
ID AAK85974 standard; DNA; 44211 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40786.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 44211;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1009
ID ADN48556 standard; DNA; 44348 BP.
DE Human Notch3 genomic DNA #2.
PN US2004102390-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.3%; Score 43; DB 12; Length 44348;

Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1010
ID AAS20000 standard; DNA; 44861 BP.
DE DNA encoding pyridoxal (pyridoxine, vitamin B6) kinase (PDXK).
PN WO200190125-A2.
PD 29-NOV-2001.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 3.3%; Score 43; DB 6; Length 44861;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1011
ID AAK72230 standard; DNA; 47319 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27042.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 47319;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1012
ID AAK64813 standard; DNA; 47319 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19625.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 47319;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1013
ID AAD52898 standard; DNA; 47999 BP.
DE Human tweety homologue 2 (TYTH2) gene.
PN WO200292629-A1.
PD 21-NOV-2002.
PA (UYQU-) UNIV QUEBENS LAND TECHNOLOGY.
Query Match 3.3%; Score 43; DB 8; Length 47999;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1014
ID AAK82338 standard; DNA; 49908 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37150.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 49908;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
RESULT 1015
ID ADA02990 standard; DNA; 51365 BP.
DE Human CD28 carcinoma associated gene, SEQ ID NO:1508.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 9; Length 51365;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1016
ID ADB72728 standard; DNA; 51365 BP.
DE Human CD28 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 10; Length 51365;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1017
ID ADC85470 standard; DNA; 51365 BP.
DE Human CD28 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 10; Length 51365;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1018
ID ADM74585 standard; DNA; 51365 BP.
DE Human carcinoma associated (CA) nucleic acid #127.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 3.3%; Score 43; DB 12; Length 51365;

Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1019
ID ADZ12723 standard; DNA; 51911 BP.
DE Human cancer-associated genomic DNA #20.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 51911;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1020
ID AEA61174 standard; DNA; 53147 BP.
DE Human CYP2C18 gene genomic sequence SEQ ID NO:84.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 3.3%; Score 43; DB 14; Length 53147;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1021
ID AAD30228 standard; DNA; 53522 BP.
DE Human PKD1 gene.
PN WO200206529-A2.
PD 24-JAN-2002.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 3.3%; Score 43; DB 6; Length 53522;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1022
ID ADU03973 standard; DNA; 53522 BP.
DE Human polycystic kidney disease 1 (PKD-1) gene.
PN CA2461106-A1.
PD 11-OCT-2004.
PA (ATHE-) ATHENA DIAGNOSTICS INC.
Query Match 3.3%; Score 43; DB 13; Length 53522;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1023
ID AEB35216 standard; DNA; 53522 BP.
DE Human Gefitinib sensitivity-related gene, PKD1 SEQ ID 80.
PN WO2005070020-A2.
PD 04-AUG-2005.
PA (COLS) UNIV COLORADO.
Query Match 3.3%; Score 43; DB 14; Length 53522;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1024
ID AAT94101 standard; DNA; 53526 BP.
DE Human PKD1 gene.
PN WO9744457-A1.
PD 27-NOV-1997.
PA (GENZ) GENZYME CORP.
Query Match 3.3%; Score 43; DB 2; Length 53526;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1025
ID AAT18551 standard; DNA; 53577 BP.
DE Human polycystic kidney disease normal PKD1 gene.
PN WO9612033-A1.
PD 25-APR-1996.
PA (IGIG-) IG LAB INC.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 3.3%; Score 43; DB 2; Length 53577;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1026
ID AAT94108 standard; DNA; 53577 BP.
DE Human PKD1 locus between chromosomal markers ATP6C and D16S84.
PN WO9744457-A1.
PD 27-NOV-1997.
PA (GENZ) GENZYME CORP.
Query Match 3.3%; Score 43; DB 2; Length 53577;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1027
ID AAK68202 standard; DNA; 56743 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23014.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 56743;

Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1028
ID AAK81760 standard; DNA; 56743 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36572.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 4; Length 56743;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1029
ID ACN44826 standard; DNA; 57243 BP.
DE Human genomic sequence hCG19805.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 57243;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1030
ID AEC32873 standard; DNA; 57759 BP.
DE Breast cancer detection estrogen receptor negative gene, SEQ ID 108.
PN US2005186577-A1.
PD 25-AUG-2005.
PA (WANG/) WANG Y.
Query Match 3.3%; Score 43; DB 14; Length 57759;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1031
ID AEC82540 standard; cDNA; 57759 BP.
DE Breast cancer associated cDNA SEQ ID NO 108.
PN WO2005083429-A2.
PD 09-SEP-2005.
PA (VERI-) VERIDEX LLC.
Query Match 3.3%; Score 43; DB 14; Length 57759;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1032
ID ABZ74619 standard; DNA; 58181 BP.
DE Secreted protein gene 372 genomic fragment HWBCN36, SEQ ID NO:1766.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 8; Length 58181;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1033
ID ADC21010 standard; DNA; 58181 BP.
DE Human secreted protein-related DNA sequence #428.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 10; Length 58181;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1034
ID ABZ68140 standard; DNA; 58181 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1663.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.3%; Score 43; DB 10; Length 58181;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1035
ID AAD36834 standard; DNA; 59215 BP.
DE Human transporter protein genomic DNA.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 60452;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1037
ID ACN44530 standard; DNA; 60500 BP.
DE Human genomic sequence hCG37125.

PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 60500;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1038
ID ACN43886 standard; DNA; 61103 BP.
DE Human genomic sequence hCG1784975.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 61103;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1039
ID ABS67634 standard; DNA; 63000 BP.
DE Human casein kinase-2 genomic DNA.
PN WO200262818-A2.
PD 15-AUG-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.3%; Score 43; DB 6; Length 63000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1040
ID ACN44106 standard; DNA; 63828 BP.
DE Human genomic sequence hCG23727.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 63828;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1041
ID AEA61156 standard; DNA; 67883 BP.
DE Human ABCG2 gene genomic sequence SEQ ID NO:66.
PN US2005130172-A1.
PD 16-JUN-2005.
PA (FARB) BAYER CORP.
Query Match 3.3%; Score 43; DB 14; Length 67883;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1042
ID AEF74801 standard; DNA; 69648 BP.
DE Human polynucleotide #315.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (VISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 3.3%; Score 43; DB 15; Length 69648;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1043
ID ADC86870 standard; DNA; 69770 BP.
DE Human GPCR gene SEQ ID NO:1323.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.3%; Score 43; DB 10; Length 69770;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1044
ID AAZ18355 standard; DNA; 72928 BP.
DE Human ASTHJ 5' genomic region.
PN WO9937809-A1.
PD 29-JUL-1999.
PA (AXYS-) AXYS PHARM INC.
Query Match 3.3%; Score 43; DB 2; Length 72928;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1045
ID AAA80253 standard; DNA; 72928 BP.
DE Human ASTHJ 5' genomic region.
PN US6087485-A.
PD 11-JUL-2000.
PA (AXYS-) AXYS PHARM INC.
Query Match 3.3%; Score 43; DB 3; Length 72928;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1046
ID ABD33385 standard; DNA; 76180 BP.

DE Human cancer-associated (CA) gene HD07-071.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 3.3%; Score 43; DB 13; Length 76180;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1047
 Query Match 3.3%; Score 43; DB 10; Length 79652;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1048
 ID ABQ88164 standard; cDNA; 86080 BP.
 DE Human osteoblast differentiation related cDNA SEQ ID NO 71.
 PN WO200250301-A2.
 PD 27-JUN-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (PROC) PROCTER & GAMBLE CO.
 Query Match 3.3%; Score 43; DB 6; Length 86080;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1049
 ID ABK83561 standard; cDNA; 86080 BP.
 DE Human cDNA differentially expressed in granulocytic cells #132.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.3%; Score 43; DB 6; Length 86080;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1050
 ID AD71054 standard; DNA; 86080 BP.
 DE Human protective protein for beta-galactosidase gene SEQ ID NO:58.
 PN WO2003061564-A2.
 PD 31-JUL-2003.
 PA (GENE-) GENE LOGIC INC.
 PA (LGBI-) LG BIOMEDICAL INST.
 Query Match 3.3%; Score 43; DB 10; Length 86080;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1051
 ID ADQ18878 standard; DNA; 86080 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1697.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 3.3%; Score 43; DB 12; Length 86080;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1052
 ID AED18140 standard; DNA; 86080 BP.
 DE Fibrotic disorder associated polynucleotide SEQ ID NO 391.
 PN WO2003098041-A2.
 PD 20-OCT-2005.
 PA (UYFL) UNIV FLORIDA RES FOUND INC.
 Query Match 3.3%; Score 43; DB 14; Length 86080;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1053
 ID ADX98572 standard; DNA; 86950 BP.
 DE Human HTO14/LOC148902/LyPLA2/GALE genomic DNA.
 Query Match 3.3%; Score 43; DB 14; Length 86950;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1054
 ID ADZ13911 standard; DNA; 89210 BP.
 DE Human cancer-associated genomic DNA #124.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 3.3%; Score 43; DB 14; Length 89210;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1055
 ID ADQ97413 standard; DNA; 90120 BP.
 DE Human cancer associated sequence HD08-045, SEQ ID 390.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 3.3%; Score 43; DB 12; Length 90120;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1056

ID ABK83576 standard; cDNA; 90220 BP.
 DE Human cDNA differentially expressed in granulocytic cells #147.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.3%; Score 43; DB 6; Length 90220;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1057
 ID ABD32673 standard; DNA; 91359 BP.
 DE Human cancer-associated genomic DNA HD13-075.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 3.3%; Score 43; DB 13; Length 91359;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1058
 ID AAL57580 standard; cDNA; 93273 BP.
 DE Human GTPase activating protein-like cDNA.
 PN WO2003059148-A2.
 PD 24-JUL-2003.
 PA (GENE-) GENE LOGIC INC.
 PA (LGBI-) LG BIOMEDICAL INST.
 Query Match 3.3%; Score 43; DB 9; Length 93273;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1059
 ID ADP08387 standard; DNA; 94400 BP.
 DE Human glycoprotein VI (platelet) (GP6;GP1V;GPVI) genomic DNA.
 Query Match 3.3%; Score 43; DB 12; Length 94400;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1060
 ID ACN44066 standard; DNA; 99886 BP.
 DE Human genomic sequence hCG15674.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 3.3%; Score 43; DB 11; Length 99886;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1061
 ID ABQ74541 standard; DNA; 100000 BP.
 DE Human transglutaminase-B gene sequence SEQ ID NO:7.
 PN WO200259265-A2.
 PD 01-AUG-2002.
 PA (DECO-) DECODE GENETICS INC.
 Query Match 3.3%; Score 43; DB 6; Length 100000;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1062
 ID AQ59518 standard; DNA; 100762 BP.
 DE Human cancer-associated (CA) gene sequence SEQ ID NO:154.
 PN WO2004058288-A1.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 3.3%; Score 43; DB 12; Length 100762;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1063
 ID ADZ13899 standard; DNA; 100822 BP.
 DE Human cancer-associated genomic DNA #122.
 PN WO2005031001-A2.
 PD 07-APR-2005.
 PA (CHIR) CHIRON CORP.
 Query Match 3.3%; Score 43; DB 14; Length 100822;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1064
 ID AQ017329 standard; DNA; 101685 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 146.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 3.3%; Score 43; DB 12; Length 101685;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 RESULT 1065
 ID ABD33432 standard; DNA; 106938 BP.
 DE Human cancer-associated (CA) gene HD07-081.
 PN WO2004058146-A2.

PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 13; Length 106938;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1066
ID ADR67034 standard; DNA; 106938 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:80.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 13; Length 106938;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1067
ID ADZ13456 standard; DNA; 107310 BP.
DE Human cancer-associated genomic DNA #83.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 107310;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1068
ID ADZ13456 standard; DNA; 107310 BP.
DE Human cancer-associated genomic DNA #83.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 107310;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1069
ID AAD16230 standard; DNA; 107820 BP.
DE Human ATP-binding cassette transporter ABCG6 (MRP6) complementary gene.
Query Match 3.3%; Score 43; DB 4; Length 107820;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1070
Query Match 3.3%; Score 43; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1071
Query Match 3.3%; Score 43; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1072
Query Match 3.3%; Score 43; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1073
Query Match 3.3%; Score 43; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1074
Query Match 3.3%; Score 43; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1075
ID ACH03408 standard; DNA; 402457 BP.
DE Genomic DNA encoding human latrophilin 3 (LPH3).
PN US2003054347-A1.
PD 20-MAR-2003.
PA (UNMI) UNIV MICHIGAN.
Query Match 3.3%; Score 43; DB 9; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1076
Query Match 3.3%; Score 43; DB 11; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1077
Query Match 3.3%; Score 43; DB 11; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1078
Query Match 3.3%; Score 43; DB 12; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1079
Query Match 3.3%; Score 43; DB 12; Length 110000;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1080
ID ADJ74882 standard; DNA; 117143 BP.
DE Marker gene SEQ ID NO:134.
PN EPI394274-A2.
PD 03-MAR-2004.

PA (GENO-) GENOX RES INC.
Query Match 3.3%; Score 43; DB 12; Length 117143;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1081
ID AED18148 standard; DNA; 117143 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 399.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 3.3%; Score 43; DB 14; Length 117143;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1082
ID AEF75107 standard; DNA; 117143 BP.
DE Human polynucleotide #621.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 3.3%; Score 43; DB 15; Length 117143;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1083
ID ADX07540 standard; DNA; 117813 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 2105.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.3%; Score 43; DB 14; Length 117813;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1084
ID AEF74585 standard; DNA; 117813 BP.
DE Human polynucleotide #99.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 3.3%; Score 43; DB 15; Length 117813;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1085
ID ADI29095 standard; DNA; 119501 BP.
DE Human MARK3 genomic DNA.
PN US2003232771-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.3%; Score 43; DB 12; Length 119501;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1086
ID ADI29095 standard; DNA; 119501 BP.
DE Human MARK3 genomic DNA.
PN US2003232771-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.3%; Score 43; DB 12; Length 119501;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1087
ID AEB34801 standard; DNA; 120890 BP.
DE Human carnitine palmitoyltransferase II, clone RP5-1024G6, DNA.
PN WO2005069855-A2.
PD 04-AUG-2005.
PA (RIGE-) RIGEL PHARM INC.
Query Match 3.3%; Score 43; DB 14; Length 120890;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1088
ID AAC66548 standard; DNA; 121162 BP.
DE Human kinesin-like protein HKLP coding sequence contig SEQ ID NO: 1.
PN WO200603375-A1.
PD 26-OCT-2000.
PA (GEST) GENSET.
Query Match 3.3%; Score 43; DB 3; Length 121162;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1089
ID ABQ88143 standard; cDNA; 121724 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 50.
PN WO200250301-A2.

PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 43; DB 6; Length 121724;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1090
ID AK83569 standard; cDNA; 122888 BP.
DE Human cDNA differentially expressed in granulocytic cells #140.
PN W0200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 43; DB 6; Length 122888;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1091
ID ASB35282 standard; DNA; 126259 BP.
DE Human Gefitinib sensitivity-related gene, SEQ ID 146.
PN W02005070020-A2.
PD 04-AUG-2005.
PA (COLS) UNIV COLORADO.
Query Match 3.3%; Score 43; DB 14; Length 126259;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1092
ID ADR52731 standard; DNA; 127917 BP.
DE Drug therapy altered expressed gene #82.
PN W02004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 3.3%; Score 43; DB 13; Length 127917;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1093
ID ADJ96282 standard; DNA; 130001 BP.
DE Human breast cancer-1 DNA #14.
PN US2004014051-A1.
PD 22-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.3%; Score 43; DB 12; Length 130001;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1094
ID ADM98070 standard; DNA; 130001 BP.
DE Human breast cancer-1 DNA, seqid:23.
PN US2005026857-A1.
PD 03-FEB-2005.
PA (BROW/) BROWN-DRIVER V L.
PA (DOBI/) DOBIE K W.
Query Match 3.3%; Score 43; DB 14; Length 130001;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1095
ID ACA64895 standard; DNA; 134292 BP.
DE Human GABBR1 DNA corresponding to AL031983.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHOARRAY GMBH.
Query Match 3.3%; Score 43; DB 8; Length 134292;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1096
ID AED18093 standard; DNA; 134292 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 344.
PN W02005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 3.3%; Score 43; DB 14; Length 134292;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1097
ID ABK83562 standard; cDNA; 139904 BP.
DE Human cDNA differentially expressed in granulocytic cells #133.
PN W0200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 43; DB 6; Length 139904;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1098
ID AQ59464 standard; DNA; 141503 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:100.
PN W02004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 12; Length 141503;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1099
ID ACN44850 standard; DNA; 142318 BP.
DE Human genomic sequence hCG33122.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 142318;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1100
ID AED17971 standard; DNA; 145616 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 222.
PN W02005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 3.3%; Score 43; DB 14; Length 145616;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1101
ID ADP45593 standard; DNA; 147300 BP.
DE Human Rho family guanine-nucleotide exchange factor KIAA0861 gDNA.
PN W02004047623-A2.
PD 10-JUN-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 3.3%; Score 43; DB 12; Length 147300;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1102
ID ADX98570 standard; DNA; 147700 BP.
DE Human guanine-nucleotide exchange factor KIAA0861 genomic DNA.
Query Match 3.3%; Score 43; DB 14; Length 147700;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1103
ID ASE96613 standard; DNA; 147700 BP.
DE KIAA0861 genomic DNA sequence, SEQ ID NO:1.
PN W02005118856-A1.
PD 15-DEC-2005.
PA (SEQU-) SEQUENOM INC.
Query Match 3.3%; Score 43; DB 15; Length 147700;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1104
ID ACN44394 standard; DNA; 150130 BP.
DE Human genomic sequence hCG28278.
PN W02003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 150130;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1105
ID AED89403 standard; DNA; 159660 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 43.
PN W02005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 3.3%; Score 43; DB 14; Length 159660;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1106
ID ASQ88179 standard; cDNA; 160771 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 86.
PN W0200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 43; DB 6; Length 160771;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1107
ID ABT11173 standard; DNA; 168174 BP.

DE Human 5-lipoxygenase gene related DNA sequence SEQ ID NO 63.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.3%; Score 43; DB 6; Length 168174;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1108
ID APT11114 standard; DNA; 168273 BP.
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID NO 2.
PN WO200262825-A2.
PD 15-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.3%; Score 43; DB 6; Length 168273;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1109
ID AED89419 standard; DNA; 168656 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 59.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 3.3%; Score 43; DB 14; Length 168656;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1110
ID ACN44262 standard; DNA; 168821 BP.
DE Human genomic sequence hCG18035.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 168821;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1111
ID AQ59434 standard; DNA; 169659 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:70.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 12; Length 169659;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1112
ID AED89418 standard; DNA; 170285 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 58.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 3.3%; Score 43; DB 14; Length 170285;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1113
ID ACF62733 standard; DNA; 172984 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:661.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 43; DB 8; Length 172984;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1114
ID ADB20848 standard; DNA; 172984 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:661.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 43; DB 8; Length 172984;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1115
ID ADB87937 standard; DNA; 172984 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:661.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 43; DB 10; Length 172984;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1116
ID ADB96920 standard; DNA; 172984 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:661.

PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 43; DB 10; Length 172984;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1117
ID ADB92111 standard; DNA; 172984 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:661.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 3.3%; Score 43; DB 10; Length 172984;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1118
ID AED18079 standard; DNA; 173354 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 330.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 3.3%; Score 43; DB 14; Length 173354;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1119
ID AEF74923 standard; DNA; 173354 BP.
DE Human polynucleotide #437.
PN WO2006013561-A2.
PD 09-FEB-2006.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
Query Match 3.3%; Score 43; DB 15; Length 173354;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1120
ID ACN43946 standard; DNA; 174448 BP.
DE Human genomic sequence hCG21793.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 174448;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1121
ID ACN44806 standard; DNA; 177587 BP.
DE Human genomic sequence hCG40093.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.3%; Score 43; DB 11; Length 177587;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1122
ID AD213195 standard; DNA; 177930 BP.
DE Human cancer-associated genomic DNA #58.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 177930;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1123
ID ABE04899 standard; DNA; 183558 BP.
DE Cancer-associated gene SEQ ID NO:217.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 183558;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1124
ID AED18538 standard; DNA; 184666 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 789.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 3.3%; Score 43; DB 14; Length 184666;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1125
ID ABT10718 standard; cDNA; 185371 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 852.

PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 43; DB 6; Length 185371;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
RESULT 1126
ID AD213735 standard; DNA; 187851 BP.
DE Human cancer-associated genomic DNA #108.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 3.3%; Score 43; DB 14; Length 187851;
RESULT 1127
ID AB033462 standard; DNA; 196063 BP.
DE Human cancer-associated (CA) gene HD07-088.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 13; Length 196063;
RESULT 1128
ID ACN44226 standard; DNA; 200418 BP.
DE Human genomic sequence hCG33697.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 3.3%; Score 43; DB 11; Length 200418;
RESULT 1129
ID AD056277 standard; DNA; 200620 BP.
DE Human presynaptic cytomatrix protein, REPS2, genomic sequence.
PN WO2004044164-A2.
PD 27-MAY-2004.
PA (SEQU-) SEQUENOM INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 12; Length 200620;
RESULT 1130
ID AEF85801 standard; DNA; 207740 BP.
DE Human chromosome 20 partial genomic sequence SEQ ID NO:1.
PN JP2006042735-A.
PD 16-FEB-2006.
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
PA (MABU/) MABUCHI A.
Query Match
Best Local Similarity 3.3%; Score 43; DB 15; Length 207740;
RESULT 1131
ID ADX80726 standard; DNA; 213300 BP.
DE Human RALBP1 associated Eps domain containing 2 (REPS2) genomic DNA.
Query Match
Best Local Similarity 3.3%; Score 43; DB 14; Length 213300;
RESULT 1132
ID ADQ97523 standard; DNA; 215974 BP.
DE Human cancer associated sequence HD09-008, SEQ ID 500.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 12; Length 215974;
RESULT 1133
ID ADX80720 standard; DNA; 221600 BP.
DE Human neurophilin 1 (NRP1) genomic DNA.
Query Match
Best Local Similarity 3.3%; Score 43; DB 14; Length 221600;
RESULT 1134
ID ABK84349 standard; cDNA; 222930 BP.
DE Human cDNA differentially expressed in granulocytic cells #920.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 6; Length 222930;
RESULT 1135

ID AED17977 standard; DNA; 222930 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 228.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 14; Length 222930;
RESULT 1136
ID ASK83497 standard; cDNA; 227968 BP.
DE Human cDNA differentially expressed in granulocytic cells #68.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 6; Length 227968;
RESULT 1137
ID ADQ18538 standard; DNA; 227968 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 12; Length 227968;
RESULT 1138
ID AED17856 standard; DNA; 227968 BP.
DE Fibrotic disorder associated polynucleotide SEQ ID NO 107.
PN WO2005098041-A2.
PD 20-OCT-2005.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 14; Length 227968;
RESULT 1139
ID ADQ97421 standard; DNA; 228835 BP.
DE Human cancer associated sequence HD08-046, SEQ ID 398.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 12; Length 228835;
RESULT 1140
ID AAV57926 standard; DNA; 235033 BP.
DE Hereditary haemochromatosis subregion from an unaffected individual.
PN WO9814466-A1.
PD 09-APR-1998.
PA (PROG-) PROCENTIOR INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 2; Length 235033;
RESULT 1141
ID AAS11614 standard; DNA; 236303 BP.
DE Human genomic DNA containing exons 2-17 of the CRIM1 gene.
PN WO200138519-A1.
PD 31-MAY-2001.
PA (UYQU) UNIV QUEENSLAND.
Query Match
Best Local Similarity 3.3%; Score 43; DB 4; Length 236303;
RESULT 1142
ID AAV57903 standard; DNA; 237326 BP.
DE Hereditary haemochromatosis subregion from an HH affected individual.
PN WO9814466-A1.
PD 09-APR-1998.
PA (PROG-) PROCENTIOR INC.
Query Match
Best Local Similarity 3.3%; Score 43; DB 2; Length 237326;
RESULT 1143
ID AEE05008 standard; DNA; 246386 BP.
DE Cancer-associated gene SEQ ID NO:326.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 3.3%; Score 43; DB 14; Length 246386;
RESULT 1144
ID ADL13684 standard; DNA; 247509 BP.

DE Osteoarthritis-associated polymorphic nucleotide #216.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.3%; Score 43; DB 10; Length 247509;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1145
ID AEF07224 standard; DNA; 259500 BP.
DE PFTK1 locus of the human genome.
PN WO2005118834-A2.
PD 15-DEC-2005.
PA (SEQU-) SEQUENOM INC. 3.3%; Score 43; DB 15; Length 259500;
Query Match 3.3%; Score 43; DB 15; Length 259500;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1146
ID ABS56564 standard; DNA; 260209 BP.
DE Human SULF2 genomic DNA sequence.
PN WO200259327-A2.
PD 01-AUG-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 3.3%; Score 43; DB 6; Length 260209;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1147
ID ADN16204 standard; DNA; 260209 BP.
DE Human sulfatase SULF1 gene.
PN WO2004031365-A2.
PD 15-APR-2004.
PA (REGC) UNIV CALIFORNIA.
PA (THIO-) THIOS PHARM INC.
Query Match 3.3%; Score 43; DB 12; Length 260209;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1148
ID AEE06394 standard; DNA; 267966 BP.
DE Glycogen synthase kinase-3beta (GSK-3beta) gene.
PN WO2005108582-A1.
PD 17-NOV-2005.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 3.3%; Score 43; DB 14; Length 267966;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1149
ID ABD32602 standard; DNA; 277616 BP.
DE Human cancer-associated genomic DNA HD7-221.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 13; Length 277616;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1150
ID ABD32602 standard; DNA; 277616 BP.
DE Human cancer-associated genomic DNA HD7-221.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 13; Length 277616;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1151
ID AEE04909 standard; DNA; 292299 BP.
DE Cancer-associated gene SEQ ID NO:227.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 292299;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1152
ID ADE86352 standard; DNA; 300000 BP.
DE Human PTPN11 genomic DNA sequence SEQ ID NO:33.
PN WO2003029422-A2.
PD 10-APR-2003.
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
Query Match 3.3%; Score 43; DB 10; Length 300000;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1153
ID ADO14076 standard; DNA; 300001 BP.
DE Human protein tyrosine phosphatase 11 gene sequence SEQ ID NO:33.
PN WO2004041216-A2.
PD 21-MAY-2004.
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
PA (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.
Query Match 3.3%; Score 43; DB 12; Length 300001;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1154
ID ABD32548 standard; DNA; 310268 BP.
DE Human cancer-associated genomic DNA HD14-033.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.3%; Score 43; DB 13; Length 310268;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1155
ID ADZ13793 standard; DNA; 342748 BP.
DE Human cancer-associated genomic DNA #113.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.3%; Score 43; DB 14; Length 342748;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1156
ID ADC86642 standard; DNA; 349881 BP.
DE Human GPCR gene SEQ ID NO:1095.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.3%; Score 43; DB 10; Length 349881;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1157
ID ADC86916 standard; DNA; 349989 BP.
DE Human GPCR gene SEQ ID NO:1369.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.3%; Score 43; DB 10; Length 349989;
Best Local Similarity 100.0%; Pred. No. 2e-09;
RESULT 1158
ID RAC11792 standard; cDNA; 253 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 15867.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.2%; Score 42; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 7.5e-09;
RESULT 1159
ID AAK73675 standard; DNA; 972 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28487.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 42; DB 4; Length 972;
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
RESULT 1160
ID AAL35319 standard; cDNA; 1151 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 661.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 42; DB 4; Length 1151;
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
RESULT 1161
ID ABX58307 standard; cDNA; 1151 BP.
DE cDNA encoding novel human musculoskeletal system antigen #651.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.

Query Match
Best Local Similarity 3.2%; Score 42; DB 8; Length 1151;
RESULT 1162
ID ADJ28034 standard; DNA; 1151 BP.
DE Human musculoskeletal system-associated contig DNA - SEQ ID 661.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.2%; Score 42; DB 12; Length 1151;
RESULT 1163
ID AB225720 standard; cDNA; 1984 BP.
DE Human topoisomerase 11.99-encoding cDNA.
PN CN1360028-A.
PD 24-JUL-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match
Best Local Similarity 3.2%; Score 42; DB 6; Length 1984;
RESULT 1164
ID AEC84311 standard; cDNA; 2247 BP.
DE Human CDNA of the invention SEQ ID NO:66.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 3.2%; Score 42; DB 11; Length 2247;
RESULT 1165
ID AEC84311 standard; cDNA; 2247 BP.
DE Human CDNA clone BLADE2004630, SEQ ID 66.
PN EPI580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 3.2%; Score 42; DB 14; Length 2247;
RESULT 1166
ID ADA52509 standard; cDNA; 2358 BP.
DE Human coding sequence, SEQ ID 77.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 3.2%; Score 42; DB 10; Length 2358;
RESULT 1167
ID ADM01675 standard; cDNA; 2532 BP.
DE Human CDNA of the invention SEQ ID NO:360.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 3.2%; Score 42; DB 11; Length 2532;
RESULT 1168
ID AEC84605 standard; cDNA; 2532 BP.
DE Human CDNA clone BRAWH20166790, SEQ ID 360.
PN EPI580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 3.2%; Score 42; DB 14; Length 2532;
RESULT 1169
ID ADM01439 standard; cDNA; 2569 BP.
DE Human CDNA of the invention SEQ ID NO:124.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 3.2%; Score 42; DB 11; Length 2569;
RESULT 1170
ID AEC84369 standard; cDNA; 2569 BP.
DE Human CDNA clone BRACE20106690, SEQ ID 124.
PN EPI580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match
Best Local Similarity 3.2%; Score 42; DB 14; Length 2569;
RESULT 1171
ID ADQ21290 standard; DNA; 4594 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4110.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 3.2%; Score 42; DB 12; Length 4594;
RESULT 1172
ID AEA15353 standard; cDNA; 4617 BP.
DE Human polynucleotide #50.
PN WO2005047534-A2.
PD 26-MAY-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match
Best Local Similarity 3.2%; Score 42; DB 14; Length 4617;
RESULT 1173
ID ADQ25169 standard; DNA; 5284 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7989.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 3.2%; Score 42; DB 12; Length 5284;
RESULT 1174
ID AAS26766 standard; DNA; 6096 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1740.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.2%; Score 42; DB 4; Length 6096;
RESULT 1175
ID ABX74115 standard; DNA; 6096 BP.
DE Human novel polynucleotide #943.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 3.2%; Score 42; DB 8; Length 6096;
RESULT 1176
ID AAK83993 standard; DNA; 6848 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38805.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.2%; Score 42; DB 4; Length 6848;
RESULT 1177
ID AAK66657 standard; DNA; 8960 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24469.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.2%; Score 42; DB 4; Length 8960;
RESULT 1178
ID AAS31470 standard; DNA; 12503 BP.
DE Human DNA for a novel extracellular matrix protein, Seq ID No 549.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.2%; Score 42; DB 4; Length 12503;
RESULT 1179
ID ABO66794 standard; DNA; 12503 BP.
DE Human polynucleotide SEQ ID NO 549.
PN US2002042386-A1.
PD 11-APR-2002.


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PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
  Query Match      3.2%; Score 42; DB 6; Length 12503;
  Best Local Similarity 100.0%; Pred. No. 6.5e-09;
RESULT 1180
ID ADC11081 standard; DNA; 12503 BP.
DE Human DNA from extracellular matrix gene 40 #1.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 10; Length 12503;
  Best Local Similarity 100.0%; Pred. No. 6.5e-09;
RESULT 1181
ID AAK65368 standard; DNA; 18564 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20180.
PN WO2001571182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 4; Length 18564;
  Best Local Similarity 100.0%; Pred. No. 6.5e-09;
RESULT 1182
ID ABZ74461 standard; DNA; 18564 BP.
DE Secreted protein gene 300 genomic fragment HSQD085, SEQ ID NO:1608.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 8; Length 18564;
  Best Local Similarity 100.0%; Pred. No. 6.5e-09;
RESULT 1183
ID ADA98881 standard; DNA; 18564 BP.
DE Human secreted protein-related DNA sequence #474.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 8; Length 18564;
  Best Local Similarity 100.0%; Pred. No. 6.5e-09;
RESULT 1184
ID ADO97295 standard; DNA; 21293 BP.
DE Human cancer associated sequence HD08-027, SEQ ID 272.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
  Query Match      3.2%; Score 42; DB 12; Length 21293;
  Best Local Similarity 100.0%; Pred. No. 6.4e-09;
RESULT 1185
ID ABA15431 standard; DNA; 25012 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7762.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 5; Length 25012;
  Best Local Similarity 100.0%; Pred. No. 6.4e-09;
RESULT 1186
ID ABZ73798 standard; DNA; 25012 BP.
DE Secreted protein gene 42 genomic fragment HBWMT11, SEQ ID NO:945.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 8; Length 25012;
  Best Local Similarity 100.0%; Pred. No. 6.4e-09;
RESULT 1187
ID ADA98470 standard; DNA; 25012 BP.
DE Human secreted protein-related DNA sequence #63.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 8; Length 25012;
  Best Local Similarity 100.0%; Pred. No. 6.4e-09;
RESULT 1188
ID ASC82969 standard; cDNA; 28247 BP.
DE Breast cancer associated cDNA SEQ ID NO 537.
PN WO2005083429-A2.

PD 09-SEP-2005.
PA (VERI-) VERIDEX LLC.
  Query Match      3.2%; Score 42; DB 14; Length 28247;
  Best Local Similarity 100.0%; Pred. No. 6.4e-09;
RESULT 1189
ID AAL36829 standard; DNA; 28313 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3194.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 4; Length 28313;
  Best Local Similarity 100.0%; Pred. No. 6.4e-09;
RESULT 1190
ID ABX59817 standard; cDNA; 28313 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2161.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
  Query Match      3.2%; Score 42; DB 8; Length 28313;
  Best Local Similarity 100.0%; Pred. No. 6.4e-09;
RESULT 1191
ID ADJ30567 standard; DNA; 28313 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3194.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 12; Length 28313;
  Best Local Similarity 100.0%; Pred. No. 6.4e-09;
RESULT 1192
ID ACN44562 standard; DNA; 28544 BP.
DE Human genomic sequence HCG15331.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
  Query Match      3.2%; Score 42; DB 11; Length 28544;
  Best Local Similarity 100.0%; Pred. No. 6.4e-09;
RESULT 1193
ID AAL36833 standard; DNA; 29228 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3198.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 4; Length 29228;
  Best Local Similarity 100.0%; Pred. No. 6.3e-09;
RESULT 1194
ID ABX59821 standard; cDNA; 29228 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2165.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
  Query Match      3.2%; Score 42; DB 8; Length 29228;
  Best Local Similarity 100.0%; Pred. No. 6.3e-09;
RESULT 1195
ID ADJ30571 standard; DNA; 29228 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3198.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      3.2%; Score 42; DB 12; Length 29228;
  Best Local Similarity 100.0%; Pred. No. 6.3e-09;
RESULT 1196
ID ADO97189 standard; DNA; 29360 BP.
DE Human cancer associated sequence HD08-012, SEQ ID 165.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
  Query Match      3.2%; Score 42; DB 12; Length 29360;
  Best Local Similarity 100.0%; Pred. No. 6.3e-09;
RESULT 1197
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ID AAK84996 standard; DNA; 39678 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39808.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 42; DB 4; Length 39678;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
RESULT 1198
ID ACN44146 standard; DNA; 50602 BP.
DE Human genomic sequence hCG28572.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 42; DB 11; Length 50602;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
RESULT 1199
ID AQO97804 standard; DNA; 50807 BP.
DE Human cancer associated sequence HD10-048, SEQ ID 781.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.2%; Score 42; DB 12; Length 50807;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
RESULT 1200
ID ABE05028 standard; DNA; 55366 BP.
DE Cancer-associated gene SEQ ID NO:346.
PN WO2005107396-A2.
PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.2%; Score 42; DB 14; Length 55366;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
RESULT 1201
ID ADZ12496 standard; DNA; 72337 BP.
DE Human cancer-associated genomic DNA #3.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.2%; Score 42; DB 14; Length 72337;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
RESULT 1202
ID ACN44090 standard; DNA; 81748 BP.
DE Human genomic sequence hCG24418.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 42; DB 11; Length 81748;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
RESULT 1203
ID ACN44090 standard; DNA; 81748 BP.
DE Human genomic sequence hCG24418.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 42; DB 11; Length 81748;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
RESULT 1204
ID AAL57572 standard; cDNA; 107818 BP.
DE Human phosphomannomutase 1 cDNA.
PN WO2003059148-A2.
PD 24-JUL-2003.
PA (GENE-) GENE LOGIC INC.
PA (LGBI-) LG BIOMEDICAL INST.
Query Match 3.2%; Score 42; DB 9; Length 107818;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
RESULT 1205
Query Match 3.2%; Score 42; DB 10; Length 110000;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
RESULT 1206
Query Match 3.2%; Score 42; DB 10; Length 110000;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
RESULT 1207
ID ACD13448 standard; DNA; 115756 BP.
DE Human DNA encoding a p53 modifier, SEQ ID 68.

PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 3.2%; Score 42; DB 8; Length 115756;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
RESULT 1208
ID ADQ97391 standard; DNA; 120447 BP.
DE Human cancer associated sequence HD08-042, SEQ ID 368.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.2%; Score 42; DB 12; Length 120447;
Best Local Similarity 100.0%; Pred. No. 6e-09;
RESULT 1209
ID ADQ80254 standard; cDNA; 127145 BP.
DE Hermaneky-Pudlak syndrome associated cDNA.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.2%; Score 42; DB 13; Length 127145;
Best Local Similarity 100.0%; Pred. No. 6e-09;
RESULT 1210
ID ADF13116 standard; DNA; 128779 BP.
DE Hypermethylation site in human breast cancer CpG island locus HBC-45.
PN US2003129602-A1.
PD 10-JUL-2003.
PA (HUAN/) HUANG T H.
Query Match 3.2%; Score 42; DB 12; Length 128779;
Best Local Similarity 100.0%; Pred. No. 6e-09;
RESULT 1211
ID ADI37262 standard; DNA; 128779 BP.
DE Hypermethylation in cancer (HBC) locus-45.
PN US6605432-B1.
PD 12-AUG-2003.
PA (UMOR) UNIV MISSOURI.
Query Match 3.2%; Score 42; DB 12; Length 128779;
Best Local Similarity 100.0%; Pred. No. 6e-09;
RESULT 1212
ID ASF19127 standard; DNA; 188056 BP.
DE Human NIPBL genomic sequence.
PN US2006003354-A1.
PD 05-JAN-2006.
PA (KRAN/) KRANTZ I D.
PA (JACK/) JACKSON L G.
Query Match 3.2%; Score 42; DB 15; Length 188056;
Best Local Similarity 100.0%; Pred. No. 6e-09;
RESULT 1213
ID AED89394 standard; DNA; 197781 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 34.
PN WO2005106044-A1.
PD 10-NOV-2005.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 3.2%; Score 42; DB 14; Length 197781;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
RESULT 1214
ID ACN44418 standard; DNA; 213040 BP.
DE Human genomic sequence hCG41574.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 42; DB 11; Length 213040;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
RESULT 1215
ID AAL03823 standard; DNA; 119 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6511.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
RESULT 1216
ID ABA07945 standard; DNA; 119 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 740.

PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
RESULT 1217
ID ABA20659 standard; DNA; 125 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12990.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
RESULT 1218
ID AAC13448 standard; cDNA; 159 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 17523.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.2%; Score 41; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
RESULT 1219
ID ADI76848 standard; DNA; 384 BP.
DE Human ovarian cancer DNA marker #9590.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 5; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1220
ID ADI70523 standard; DNA; 384 BP.
DE Human ovarian cancer DNA marker #3365.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 5; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1221
ID AAH30334 standard; cDNA; 405 BP.
DE Human colon cancer cell line Kmi2L4-A cDNA library derived sequence #269.
PN WO200018916-A2.
PD 06-APR-2000.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.2%; Score 41; DB 3; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1222
ID ACH49493 standard; cDNA; 415 BP.
DE Human leukocyte cDNA #1087.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.2%; Score 41; DB 9; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1223
ID RAP64741 standard; cDNA; 449 BP.
DE Novel human polynucleotide, SEQ ID NO: 497.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.2%; Score 41; DB 5; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1224
ID ABV05097 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 5088.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 3.2%; Score 41; DB 5; Length 459;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1225
ID ABV57954 standard; cDNA; 497 BP.
DE Human prostate expression marker cDNA 57945.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 5; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1226
ID ACL59582 standard; cDNA; 515 BP.
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:5717.
PN WO2005000087-A2.
PD 06-JAN-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.2%; Score 41; DB 14; Length 515;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1227
ID AAL12051 standard; cDNA; 519 BP.
DE Human breast cancer expressed polynucleotide 4508.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 4; Length 519;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1228
ID AAK92502 standard; cDNA; 561 BP.
DE Human cDNA 3'-end sequence, SEQ ID NO: 962.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.2%; Score 41; DB 4; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1229
ID ADL42084 standard; DNA; 561 BP.
DE Human ovarian cancer DNA marker #15974.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 5; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1230
ID ADL8929 standard; cDNA; 561 BP.
DE 3' end of a human cDNA molecule SeqID 962.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.2%; Score 41; DB 12; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1231
ID ABQ58089 standard; cDNA; 563 BP.
DE Human colon cancer related nucleotide sequence SEQ ID NO:1784.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FARB) BAYER CORP.
Query Match 3.2%; Score 41; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1232
ID ABV14266 standard; cDNA; 564 BP.
DE Human prostate expression marker cDNA 14257.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 5; Length 564;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1233
ID AAL11911 standard; cDNA; 575 BP.
DE Human breast cancer expressed polynucleotide 4368.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 4; Length 575;

Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1234
ID ACL54220 standard; cDNA; 575 BP.
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:355.
PN WO2005000087-A2.
PD 06-JAN-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.2%; Score 41; DB 14; Length 575;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1235
ID ABV57912 standard; cDNA; 577 BP.
DE Human prostate expression marker cDNA 57903.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 5; Length 577;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1236
ID AAH13120 standard; cDNA; 585 BP.
DE Human CDNA clone (3'-primer) SEQ ID NO:9955.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.2%; Score 41; DB 4; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1237
ID ABV35359 standard; cDNA; 586 BP.
DE Human prostate expression marker cDNA 35350.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 5; Length 586;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1238
ID ABV44190 standard; cDNA; 586 BP.
DE Human prostate expression marker cDNA 44181.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 5; Length 586;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1239
ID AAL20936 standard; cDNA; 592 BP.
DE Human breast cancer expressed polynucleotide 13393.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1240
ID AAL20801 standard; cDNA; 592 BP.
DE Human breast cancer expressed polynucleotide 13258.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1241
ID ACN82104 standard; DNA; 652 BP.
DE Breast cancer related marker, seq id 3254.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.2%; Score 41; DB 11; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1242
ID AAA16296 standard; DNA; 655 BP.
DE Human colon cancer differentially expressed nucleotide sequence #301.
PN WO20012702-A2.
PD 09-MAR-2000.
PA (FARB) BAYER CORP.
Query Match 3.2%; Score 41; DB 3; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;

RESULT 1243
ID AAD19494 standard; DNA; 655 BP.
DE Human c-myb-related gene #2.
PN WO200172843-A2.
PD 04-OCT-2001.
PA (FARB) BAYER AG.
Query Match 3.2%; Score 41; DB 4; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1244
ID AAL97047 standard; cDNA; 729 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 3122.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 3.2%; Score 41; DB 4; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1245
ID AAH04073 standard; cDNA; 786 BP.
DE Human CDNA clone (5'-primer) SEQ ID NO:908.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.2%; Score 41; DB 4; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1246
ID AAL94455 standard; cDNA; 791 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 530.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 3.2%; Score 41; DB 4; Length 791;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1247
ID ABT42775 standard; DNA; 791 BP.
DE Human neuroblastoma-related DNA sequence, SEQ ID NO:56.
PN WO2002103017-A1.
PD 27-DEC-2002.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 3.2%; Score 41; DB 8; Length 791;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1248
ID AAH04407 standard; cDNA; 810 BP.
DE Human CDNA clone (5'-primer) SEQ ID NO:1242.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.2%; Score 41; DB 4; Length 810;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1249
ID AAK91480 standard; DNA; 1011 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5056.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 1011;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1250
ID AAK91481 standard; DNA; 1011 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5057.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 1011;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
RESULT 1251
ID ACN90553 standard; DNA; 1331 BP.
DE Breast cancer related marker, seq id 11703.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 3.2%; Score 41; DB 11; Length 1331;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1252
ID AAK51869 standard; cDNA; 1386 BP.
DE Human polynucleotide SEQ ID NO 414.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.2%; Score 41; DB 4; Length 1386;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1253
ID AAH17199 standard; cDNA; 1701 BP.
DE Human cDNA sequence SEQ ID NO:16569.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.2%; Score 41; DB 4; Length 1701;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1254
ID AAH15530 standard; cDNA; 1713 BP.
DE Human cDNA sequence SEQ ID NO:13800.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.2%; Score 41; DB 4; Length 1713;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1255
ID ADQ23477 standard; DNA; 1863 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6297.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.2%; Score 41; DB 12; Length 1863;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1256
ID AAK94191 standard; cDNA; 1903 BP.
DE Human full-length cDNA, SEQ ID NO: 2743.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.2%; Score 41; DB 4; Length 1903;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1257
ID ADL30710 standard; cDNA; 1903 BP.
DE Full length human cDNA clone seqID 2743.
PN EPI1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.2%; Score 41; DB 12; Length 1903;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1258
ID AAH16586 standard; cDNA; 2040 BP.
DE Human cDNA sequence SEQ ID NO:15671.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.2%; Score 41; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1259
ID ADM02073 standard; cDNA; 2547 BP.
DE Human cDNA of the invention SEQ ID NO:758.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.2%; Score 41; DB 11; Length 2547;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1260
ID ASC85003 standard; cDNA; 2547 BP.
DE Human cDNA clone FCBBF20006780, SEQ ID 758.
PN EPI580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.2%; Score 41; DB 14; Length 2547;

Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1261
ID AAL35789 standard; DNA; 2633 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2154.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 2633;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1262
ID ABX58777 standard; cDNA; 2633 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1121.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.2%; Score 41; DB 8; Length 2633;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1263
ID ADJ29527 standard; DNA; 2633 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2154.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 12; Length 2633;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1264
ID AAS33172 standard; cDNA; 2704 BP.
DE DNA encoding human secreted protein, Seq ID No 131.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 2704;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1265
ID ADM02712 standard; cDNA; 3294 BP.
DE Human cDNA of the invention SEQ ID NO:1397.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.2%; Score 41; DB 11; Length 3294;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1266
ID AEC85642 standard; cDNA; 3294 BP.
DE Human cDNA clone OCBBF20130910, SEQ ID 1397.
PN EPI580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.2%; Score 41; DB 14; Length 3294;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1267
ID ADR06660 standard; cDNA; 4001 BP.
DE Full length human cDNA useful for treating neurological disease Seq 166.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.2%; Score 41; DB 13; Length 4001;
Best Local Similarity 100.0%; Pred. No. 2e-08;
RESULT 1268
ID AAS31467 standard; DNA; 6461 BP.
DE Human DNA for a novel extracellular matrix protein, Seq ID No 546.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 6461;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1269
ID ABQ66791 standard; DNA; 6461 BP.
DE Human polynucleotide SEQ ID NO 546.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.2%; Score 41; DB 6; Length 6461;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1270
ID ADC11078 standard; DNA; 6461 BP.
DE Human DNA from extracellular matrix gene 2 #2.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 10; Length 6461;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1271
ID AAL05754 standard; DNA; 6647 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8442.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 6647;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1272
ID ABA20362 standard; DNA; 6647 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12693.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 5; Length 6647;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1273
ID ADM87583 standard; cDNA; 7251 BP.
DE Human EST derived nucleotide sequence SEQ ID NO:676.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 3.2%; Score 41; DB 12; Length 7251;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1274
ID AAD49169 standard; DNA; 12091 BP.
DE CET11010 vector DNA.
PN WO200281677-A2.
PD 17-OCT-2002.
PA (COBR-) COBRA THERAPEUTICS LTD.
Query Match 3.2%; Score 41; DB 8; Length 12091;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1275
ID AAK83784 standard; DNA; 12112 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38596.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 12112;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1276
ID AAD49172 standard; DNA; 12321 BP.
DE CET1110 vector DNA.
PN WO200281677-A2.
PD 17-OCT-2002.
PA (COBR-) COBRA THERAPEUTICS LTD.
Query Match 3.2%; Score 41; DB 8; Length 12321;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1277
ID ABZ73998 standard; DNA; 13186 BP.
DE Secreted protein gene 136 genomic fragment HFTAS49, SEQ ID NO:1145.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 8; Length 13186;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1278
ID ADC20710 standard; DNA; 13187 BP.
DE Human secreted protein-related DNA sequence #128.
PN WO200292787-A2.
PD 21-NOV-2002.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 10; Length 13187;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1279
ID AAD49161 standard; DNA; 13547 BP.
DE CET720 vector DNA.
PN WO200281677-A2.
PD 17-OCT-2002.
PA (COBR-) COBRA THERAPEUTICS LTD.
Query Match 3.2%; Score 41; DB 8; Length 13547;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1280
ID ABZ73997 standard; DNA; 13862 BP.
DE Secreted protein gene 136 genomic fragment HFTAS49, SEQ ID NO:1144.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 8; Length 13862;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1281
ID ADC20709 standard; DNA; 13862 BP.
DE Human secreted protein-related DNA sequence #127.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 10; Length 13862;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1282
ID AAD54675 standard; DNA; 14262 BP.
DE CET720GFP vector DNA used in the exemplification of the invention.
PN WO200299089-A1.
PD 12-DEC-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.2%; Score 41; DB 8; Length 14262;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1283
ID ABT16402 standard; DNA; 14262 BP.
DE Recombinant protein production related vector DNA SEQ ID No 9.
PN WO200299070-A2.
PD 12-DEC-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.2%; Score 41; DB 10; Length 14262;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1284
ID AAS42037 standard; DNA; 14970 BP.
DE Genomic sequence #353 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 14970;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1285
ID AAZ58411 standard; DNA; 15071 BP.
DE hmrNP A2 genomic clone including UCOE.
PN WO200005393-A2.
PD 03-FEB-2000.
PA (COBR-) COBRA THERAPEUTICS LTD.
Query Match 3.2%; Score 41; DB 3; Length 15071;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1286
ID AAI62620 standard; DNA; 16163 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 270.
PN WO200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 16163;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1287
ID AAK83901 standard; DNA; 16163 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38713.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.2%; Score 41; DB 4; Length 16163;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1288
ID AAK87161 standard; DNA; 16163 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41973.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 16163;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1289
ID AAL03817 standard; DNA; 16163 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6505.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 16163;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1290
ID AAL05755 standard; DNA; 16579 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8443.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 16579;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1291
ID ABA20363 standard; DNA; 16579 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12694.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 5; Length 16579;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1292
ID ABZ74059 standard; DNA; 17570 BP.
DE Secreted protein gene 176 genomic fragment HLIC010, SEQ ID NO:1206.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 8; Length 17570;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1293
ID ADA98657 standard; DNA; 17570 BP.
DE Human secreted protein-related DNA sequence #250.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 8; Length 17570;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1294
ID ABZ67655 standard; DNA; 17570 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1178.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 10; Length 17570;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1295
ID ADL62089 standard; DNA; 18968 BP.
DE Human ovarian cancer DNA marker #20301.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 41; DB 5; Length 18968;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1296
ID AAK80351 standard; DNA; 19441 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35163.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 19441;

Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1297
ID ADT77140 standard; DNA; 20001 BP.
DE Type II diabetes gene SEQ ID NO 17.
PN WO2004084797-A2.
PD 07-OCT-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (DAIM-) DAIMON M.
PA (KATO/) KATO T.
Query Match 3.2%; Score 41; DB 13; Length 20001;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1298
ID AAL36361 standard; DNA; 20467 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2726.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 20467;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1299
ID AAL36360 standard; DNA; 20467 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2725.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 20467;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1300
ID ABX59348 standard; cDNA; 20467 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1692.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.2%; Score 41; DB 8; Length 20467;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1301
ID ABX59349 standard; cDNA; 20467 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1693.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.2%; Score 41; DB 8; Length 20467;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1302
ID ADJ30098 standard; DNA; 20467 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2725.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 12; Length 20467;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1303
ID ADJ30099 standard; DNA; 20467 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2726.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 12; Length 20467;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1304
ID ABK42793 standard; DNA; 21761 BP.
DE Genomic sequence #692 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 21761;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1305
ID AAK66660 standard; DNA; 21761 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21472.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 21761;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1306
ID ADB60949 standard; DNA; 21761 BP.
DE Connective tissue related genomic DNA #692.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 9; Length 21761;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
RESULT 1307
ID AAK86398 standard; DNA; 26191 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41210.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 26191;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1308
ID AAS28612 standard; DNA; 27148 BP.
DE Genomic sequence #452 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 27148;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1309
ID ADG41808 standard; DNA; 27148 BP.
DE Human respiratory system associated genomic DNA seq id 1046.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 10; Length 27148;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1310
ID ADI97582 standard; DNA; 27148 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID1046.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 11; Length 27148;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1311
ID ABS98441 standard; DNA; 28123 BP.
DE Human multidrug resistance associated protein 3 gene sequence exons 1-11.
PN WO200257410-A2.
PD 25-JUL-2002.
PA (DNAS-) DNA SCI LAB INC.
Query Match 3.2%; Score 41; DB 6; Length 28123;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1312
ID ACN44954 standard; DNA; 31116 BP.
DE Human genomic sequence hCG38822.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 11; Length 31116;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1313
ID ADI21355 standard; DNA; 31279 BP.
DE Human cancer-associated genomic DNA #63.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Query Match 3.2%; Score 41; DB 14; Length 31279;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1314
ID AAD26830 standard; DNA; 36797 BP.
DE Human SNAP29 gene allelic variant.

PN WO200190126-A2.
PD 29-NOV-2001.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 3.2%; Score 41; DB 6; Length 36797;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1315
ID AAD26738 standard; DNA; 36797 BP.
DE Human synaptosomal-associated protein, 29 kD (SNAP29) encoding gene.
PN WO200190126-A2.
PD 29-NOV-2001.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 3.2%; Score 41; DB 6; Length 36797;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1316
ID ABZ74034 standard; DNA; 39119 BP.
DE Secreted protein gene 163 genomic fragment HUPCH08, SEQ ID NO:1181.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 8; Length 39119;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1317
ID ADA98641 standard; DNA; 39119 BP.
DE Human secreted protein-related DNA sequence #234.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 8; Length 39119;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1318
ID ADC20764 standard; DNA; 39119 BP.
DE Human secreted protein-related DNA sequence #182.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 10; Length 39119;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1319
ID ASZ67621 standard; DNA; 39119 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1144.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 10; Length 39119;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1320
ID ADE82954 standard; DNA; 39785 BP.
DE Parkinson's disease gene PARK8 genomic sequence.
PN WO2003076658-A2.
PD 18-SEP-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 3.2%; Score 41; DB 10; Length 39785;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1321
ID ADQ97629 standard; DNA; 41199 BP.
DE Human cancer associated sequence HD10-017, SEQ ID 606.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.2%; Score 41; DB 12; Length 41199;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1322
ID ABD33466 standard; DNA; 42360 BP.
DE Human cancer-associated (CA) gene HD07-089.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.2%; Score 41; DB 13; Length 42360;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1323
ID ABD33436 standard; DNA; 52710 BP.
DE Human cancer-associated (CA) gene HD07-082.
PN WO2004058146-A2.

PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.2%; Score 41; DB 13; Length 52710;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1324
ID ADA02540 standard; DNA; 58822 BP.
DE Human TCOP1 carcinoma associated gene, SEQ ID NO:1058.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 9; Length 58822;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1325
ID ADB72278 standard; DNA; 58822 BP.
DE Human TCOP1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 10; Length 58822;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1326
ID ADE95788 standard; DNA; 58822 BP.
DE Human TCOP1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 10; Length 58822;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1327
ID ADJ53477 standard; DNA; 70000 BP.
DE Human PPP3CB genomic DNA #3.
PN US2004023382-A1.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.2%; Score 41; DB 12; Length 70000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1328
ID ADZ12887 standard; DNA; 72586 BP.
DE Human cancer-associated genomic DNA #35.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.2%; Score 41; DB 14; Length 72586;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1329
ID ADZ42280 standard; DNA; 73100 BP.
DE Human endothelin converting-enzyme 1 gene with C776A/ T66564C SNPs Seq 7.
PN JP2005110606-A.
PD 28-APR-2005.
PA (KOKU-) KOKURITSU JUNKANKI BYO CENT SOCHO.
PA (DOKU-) DOKURITSU GYOSEI HOJIN IYAKUJIN IRYO KIK.
Query Match 3.2%; Score 41; DB 11; Length 73100;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1330
ID ACN44030 standard; DNA; 73145 BP.
DE Human genomic sequence hCG23021.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 11; Length 73145;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1331
ID ADO59187 standard; DNA; 73583 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:24.
PN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
Query Match 3.2%; Score 41; DB 12; Length 73583;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1332

ID ACN44594 standard; DNA; 74234 BP.
DE Human genomic sequence HCG15373.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 11; Length 74234;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1333
ID AAK85590 standard; DNA; 75384 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:40402.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 41; DB 4; Length 75384;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1334
ID ADQ97623 standard; DNA; 86764 BP.
DE Human cancer associated sequence HD10-016, SEQ ID 600.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.2%; Score 41; DB 12; Length 86764;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1335
ID ADX98572 standard; DNA; 86950 BP.
DE Human HT014/LOC148902/LYPLA2/GALE genomic DNA.
Query Match 3.2%; Score 41; DB 14; Length 86950;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1336
ID ADA03032 standard; DNA; 99957 BP.
DE Human MCG10516 homologue carcinoma associated gene, SEQ ID NO:1550.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 9; Length 99957;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1337
ID ADB72770 standard; DNA; 99957 BP.
DE Human CA gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 10; Length 99957;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1338
ID ADC85512 standard; DNA; 99957 BP.
DE Human genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 10; Length 99957;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1339
ID ADM74627 standard; DNA; 99957 BP.
DE Human carcinoma associated (CA) nucleic acid #148.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 3.2%; Score 41; DB 12; Length 99957;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1340
Query Match 3.2%; Score 41; DB 14; Length 101433;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1341
ID ADX06943 standard; DNA; 103738 BP.
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1508.
PN WO2005012875-A2.
PD 10-FEB-2005.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 3.2%; Score 41; DB 14; Length 103738;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1342

ID ADV70791 standard; DNA; 104424 BP.
DE Human soluble adenylyl cyclase (SAC) gene SEQ ID NO:21.
PN CN1548557-A.
PD 24-NOV-2004.
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
Query Match 3.2%; Score 41; DB 14; Length 104424;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1343
ID AD246659 standard; DNA; 104424 BP.
DE Type-II diabetes susceptibility gene SAC, SEQ ID 27.
PN CN1548553-A.
PD 24-NOV-2004.
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
Query Match 3.2%; Score 41; DB 14; Length 104424;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1344
ID ABK94411 standard; DNA; 109906 BP.
DE DNA encoding endothelin converting enzyme 1 (ECE-1) #1.
PN WO200224747-A2.
PD 28-MAR-2002.
PA (EPID-) EPIDAUS BIOTECHNOLOGIE AG.
Query Match 3.2%; Score 41; DB 6; Length 109906;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1345
ID ADL08112 standard; DNA; 109906 BP.
DE Human gene associated with low HDL-C ECE1.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 3.2%; Score 41; DB 12; Length 109906;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1346
Query Match 3.2%; Score 41; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1347
Query Match 3.2%; Score 41; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1348
Query Match 3.2%; Score 41; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1349
Query Match 3.2%; Score 41; DB 4; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1350
Query Match 3.2%; Score 41; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1351
Query Match 3.2%; Score 41; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1352
Query Match 3.2%; Score 41; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1353
Query Match 3.2%; Score 41; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1354
Query Match 3.2%; Score 41; DB 10; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1355
ID ADG70184 standard; DNA; 379652 BP.
DE DNA of BAC bA236m15-00303.
PN WO2003000727-A2.
PD 03-JAN-2003.
PA (ISIS-) ISIS INNOVATIONS LTD.
Query Match 3.2%; Score 41; DB 10; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1356
Query Match 3.2%; Score 41; DB 10; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1357
Query Match 3.2%; Score 41; DB 11; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1358
Query Match 3.2%; Score 41; DB 11; Length 128668;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1359
Query Match 3.2%; Score 41; DB 11; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1360
Query Match 3.2%; Score 41; DB 12; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1361
Query Match 3.2%; Score 41; DB 12; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1362
ID ADR52890 standard; DNA; 115935 BP.
DE Drug therapy altered expressed gene #241.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AWHP) WIETH.
PA (BURC) BURCZYNSKI M.
PA (TWIN) TWINE N.
PA (DORN) DORNER A J.
PA (TREP) TREPICCHIO W L.
Query Match 3.2%; Score 41; DB 13; Length 115935;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1363
ID ABK83569 standard; CDNA; 122888 BP.
DE Human cDNA differentially expressed in granulocytic cells #140.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.2%; Score 41; DB 6; Length 122888;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
RESULT 1364
ID ADE43582 standard; DNA; 128034 BP.
DE Polymorphic human IDE genomic sequence, SEQ ID 187.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.2%; Score 41; DB 10; Length 128034;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1365
ID ADE43581 standard; DNA; 128034 BP.
DE Human IDE genomic sequence, SEQ ID 186.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.2%; Score 41; DB 10; Length 128034;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1366
ID ADH54059 standard; DNA; 128034 BP.
DE Human IDE gene DNA sequence SeqID186.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.2%; Score 41; DB 12; Length 128034;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1367
ID ADH54060 standard; DNA; 128034 BP.
DE Human IDE gene variant DNA sequence SeqID187.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.2%; Score 41; DB 12; Length 128034;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1368
ID ACN44074 standard; DNA; 128668 BP.
DE Human genomic sequence hCG40471.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 11; Length 128668;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;

RESULT 1369
ID ABD32827 standard; DNA; 129381 BP.
DE Human cancer-associated genomic DNA HD17-008.
PN WO2004074320-A2.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 3.2%; Score 41; DB 13; Length 129381;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1370
ID ADP67269 standard; DNA; 152501 BP.
DE Human chromosome 1 7500-16000bp.
PN US2004110143-A1.
PD 10-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.2%; Score 41; DB 12; Length 152501;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1371
ID ADL13748 standard; DNA; 169144 BP.
DE Osteoarthritis-associated polymorphic nucleotide #280.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.2%; Score 41; DB 10; Length 169144;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1372
ID ABQ88186 standard; cDNA; 169739 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 93.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 3.2%; Score 41; DB 6; Length 169739;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1373
ID AD89380 standard; DNA; 191331 BP.
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 20.
PN WO2005106044-A1.
PA (EXAG-) EXAGEN DIAGNOSTICS INC.
Query Match 3.2%; Score 41; DB 14; Length 191331;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1374
ID ADE43315 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.2%; Score 41; DB 10; Length 202100;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1375
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO) GEN HOSPITAL CORP.
Query Match 3.2%; Score 41; DB 12; Length 202100;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1376
ID ABR16034 standard; DNA; 203654 BP.
DE Human gene encoding calcium channel transporter family member.
PN US2002142938-A1.
PD 03-OCT-2002.
PA (YANG/) YAN C.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 3.2%; Score 41; DB 10; Length 203654;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1377
ID AEE04958 standard; DNA; 212235 BP.
DE Cancer-associated gene SEQ ID NO:276.
PN WO2005107396-A2.

PD 17-NOV-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.2%; Score 41; DB 14; Length 212235;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1378
ID ABO76678 standard; DNA; 218336 BP.
DE Androgen receptor signalling pathway-associated DNA AF067844.
PN WO200282081-A2.
PD 17-OCT-2002.
PA (UYRP) UNIV ROCHESTER.
Query Match 3.2%; Score 41; DB 8; Length 218336;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1379
ID ACN4702 standard; DNA; 220224 BP.
DE Human genomic sequence hCG1788599.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 11; Length 220224;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1380
ID ACN44210 standard; DNA; 238484 BP.
DE Human genomic sequence hCG28803.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 41; DB 11; Length 238484;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1381
ID ADL13684 standard; DNA; 247509 BP.
DE Osteoarthritis-associated polymorphic nucleotide #216.
PN WO2003054186-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.2%; Score 41; DB 10; Length 247509;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1382
ID ADV16961 standard; DNA; 290040 BP.
DE Human protein associated with myc (PAM) genomic DNA.
PN EP1481685-A1.
PD 01-DEC-2004.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Query Match 3.2%; Score 41; DB 14; Length 290040;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1383
ID ADU92049 standard; DNA; 290040 BP.
DE Human PAM (protein associated with myc) genomic DNA.
PN EP1481680-A1.
PD 01-DEC-2004.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Query Match 3.2%; Score 41; DB 14; Length 290040;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1384
ID ADP69744 standard; DNA; 312477 BP.
DE Human ROCK 1 DNA #2.
PN US2004115641-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.2%; Score 41; DB 12; Length 312477;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
RESULT 1385
ID AAK74210 standard; DNA; 120 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29022.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
RESULT 1386
ID ABA15417 standard; DNA; 134 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7748.
PN WO200159063-A2.
PD 16-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 5; Length 134;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
RESULT 1387
ID AAK82004 standard; DNA; 137 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36816.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
RESULT 1388
ID AAK82003 standard; DNA; 137 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36815.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
RESULT 1389
ID AAC11916 standard; cDNA; 212 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 15991.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.1%; Score 40; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
RESULT 1390
ID AAC11848 standard; cDNA; 212 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 15923.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.1%; Score 40; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
RESULT 1391
ID ADC20727 standard; DNA; 282 BP.
DE Human secreted protein-related DNA sequence #145.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
RESULT 1392
ID AST16934 standard; DNA; 282 BP.
DE Human secreted protein-related DNA sequence - SEQ ID No 288.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
RESULT 1393
ID ABZ67591 standard; DNA; 282 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1114.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 282;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
RESULT 1394
ID AAC05509 standard; cDNA; 301 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 9584.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.1%; Score 40; DB 3; Length 301;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
RESULT 1395
ID ABV10916 standard; cDNA; 369 BP.
DE Human prostate expression marker cDNA 10907.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 3.1%; Score 40; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1396
ID AAF67029 standard; cDNA; 378 BP.
DE Novel human polynucleotide, SEQ ID NO: 2785.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 5; Length 378;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1397
ID ABV26938 standard; cDNA; 387 BP.
DE Human prostate expression marker cDNA 26929.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1398
ID ABV21097 standard; cDNA; 387 BP.
DE Human prostate expression marker cDNA 21088.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1399
ID ABV21076 standard; cDNA; 387 BP.
DE Human prostate expression marker cDNA 21067.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1400
ID ABV26919 standard; cDNA; 387 BP.
DE Human prostate expression marker cDNA 26910.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1401
ID ABV10883 standard; cDNA; 389 BP.
DE Human prostate expression marker cDNA 10874.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 389;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1402
ID ABV01714 standard; cDNA; 390 BP.
DE Human prostate expression marker cDNA 1705.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 390;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1403
ID ABV01747 standard; cDNA; 394 BP.
DE Human prostate expression marker cDNA 1738.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1404
ID AAI89050 standard; cDNA; 397 BP.
DE Human polynucleotide SEQ ID NO 9110.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.

Query Match 3.1%; Score 40; DB 4; Length 397;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1405
ID ABV32067 standard; cDNA; 407 BP.
DE Human prostate expression marker cDNA 32058.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 407;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1406
ID AAF68854 standard; cDNA; 425 BP.
DE Novel human polynucleotide, SEQ ID NO: 2610.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 5; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1407
ID AAL03569 standard; DNA; 433 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6257.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1408
ID ABA07778 standard; DNA; 433 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 573.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1409
ID AAI91077 standard; cDNA; 465 BP.
DE Human polynucleotide SEQ ID NO 11137.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1410
ID ABL84083 standard; cDNA; 472 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:7061.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.1%; Score 40; DB 6; Length 472;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1411
ID ABV41005 standard; cDNA; 481 BP.
DE Human prostate expression marker cDNA 40996.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1412
ID ABV32038 standard; cDNA; 481 BP.
DE Human prostate expression marker cDNA 32029.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1413
ID ABV40977 standard; cDNA; 481 BP.
DE Human prostate expression marker cDNA 40968.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 3.1%; Score 40; DB 5; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 1414
ID ADM99934 standard; DNA; 507 BP.
DE Human NR3C1 SNP (single nucleotide polymorphism)-containing DNA 14.
PN WO2004033650-A2.
PD 22-APR-2004.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 3.1%; Score 40; DB 12; Length 507;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1415
ID ABV56815 standard; cDNA; 530 BP.
DE Human prostate expression marker cDNA 56806.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 40; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1416
ID ABN63052 standard; cDNA; 556 BP.
DE Human cancer related polynucleotide SEQ ID NO 3019.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 6; Length 556;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1417
ID ACL56939 standard; cDNA; 562 BP.
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:3074.
PN WO2005000087-A2.
PD 06-JAN-2005.
PA (CHIR) CHIRON CORP.
Query Match 3.1%; Score 40; DB 14; Length 562;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1418
ID ABL38071 standard; cDNA; 584 BP.
DE Human colon tumour antigen polynucleotide SEQ ID NO:1660.
PN WO200196388-A2.
PD 20-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.1%; Score 40; DB 6; Length 584;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1419
ID ADV15705 standard; DNA; 601 BP.
DE Human osteoporosis related gene SNP flanking sequence, seq id 446.
PN US6825336-B1.
PD 30-NOV-2004.
PA (APPL-) APPLERA CORP.
Query Match 3.1%; Score 40; DB 13; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1420
ID AEB33638 standard; DNA; 601 BP.
DE Human DNA polymorphic region #1218.
PN US2005147987-A1.
PD 07-JUL-2005.
PA (APPL-) APPLERA CORP NY.
Query Match 3.1%; Score 40; DB 14; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1421
ID ADB81874 standard; cDNA; 668 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID 186).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 9; Length 668;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1422
ID ADB82636 standard; cDNA; 733 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID 948).
PN WO2003050236-A2.
PD 19-JUN-2003.

PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 9; Length 733;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1423
ID AAK78061 standard; DNA; 745 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32873.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1424
ID AAK78060 standard; DNA; 745 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32872.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1425
ID ABQ88930 standard; cDNA; 755 BP.
DE Human prostate expressed polynucleotide SEQ ID NO 186.
PN WO200255700-A2.
PD 18-JUL-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 6; Length 755;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1426
ID ABQ89696 standard; cDNA; 757 BP.
DE Human prostate expressed polynucleotide SEQ ID NO 952.
PN WO200255700-A2.
PD 18-JUL-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 6; Length 757;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1427
ID AAK65246 standard; DNA; 761 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20058.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 761;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
RESULT 1428
ID ABZ73959 standard; DNA; 800 BP.
DE Secreted protein gene 120 genomic fragment HEQBF89, SEQ ID NO:1106.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 800;
Best Local Similarity 100.0%; Pred. No. 6e-08;
RESULT 1429
ID ADA98583 standard; DNA; 800 BP.
DE Human secreted protein-related DNA sequence #176.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 800;
Best Local Similarity 100.0%; Pred. No. 6e-08;
RESULT 1430
ID ABQ89053 standard; cDNA; 802 BP.
DE Human prostate expressed polynucleotide SEQ ID NO 309.
PN WO200255700-A2.
PD 18-JUL-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 6; Length 802;
Best Local Similarity 100.0%; Pred. No. 6e-08;
RESULT 1431
ID AD861997 standard; cDNA; 802 BP.

DE Human cDNA sequence useful for the treatment of cancer (SeqID 309).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 40; DB 9; Length 802;
Best Local Similarity 100.0%; Pred. No. 6e-08;
RESULT 1432
ID ABZ73960 standard; DNA; 827 BP.
DE Secreted protein gene 120 genomic fragment HEQBF89, SEQ ID NO:1107.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 827;
Best Local Similarity 100.0%; Pred. No. 6e-08;
RESULT 1433
ID ADA98584 standard; DNA; 827 BP.
DE Human secreted protein-related DNA sequence #177.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 827;
Best Local Similarity 100.0%; Pred. No. 6e-08;
RESULT 1434
ID AAL06364 standard; DNA; 998 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9052.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 998;
Best Local Similarity 100.0%; Pred. No. 6e-08;
RESULT 1435
ID ABL58622 standard; cDNA; 1743 BP.
DE Human macroprotein 10.01 cDNA.
PN CN1331233-A.
PD 16-JAN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 3.1%; Score 40; DB 6; Length 1743;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
RESULT 1436
ID ABK14083 standard; cDNA; 1743 BP.
DE Human large protein 10.01 cDNA.
PN WO200206334-A1.
PD 24-JAN-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 3.1%; Score 40; DB 6; Length 1743;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
RESULT 1437
ID ADB61947 standard; cDNA; 1916 BP.
DE Human cDNA encoding clone BRACE20059110.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.1%; Score 40; DB 10; Length 1916;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
RESULT 1438
ID AA198082 standard; cDNA; 2393 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 25.
PN WO200166733-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 3.1%; Score 40; DB 4; Length 2393;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
RESULT 1439
ID ADM01671 standard; cDNA; 2652 BP.
DE Human cDNA of the invention SEQ ID NO:356.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.1%; Score 40; DB 11; Length 2652;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;

RESULT 1440
ID ASC84601 standard; cDNA; 2652 BP.
DE Human cDNA clone BRAHW20158530, SEQ ID 356.
PN EP1580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.1%; Score 40; DB 14; Length 2652;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
RESULT 1441
ID ADR10422 standard; cDNA; 2800 BP.
DE Full length human cDNA useful for treating neurological disease Seq 3928.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.1%; Score 40; DB 13; Length 2800;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
RESULT 1442
ID ADR08229 standard; cDNA; 3430 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1735.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.1%; Score 40; DB 13; Length 3430;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1443
ID AAK73534 standard; DNA; 3622 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28346.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 3622;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1444
ID ADR07011 standard; cDNA; 3847 BP.
DE Full length human cDNA useful for treating neurological disease Seq 517.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.1%; Score 40; DB 13; Length 3847;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1445
ID AAS42190 standard; DNA; 4242 BP.
DE Genomic sequence #506 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 4242;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1446
ID AAZ25338 standard; cDNA; 4285 BP.
DE Human nephrin nucleotide sequence.
PN WO9947562-A1.
PD 23-SEP-1999.
PA (BIOS-) BIOSTRATUM INC.
Query Match 3.1%; Score 40; DB 2; Length 4285;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1447
ID ACD13372 standard; cDNA; 4285 BP.
DE Human DNA encoding a p53 modifier, SEQ ID 42.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 3.1%; Score 40; DB 8; Length 4285;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1448
ID ADI47425 standard; cDNA; 4285 BP.
DE Human nephrin cDNA, SEQ ID NO:2.
PN WO2004009102-A1.
PD 29-JAN-2004.
PA (GLOW-) GLOWEGA INC OY.
Query Match 3.1%; Score 40; DB 12; Length 4285;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1449

ID AAS36514 standard; DNA; 4409 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2014.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 4409;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1450
ID ADE47208 standard; DNA; 4409 BP.
DE Human cardiovascular system related genomic DNA #774.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 4409;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1451
ID ADJ08626 standard; DNA; 4409 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2014.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 13; Length 4409;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1452
ID AAS36512 standard; DNA; 4494 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2012.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 4494;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1453
ID ADE47206 standard; DNA; 4494 BP.
DE Human cardiovascular system related genomic DNA #772.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 4494;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1454
ID ADJ08624 standard; DNA; 4494 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2012.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 13; Length 4494;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1455
ID AAS36511 standard; DNA; 4495 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2011.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 4495;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1456
ID ADE47205 standard; DNA; 4495 BP.
DE Human cardiovascular system related genomic DNA #771.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 4495;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1457
ID ADJ08623 standard; DNA; 4495 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2011.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 13; Length 4495;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1458
ID ABZ74184 standard; DNA; 4635 BP.

DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1331.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 4635;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1459
ID ADA98713 standard; DNA; 4635 BP.
DE Human secreted protein-related DNA sequence #306.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 4635;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1460
ID ABZ67750 standard; DNA; 4635 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1273.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 4635;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1461
ID AAK81742 standard; DNA; 5013 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36554.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 5013;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1462
ID AAK81743 standard; DNA; 5111 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36555.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 5111;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1463
ID AAL62686 standard; DNA; 5377 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 336.
PN WO200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 5377;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1464
ID AAL06805 standard; DNA; 5377 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9493.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 5377;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
RESULT 1465
ID ASK14608 standard; DNA; 7736 BP.
DE Genomic DNA encoding novel human ion channel, 5HT3D.
PN WO200202639-A2.
PD 10-JAN-2002.
PA (PHAA-) PHARMACIA & UPJOHN CO.
Query Match 3.1%; Score 40; DB 6; Length 7736;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
RESULT 1466
ID AAS27646 standard; DNA; 8472 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1306.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 8472;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
RESULT 1467
ID AAS27647 standard; DNA; 8472 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1307.

PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 8472;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
RESULT 1468
ID ADB94449 standard; DNA; 8472 BP.
DE Novel human protein DNA #58.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.1%; Score 40; DB 10; Length 8472;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
RESULT 1469
ID ADB94450 standard; DNA; 8472 BP.
DE Novel human protein DNA #59.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.1%; Score 40; DB 10; Length 8472;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
RESULT 1470
ID ASK50441 standard; DNA; 9302 BP.
DE Human ADMR genomic DNA.
PN WO200226770-A2.
PD 04-APR-2002.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 3.1%; Score 40; DB 6; Length 9302;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
RESULT 1471
ID ADM97822 standard; DNA; 9597 BP.
DE pCDGal4-DBD-GR vector SEQ ID NO: 75.
PN WO2004031415-A2.
PD 15-APR-2004.
PA (VERT-) VERTEX PHARM INC.
Query Match 3.1%; Score 40; DB 12; Length 9597;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1472
ID ABK69846 standard; DNA; 9796 BP.
DE Human secreted protein gene 22 genomic DNA fragment #7.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 6; Length 9796;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1473
ID ACC50861 standard; CDNA; 9796 BP.
DE Human secreted protein BAC clone SEQ ID NO 1041.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 9796;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1474
ID ABZ71483 standard; DNA; 9796 BP.
DE Secreted protein gene 12 genomic fragment HAUAI83, SEQ ID NO:593.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 9796;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1475
ID ADB91839 standard; DNA; 9796 BP.
DE Human secreted protein related DNA #SEQ ID 785.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 9; Length 9796;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;


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RESULT 1476
ID ADC74614 standard; DNA; 9796 BP.
DE Human secreted protein-related DNA - SEQ ID 1247.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 9796;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1477
ID ADD38134 standard; cDNA; 9796 BP.
DE CDNA clone in ATCC deposit #28.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 9796;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1478
ID ADA57728 standard; DNA; 9796 BP.
DE BAC fragment containing human secreted protein gene #302.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 9796;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1479
ID AAK83281 standard; DNA; 9918 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2857.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 9796;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1480
ID ADM97823 standard; DNA; 10872 BP.
DE PKI-Gal4-DBD-GR vector SEQ ID NO: 76.
PN WO2004031415-A2.
PD 15-APR-2004.
PA (VERT-) VERTEX PHARM INC.
Query Match 3.1%; Score 40; DB 12; Length 10872;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1481
ID AAK86165 standard; DNA; 10898 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40977.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 10898;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1482
ID AAF80047 standard; DNA; 13591 BP.
DE Nucleotide sequence of odorant binding polypeptide OBPIIb gene.
PN WO200112806-A2.
PD 22-FEB-2001.
PA (UYAU-) UNIV AUVERGNE.
PA (PITI/) PITIOT G.
Query Match 3.1%; Score 40; DB 5; Length 13591;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1483
ID AAK83210 standard; DNA; 14258 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38022.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 14258;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1484
ID AAK83183 standard; DNA; 14260 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37995.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 14260;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1485
ID AAK83217 standard; DNA; 14260 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38029.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 14260;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1486
ID AAK69164 standard; DNA; 14294 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23976.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 14294;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1487
ID AAK83152 standard; DNA; 15364 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37964.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 15364;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1488
ID AAK83220 standard; DNA; 15772 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38032.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 15772;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
RESULT 1489
ID ADA98562 standard; DNA; 16301 BP.
DE Human secreted protein-related DNA sequence #155.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 16301;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1490
ID ADA44300 standard; DNA; 16301 BP.
DE Human secreted protein DNA SEQ ID 493.
PN WO2003000885-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 8; Length 16301;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1491
ID ADC20672 standard; DNA; 16301 BP.
DE Human secreted protein-related DNA sequence #90.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 16301;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1492
ID ADF10865 standard; DNA; 16301 BP.
DE Human secreted protein encoding sequence #187.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 10; Length 16301;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1493
ID AAK77656 standard; DNA; 16499 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32468.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 16499;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1494
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ID ABK42608 standard; DNA; 16825 BP.
DE Genomic sequence #507 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 16825;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1495
ID ADB60764 standard; DNA; 16825 BP.
DE Connective tissue related genomic DNA #507.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 9; Length 16825;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1496
ID AAL36869 standard; DNA; 17286 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3234.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 17286;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1497
ID ABX59857 standard; cDNA; 17286 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2201.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.1%; Score 40; DB 8; Length 17286;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1498
ID ADJ30607 standard; DNA; 17286 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3234.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 12; Length 17286;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1499
ID AAZ50904 standard; DNA; 17590 BP.
DE Human TBC-1 partial genomic DNA comprising 5' end sequence.
PN WO200008209-A2.
PD 17-FEB-2000.
PA (GEST) GENSET.
Query Match 3.1%; Score 40; DB 3; Length 17590;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
RESULT 1500
ID AAK83173 standard; DNA; 18488 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37985.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 40; DB 4; Length 18488;
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2006, 20:28:02 ; Search time 306 Seconds
(without alignments)
7918.581 Million cell updates/sec

Title: US-10-785-221-8
Perfect score: 1295
Sequence: 1 ccgaagttcaaggccccc.....ataaatagcttgatattc 1295

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 1403666 seqs, 93554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database : Issued Patents_NA:*
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10: /EMC Celerra_SID33/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1 1295 100.0 1295 3 US-09-254-465A-8 Sequence 8, Appli
2 1295 100.0 1295 3 US-09-907-794A-63 Sequence 63, Appl
3 1295 100.0 1295 3 US-09-905-125A-63 Sequence 63, Appl
4 1295 100.0 1295 3 US-09-902-775A-63 Sequence 63, Appl
5 1295 100.0 1295 3 US-09-906-700-63 Sequence 63, Appl
6 1295 100.0 1295 3 US-09-903-603A-63 Sequence 63, Appl
7 1295 100.0 1295 3 US-09-904-520A-63 Sequence 63, Appl
8 1295 100.0 1295 3 US-09-909-064-63 Sequence 63, Appl
9 1295 100.0 1295 3 US-09-905-381A-63 Sequence 63, Appl
10 1295 100.0 1295 3 US-09-906-618-63 Sequence 8, Appli
11 1295 100.0 1295 3 US-09-953-499-8 Sequence 63, Appl
12 1295 100.0 1295 3 US-09-906-646-63 Sequence 63, Appl
13 1295 100.0 1295 3 US-09-904-462-63 Sequence 63, Appl
14 1295 100.0 1295 3 US-09-902-736A-63 Sequence 63, Appl
15 1295 100.0 1295 3 US-09-906-722A-63 Sequence 63, Appl
16 1295 100.0 1295 4 US-09-905-449-63 Sequence 63, Appl
17 1295 100.0 1295 4 US-09-903-562B-63 Sequence 63, Appl
18 1295 100.0 1295 4 US-09-906-679A-63 Sequence 63, Appl
19 1295 100.0 1295 5 US-09-907-841-63 Sequence 63, Appl
20 821 63.4 1022 3 US-09-152-060-35 Sequence 35, Appl
21 821 63.4 1022 3 US-09-852-797-35 Sequence 35, Appl
22 821 63.4 1022 3 US-09-853-161-35 Sequence 35, Appl
23 821 63.4 1022 3 US-10-058-993-35 Sequence 35, Appl

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373 28.8 413 3 US-09-254-465A-27 Sequence 27, Appl
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61 4.7 601 3 US-09-949-016-88099 Sequence 88099, A
61 4.7 601 3 US-09-949-016-88100 Sequence 88100, A
61 4.7 5934 3 US-09-949-016-14235 Sequence 14235, A
61 4.7 10344 3 US-09-949-016-14208 Sequence 14208, A
61 4.7 38538 3 US-09-949-016-13150 Sequence 13150, A
61 4.7 110243 3 US-09-949-016-13698 Sequence 13698, A
58 4.5 87648 3 US-09-949-016-13655 Sequence 13655, A
56 4.3 142504 3 US-09-949-016-13693 Sequence 13693, A
56 4.3 142506 3 US-09-949-016-12474 Sequence 12474, A
55 4.2 186734 3 US-09-949-016-14870 Sequence 14870, A
55 4.2 193689 3 US-09-949-016-12350 Sequence 12350, A
55 4.2 193689 3 US-09-949-016-13088 Sequence 13088, A
53 4.1 15586 3 US-09-949-016-13859 Sequence 13859, A
53 4.1 47698 3 US-09-949-016-13514 Sequence 13514, A
53 4.1 49971 3 US-09-949-016-16688 Sequence 16688, A
52 4.0 5931 3 US-09-949-016-11975 Sequence 11975, A
52 4.0 5932 3 US-09-949-016-15500 Sequence 15500, A
52 4.0 91559 3 US-09-949-016-12581 Sequence 12581, A
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51 3.9 601 3 US-09-949-016-37353 Sequence 37353, A
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C 281	44	3.4	51822	3	US-09-949-016-15232	Sequence 15232, A	C 354	43	3.3	601	3	US-09-949-016-172791	Sequence 172791, A
C 282	44	3.4	58593	3	US-09-949-016-12233	Sequence 12232, A	C 355	43	3.3	601	3	US-09-949-016-177642	Sequence 177642, A
C 283	44	3.4	65300	3	US-09-949-016-16813	Sequence 16813, A	C 356	43	3.3	601	3	US-09-949-016-184559	Sequence 184559, A
C 284	44	3.4	96202	3	US-09-949-016-16433	Sequence 16433, A	C 357	43	3.3	601	3	US-09-949-016-189383	Sequence 189383, A
C 285	44	3.4	98302	3	US-09-949-016-16847	Sequence 16847, A	C 358	43	3.3	601	3	US-09-949-016-189384	Sequence 189384, A
C 286	44	3.4	112874	3	US-09-949-016-13180	Sequence 13180, A	C 359	43	3.3	601	3	US-09-949-016-189484	Sequence 189484, A
C 287	44	3.4	125672	3	US-09-949-016-16956	Sequence 16956, A	C 360	43	3.3	601	3	US-09-949-016-191446	Sequence 191446, A
C 288	44	3.4	141589	5	US-09-543-679A-2480	Sequence 1956, A	C 361	43	3.3	601	3	US-09-949-016-191447	Sequence 191447, A
C 289	44	3.4	141589	5	US-09-543-679A-2694	Sequence 2694, Ap	C 362	43	3.3	601	3	US-09-949-016-191448	Sequence 191448, A
C 290	44	3.4	146982	5	US-09-543-679A-2719	Sequence 2719, Ap	C 363	43	3.3	601	3	US-09-949-016-191449	Sequence 191449, A
C 291	44	3.4	162465	3	US-09-949-016-14264	Sequence 3009, Ap	C 364	43	3.3	601	3	US-09-949-016-197190	Sequence 197190, A
C 292	44	3.4	209274	5	US-09-543-679A-3004	Sequence 14264, A	C 365	43	3.3	601	3	US-09-949-016-197191	Sequence 197191, A
C 293	44	3.4	235452	3	US-09-949-016-13675	Sequence 3004, Ap	C 366	43	3.3	601	3	US-09-949-016-197192	Sequence 197192, A
C 294	44	3.4	235452	3	US-09-949-016-13675	Sequence 13675, A	C 367	43	3.3	601	3	US-09-949-016-197308	Sequence 197308, A
C 295	43	3.3	198	3	US-09-513-999C-25163	Sequence 25163, A	C 368	43	3.3	601	3	US-09-949-016-197309	Sequence 197309, A
C 296	43	3.3	251	3	US-09-513-999C-18969	Sequence 18969, A	C 369	43	3.3	601	3	US-09-949-016-197310	Sequence 197310, A
C 297	43	3.3	278	3	US-09-513-999C-9040	Sequence 9040, Ap	C 370	43	3.3	601	3	US-09-949-016-197426	Sequence 197426, A
C 298	43	3.3	298	3	US-09-513-999C-19889	Sequence 19889, A	C 371	43	3.3	601	3	US-09-949-016-197427	Sequence 197427, A
C 299	43	3.3	358	3	US-09-621-976-9061	Sequence 9061, Ap	C 372	43	3.3	601	3	US-09-949-016-197428	Sequence 197428, A
C 300	43	3.3	475	3	US-09-621-976-9358	Sequence 9358, Ap	C 373	43	3.3	601	3	US-09-949-016-197544	Sequence 197544, A
C 301	43	3.3	601	3	US-09-949-016-25330	Sequence 25330, A	C 374	43	3.3	601	3	US-09-949-016-197545	Sequence 197545, A
C 302	43	3.3	601	3	US-09-949-016-25391	Sequence 25391, A	C 375	43	3.3	601	3	US-09-949-016-197546	Sequence 197546, A
C 303	43	3.3	601	3	US-09-949-016-35831	Sequence 35831, A	C 376	43	3.3	601	3	US-09-949-016-198142	Sequence 198142, A
C 304	43	3.3	601	3	US-09-949-016-35832	Sequence 35832, A	C 377	43	3.3	601	3	US-09-949-016-200613	Sequence 200613, A
C 305	43	3.3	601	3	US-09-949-016-35833	Sequence 35833, A	C 378	43	3.3	601	3	US-09-949-016-200759	Sequence 200759, A
C 306	43	3.3	601	3	US-09-949-016-35908	Sequence 35908, A	C 379	43	3.3	601	3	US-09-949-016-206135	Sequence 206135, A
C 307	43	3.3	601	3	US-09-949-016-35909	Sequence 35909, A	C 380	43	3.3	601	3	US-09-949-016-206136	Sequence 206136, A
C 308	43	3.3	601	3	US-09-949-016-35910	Sequence 35910, A	C 381	43	3.3	601	3	US-09-949-002-6896	Sequence 6896, Ap
C 309	43	3.3	601	3	US-09-949-016-35955	Sequence 35955, A	C 382	43	3.3	601	3	US-09-949-002-6897	Sequence 6897, Ap
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C 313	43	3.3	601	3	US-09-949-016-36115	Sequence 36115, A	C 386	43	3.3	601	3	US-09-949-002-6937	Sequence 6937, Ap
C 314	43	3.3	601	3	US-09-949-016-36116	Sequence 36116, A	C 387	43	3.3	601	3	US-09-949-002-7157	Sequence 7157, Ap
C 315	43	3.3	601	3	US-09-949-016-36439	Sequence 36439, A	C 388	43	3.3	601	3	US-09-949-002-7163	Sequence 7163, Ap

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C 390	43	3.3	700	3	US-09-735-271-481	Sequence 481, App	C 463	43	3.3	49818	3	US-09-949-016-12458	Sequence 12458, A
C 391	43	3.3	2214	3	US-09-684-405-10	Sequence 10, Appl	C 464	43	3.3	49829	3	US-09-949-016-14011	Sequence 14011, A
C 392	43	3.3	3903	3	US-09-622-745B-1	Sequence 1, Appl	C 465	43	3.3	49848	3	US-09-949-016-15675	Sequence 15675, A
C 393	43	3.3	4421	2	US-08-257-963B-9	Sequence 9, Appl	C 466	43	3.3	51043	3	US-09-949-016-12739	Sequence 12739, A
C 394	43	3.3	4421	3	US-08-367-841A-9	Sequence 9, Appl	C 467	43	3.3	51046	3	US-09-949-016-13946	Sequence 13946, A
C 395	43	3.3	4421	3	US-08-520-373D-6	Sequence 6, Appl	C 468	43	3.3	51773	3	US-09-949-016-16002	Sequence 16002, A
C 396	43	3.3	4421	7	PCT-US95-07201-9	Sequence 9, Appl	C 469	43	3.3	52667	3	US-09-949-016-12019	Sequence 12019, A
C 397	43	3.3	5375	3	US-08-757-223-7	Sequence 7, Appl	C 470	43	3.3	53526	3	US-08-658-136-2	Sequence 2, Appl
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C 399	43	3.3	6872	3	US-09-949-016-15483	Sequence 15483, A	C 472	43	3.3	53577	3	US-08-460-215A-1	Sequence 1, Appl
C 400	43	3.3	7452	3	US-08-592-500-1	Sequence 1, Appl	C 473	43	3.3	55130	3	US-09-949-016-11850	Sequence 11850, A
C 401	43	3.3	7452	3	US-08-195-006-1	Sequence 1, Appl	C 474	43	3.3	56147	3	US-09-949-016-16352	Sequence 16352, A
C 402	43	3.3	7452	3	US-09-775-803-13	Sequence 13, Appl	C 475	43	3.3	58593	3	US-09-949-016-12232	Sequence 12232, A
C 403	43	3.3	7452	7	PCT-US94-0764A-1	Sequence 1, Appl	C 476	43	3.3	59719	3	US-09-949-016-15616	Sequence 15616, A
C 404	43	3.3	7452	3	US-09-949-016-16886	Sequence 16886, A	C 477	43	3.3	63000	3	US-09-780-172-18	Sequence 18, Appl
C 405	43	3.3	8559	3	US-09-949-016-13412	Sequence 13412, A	C 478	43	3.3	63187	3	US-09-949-016-12682	Sequence 12682, A
C 406	43	3.3	9928	3	US-09-949-016-16885	Sequence 16885, A	C 479	43	3.3	63187	3	US-09-949-016-16288	Sequence 16288, A
C 407	43	3.3	10317	3	US-09-949-016-11897	Sequence 11897, A	C 480	43	3.3	63926	3	US-09-949-016-16473	Sequence 16473, A
C 408	43	3.3	10320	3	US-09-949-016-12117	Sequence 12117, A	C 481	43	3.3	64626	3	US-09-949-016-12011	Sequence 12011, A
C 409	43	3.3	10321	3	US-09-949-016-16155	Sequence 16155, A	C 482	43	3.3	64638	3	US-09-949-016-11767	Sequence 11767, A
C 410	43	3.3	11490	3	US-09-949-016-14149	Sequence 14149, A	C 483	43	3.3	64639	3	US-09-949-016-13520	Sequence 13520, A
C 411	43	3.3	11673	3	US-09-949-016-13671	Sequence 13671, A	C 484	43	3.3	69701	3	US-09-949-016-14187	Sequence 14187, A
C 412	43	3.3	13821	3	US-09-949-016-13590	Sequence 13590, A	C 485	43	3.3	71278	3	US-09-949-016-11851	Sequence 11851, A
C 413	43	3.3	14485	3	US-09-876-216-3	Sequence 3, Appl	C 486	43	3.3	71278	3	US-09-949-016-117563	Sequence 117563, A
C 414	43	3.3	14485	3	US-10-359-076-3	Sequence 3, Appl	C 487	43	3.3	72328	3	US-09-009-913-1	Sequence 1, Appl
C 415	43	3.3	15454	3	US-09-949-016-16679	Sequence 16679, A	C 488	43	3.3	72392	3	US-09-949-016-11592	Sequence 11592, A
C 416	43	3.3	15652	3	US-09-422-936-60	Sequence 60, Appl	C 489	43	3.3	73308	3	US-09-949-016-16326	Sequence 16326, A
C 417	43	3.3	15975	3	US-09-949-016-17469	Sequence 17469, A	C 490	43	3.3	74940	3	US-09-949-016-17512	Sequence 17512, A
C 418	43	3.3	18319	3	US-09-949-016-17446	Sequence 17446, A	C 491	43	3.3	77626	3	US-09-949-016-13608	Sequence 12608, A
C 419	43	3.3	18970	3	US-09-949-016-15319	Sequence 15319, A	C 492	43	3.3	80269	3	US-09-949-016-15681	Sequence 15681, A
C 420	43	3.3	20103	3	US-09-949-016-17223	Sequence 17223, A	C 493	43	3.3	80858	3	US-09-949-016-12659	Sequence 12659, A
C 421	43	3.3	20221	3	US-09-949-016-15366	Sequence 15366, A	C 494	43	3.3	80859	3	US-09-949-016-15715	Sequence 15715, A
C 422	43	3.3	20721	3	US-09-949-016-16257	Sequence 16257, A	C 495	43	3.3	81927	3	US-09-949-016-15623	Sequence 15623, A
C 423	43	3.3	22287	3	US-09-949-016-16820	Sequence 16820, A	C 496	43	3.3	84558	3	US-09-949-016-15752	Sequence 15752, A
C 424	43	3.3	23109	3	US-09-949-002-648	Sequence 648, App	C 497	43	3.3	84761	3	US-09-949-016-11919	Sequence 11919, A
C 425	43	3.3	23116	3	US-09-949-002-791	Sequence 791, App	C 498	43	3.3	84763	3	US-09-949-016-13914	Sequence 13914, A
C 426	43	3.3	24942	3	US-09-949-016-13318	Sequence 13318, A	C 499	43	3.3	84875	3	US-09-949-016-117334	Sequence 117334, A
C 427	43	3.3	25160	3	US-09-949-016-12691	Sequence 12691, A	C 500	43	3.3	84875	3	US-09-949-016-17335	Sequence 17335, A
C 428	43	3.3	25162	3	US-09-949-016-13065	Sequence 13065, A	C 501	43	3.3	84875	3	US-09-949-016-17336	Sequence 17336, A
C 429	43	3.3	25162	3	US-09-949-016-13066	Sequence 13066, A	C 502	43	3.3	84875	3	US-09-949-016-17337	Sequence 17337, A
C 430	43	3.3	26104	3	US-09-949-016-14045	Sequence 14045, A	C 503	43	3.3	85122	3	US-09-949-016-14693	Sequence 14693, A
C 431	43	3.3	26334	3	US-09-949-016-17354	Sequence 17354, A	C 504	43	3.3	85152	3	US-09-949-016-12665	Sequence 12665, A
C 432	43	3.3	26684	3	US-09-949-016-15109	Sequence 15109, A	C 505	43	3.3	85152	3	US-09-949-016-12666	Sequence 12666, A
C 433	43	3.3	26684	3	US-09-949-016-15110	Sequence 15110, A	C 506	43	3.3	85152	3	US-09-949-016-12667	Sequence 12667, A
C 434	43	3.3	26684	3	US-09-949-016-17409	Sequence 17409, A	C 507	43	3.3	85152	3	US-09-949-016-12668	Sequence 12668, A
C 435	43	3.3	26684	3	US-09-949-016-17410	Sequence 17410, A	C 508	43	3.3	85854	3	US-09-949-016-12908	Sequence 12908, A
C 436	43	3.3	26769	3	US-09-949-016-14934	Sequence 14934, A	C 509	43	3.3	85963	3	US-09-949-016-13804	Sequence 13804, A
C 437	43	3.3	28233	3	US-09-949-002-761	Sequence 761, App	C 510	43	3.3	86273	3	US-09-949-016-15273	Sequence 15273, A
C 438	43	3.3	28253	3	US-09-949-002-762	Sequence 762, App	C 511	43	3.3	88557	3	US-09-949-016-17028	Sequence 17028, A
C 439	43	3.3	28257	3	US-09-949-016-13076	Sequence 13076, A	C 512	43	3.3	89210	3	US-09-949-016-16988	Sequence 16988, A
C 440	43	3.3	28316	3	US-09-949-002-766	Sequence 766, App	C 513	43	3.3	90472	3	US-09-949-016-14038	Sequence 14038, A
C 441	43	3.3	28316	3	US-09-949-002-767	Sequence 767, App	C 514	43	3.3	90900	3	US-09-949-016-13034	Sequence 13034, A
C 442	43	3.3	28843	3	US-09-949-016-12515	Sequence 12515, A	C 515	43	3.3	92074	3	US-09-949-016-17163	Sequence 17163, A
C 443	43	3.3	29960	3	US-09-949-016-11978	Sequence 11978, A	C 516	43	3.3	94593	3	US-09-949-016-16324	Sequence 16324, A
C 444	43	3.3	30054	3	US-09-949-016-16100	Sequence 16100, A	C 517	43	3.3	98037	3	US-09-949-016-16523	Sequence 16523, A
C 445	43	3.3	30851	3	US-09-949-016-17418	Sequence 17418, A	C 518	43	3.3	98828	3	US-09-949-016-16630	Sequence 16630, A
C 446	43	3.3	31571	2	US-08-323-443B-1	Sequence 1, Appl	C 519	43	3.3	106256	3	US-09-949-016-16858	Sequence 16858, A
C 447	43	3.3	31623	3	US-09-949-016-15945	Sequence 15945, A	C 520	43	3.3	107820	3	US-09-792-616-1	Sequence 1, Appl
C 448	43	3.3	32665	3	US-09-949-016-14098	Sequence 14098, A	C 521	43	3.3	107941	3	US-09-949-016-14206	Sequence 14206, A
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C 450	43	3.3	34047	3	US-09-949-016-13503	Sequence 13503, A	C 523	43	3.3	115814	3	US-09-949-016-16205	Sequence 16205, A
C 451	43	3.3	35207	3	US-09-949-016-17069	Sequence 17069, A	C 524	43	3.3	119214	3	US-09-949-016-12507	Sequence 12507, A
C 452	43	3.3	36227	3	US-09-949-016-13951	Sequence 13951, A	C 525	43	3.3	121982	3	US-09-949-016-12085	Sequence 12085, A
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C 455	43	3.3	40168	3	US-09-949-016-13225	Sequence 13225, A	C 528	43	3.3	121982	3	US-09-949-016-14105	Sequence 14105, A
C 456	43	3.3	40546	3	US-09-949-016-12847	Sequence 12847, A	C 529	43	3.3	133278	3	US-09-949-016-12524	Sequence 12524, A
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C 459	43	3.3	40641	3	US-09-949-016-13376	Sequence 13376, A	C 532	43	3.3	136265	3	US-09-949-016-12756	Sequence 12756, A
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537	43	3.3	143644	3	US-09-949-016-15238	Sequence 15238, A	610	42	3.2	44555	3	US-09-949-016-12043	Sequence 12043, A
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539	43	3.3	145241	3	US-09-949-016-17395	Sequence 17395, A	c 612	42	3.2	48318	3	US-09-949-016-15717	Sequence 15717, A
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544	43	3.3	152145	3	US-09-949-016-12371	Sequence 12371, A	617	42	3.2	117937	3	US-09-949-016-15775	Sequence 15775, A
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551	43	3.3	152822	3	US-09-949-016-17519	Sequence 17519, A	624	41	3.2	601	3	US-09-949-016-38401	Sequence 38401, A
552	43	3.3	154600	3	US-09-949-016-14757	Sequence 14757, A	625	41	3.2	601	3	US-09-949-016-46650	Sequence 46650, A
553	43	3.3	160759	3	US-09-949-016-16514	Sequence 16514, A	c 626	41	3.2	601	3	US-09-949-016-52793	Sequence 52793, A
554	43	3.3	162914	3	US-09-949-016-15578	Sequence 15578, A	c 627	41	3.2	601	3	US-09-949-016-52794	Sequence 52794, A
555	43	3.3	168174	3	US-10-071-411A-63	Sequence 63, Appl	c 628	41	3.2	601	3	US-09-949-016-60253	Sequence 60253, A
556	43	3.3	168273	3	US-09-949-016-15494	Sequence 2, Appl	c 629	41	3.2	601	3	US-09-949-016-60254	Sequence 60254, A
557	43	3.3	183770	3	US-09-949-016-12111	Sequence 15494, A	c 630	41	3.2	601	3	US-09-949-016-60255	Sequence 60255, A
558	43	3.3	187848	3	US-09-949-016-12111	Sequence 12111, A	c 631	41	3.2	601	3	US-09-949-016-78138	Sequence 78138, A
559	43	3.3	190078	3	US-09-949-016-12707	Sequence 12707, A	c 632	41	3.2	601	3	US-09-949-016-103778	Sequence 103778, A
560	43	3.3	190078	3	US-09-949-016-17026	Sequence 17026, A	c 633	41	3.2	601	3	US-09-949-016-110161	Sequence 110161, A
561	43	3.3	193169	3	US-09-949-016-15091	Sequence 15091, A	c 634	41	3.2	601	3	US-09-949-016-110161	Sequence 110161, A
562	43	3.3	235033	5	US-08-852-495C-1	Sequence 1, Appl	c 635	41	3.2	601	3	US-09-949-016-110727	Sequence 110727, A
563	43	3.3	237326	5	US-08-852-495C-2	Sequence 2, Appl	c 636	41	3.2	601	3	US-09-949-016-110888	Sequence 110888, A
564	43	3.3	237863	3	US-09-949-016-13404	Sequence 13404, A	c 637	41	3.2	601	3	US-09-949-016-111049	Sequence 111049, A
565	43	3.3	246240	2	US-08-724-394A-20	Sequence 20, Appl	c 638	41	3.2	601	3	US-09-949-016-11210	Sequence 11210, A
566	43	3.3	246240	2	US-08-724-394A-21	Sequence 21, Appl	c 639	41	3.2	601	3	US-09-949-016-120460	Sequence 120460, A
567	43	3.3	246240	2	US-08-724-394A-22	Sequence 22, Appl	c 640	41	3.2	601	3	US-09-949-016-137353	Sequence 137353, A
568	43	3.3	247299	3	US-09-949-016-17590	Sequence 17590, A	c 641	41	3.2	601	3	US-09-949-016-145751	Sequence 145751, A
569	43	3.3	251769	3	US-09-949-016-13185	Sequence 13185, A	c 642	41	3.2	601	3	US-09-949-016-145752	Sequence 145752, A
570	43	3.3	251769	3	US-09-949-016-13186	Sequence 13186, A	c 643	41	3.2	601	3	US-09-949-016-146019	Sequence 146019, A
571	43	3.3	260247	3	US-09-949-016-13358	Sequence 13358, A	c 644	41	3.2	601	3	US-09-949-016-146020	Sequence 146020, A
572	43	3.3	260247	3	US-09-949-016-13358	Sequence 13358, A	c 645	41	3.2	601	3	US-09-949-016-146287	Sequence 146287, A
573	43	3.3	266748	3	US-09-949-016-13187	Sequence 13187, A	c 646	41	3.2	601	3	US-09-949-016-146288	Sequence 146288, A
574	43	3.3	266748	3	US-09-949-016-13188	Sequence 13188, A	647	41	3.2	601	3	US-09-949-016-149450	Sequence 149450, A
575	43	3.3	275110	3	US-09-949-016-12706	Sequence 12706, A	648	41	3.2	601	3	US-09-949-016-149451	Sequence 149451, A
576	43	3.3	275110	3	US-09-949-016-16070	Sequence 16070, A	649	41	3.2	601	3	US-09-949-016-167019	Sequence 167019, A
577	43	3.3	304533	3	US-09-949-016-15371	Sequence 15371, A	c 650	41	3.2	601	3	US-09-949-016-175296	Sequence 175296, A
578	43	3.3	304533	3	US-09-949-016-15372	Sequence 15372, A	c 651	41	3.2	601	3	US-09-949-016-175297	Sequence 175297, A
579	43	3.3	360470	3	US-09-949-016-13173	Sequence 13173, A	c 652	41	3.2	601	3	US-09-949-016-176499	Sequence 176499, A
580	43	3.3	363032	3	US-09-949-016-12415	Sequence 12415, A	c 653	41	3.2	601	3	US-09-949-016-176500	Sequence 176500, A
581	43	3.3	363032	3	US-09-949-016-15754	Sequence 15754, A	c 654	41	3.2	601	3	US-09-949-016-176501	Sequence 176501, A
582	43	3.3	462589	3	US-09-949-016-12900	Sequence 12900, A	c 655	41	3.2	601	3	US-09-949-016-181048	Sequence 181048, A
583	43	3.3	476044	3	US-09-949-016-12412	Sequence 12412, A	c 656	41	3.2	601	3	US-09-949-016-181049	Sequence 181049, A
584	43	3.3	636591	3	US-09-949-016-11808	Sequence 11808, A	c 657	41	3.2	601	3	US-09-949-016-198212	Sequence 198212, A
585	43	3.3	636591	3	US-09-949-016-11388	Sequence 13888, A	c 658	41	3.2	601	3	US-09-949-016-198213	Sequence 198213, A
586	43	3.3	786431	3	US-09-751-389-3	Sequence 3, Appl	c 659	41	3.2	601	3	US-09-949-016-204424	Sequence 204424, A
587	42	3.2	253	3	US-09-513-999C-15867	Sequence 15867, A	c 660	41	3.2	601	3	US-09-949-016-204426	Sequence 204426, A
588	42	3.2	601	3	US-09-949-016-33988	Sequence 33988, A	c 661	41	3.2	601	3	US-09-949-016-204494	Sequence 204494, A
589	42	3.2	601	3	US-09-949-016-45669	Sequence 45669, A	c 662	41	3.2	601	3	US-09-949-016-204496	Sequence 204496, A
590	42	3.2	601	3	US-09-949-016-94613	Sequence 94613, A	c 663	41	3.2	601	3	US-09-949-016-206047	Sequence 206047, A
591	42	3.2	601	3	US-09-949-016-94614	Sequence 94614, A	664	41	3.2	601	3	US-09-949-002-1960	Sequence 1960, Ap
592	42	3.2	601	3	US-09-949-016-94615	Sequence 94615, A	665	41	3.2	601	3	US-09-949-002-5343	Sequence 5343, Ap
593	42	3.2	601	3	US-09-949-016-121478	Sequence 121478, A	666	41	3.2	601	3	US-09-949-002-9560	Sequence 9560, Ap
594	42	3.2	601	3	US-09-949-016-123894	Sequence 123894, A	667	41	3.2	655	3	US-09-385-982-301	Sequence 301, App
595	42	3.2	601	3	US-09-949-002-2140	Sequence 2140, Ap	668	41	3.2	5837	3	US-09-949-002-612	Sequence 612, App
596	42	3.2	601	3	US-09-949-002-8111	Sequence 8111, Ap	669	41	3.2	8610	3	US-09-949-016-14614	Sequence 14614, A
597	42	3.2	2358	4	US-10-094-749-77	Sequence 77, Appl	c 670	41	3.2	10980	3	US-09-949-016-14471	Sequence 14471, A
598	42	3.2	11280	3	US-09-949-016-15203	Sequence 15203, A	c 671	41	3.2	14156	3	US-09-949-016-16772	Sequence 16772, A
599	42	3.2	11280	3	US-09-949-016-15204	Sequence 15204, A	c 672	41	3.2	14574	3	US-09-949-016-16439	Sequence 29, Appl
600	42	3.2	17584	3	US-09-949-016-13743	Sequence 13743, A	c 673	41	3.2	15071	3	US-09-358-082A-29	Sequence 29, Appl
601	42	3.2	17584	3	US-09-949-016-13743	Sequence 13743, A	c 674	41	3.2	15071	3	US-09-358-082A-29	Sequence 29, Appl
602	42	3.2	12523	3	US-09-949-016-15131	Sequence 15131, A	c 675	41	3.2	15071	4	US-10-225-073-29	Sequence 29, Appl
603	42	3.2	22821	3	US-09-949-016-14778	Sequence 14778, A	c 676	41	3.2	15071	4	US-10-225-418-29	Sequence 29, Appl
604	42	3.2	23533	3	US-09-949-016-15377	Sequence 15377, A	c 677	41	3.2	15116	3	US-09-949-016-12354	Sequence 12354, A
605	42	3.2	24971	3	US-09-949-016-14444	Sequence 14444, A	c 678	41	3.2	15117	3	US-09-949-016-16260	Sequence 16260, A
606	42	3.2	24972	3	US-09-949-016-15059	Sequence 15059, A	c 679	41	3.2	15564	3	US-09-949-016-12783	Sequence 12783, A
607	42	3.2	25274	3	US-09-949-016-16682	Sequence 16682, A	680	41	3.2	20677	3	US-09-949-002-724	Sequence 724, App

C 681	41	3.2	22539	3	US-09-949-016-15931	Sequence 15931, A	754	41	3.2	283538	3	US-09-949-016-13506	Sequence 13506, A
C 682	41	3.2	23535	3	US-09-949-016-14630	Sequence 14630, A	755	41	3.2	767677	3	US-09-949-016-12147	Sequence 12147, A
C 683	41	3.2	23538	3	US-09-949-016-12649	Sequence 12649, A	756	41	3.2	767677	3	US-09-949-016-17361	Sequence 17361, A
C 684	41	3.2	23539	3	US-09-949-016-17558	Sequence 17558, A	757	40	3.1	212	3	US-09-513-999C-15923	Sequence 15923, A
C 685	41	3.2	24166	3	US-09-949-016-13755	Sequence 13755, A	758	40	3.1	212	3	US-09-513-999C-15991	Sequence 15991, A
C 686	41	3.2	29453	3	US-09-949-016-12939	Sequence 12939, A	759	40	3.1	297	3	US-09-621-976-12888	Sequence 12888, A
C 687	41	3.2	29453	3	US-09-949-016-12940	Sequence 12940, A	760	40	3.1	301	3	US-09-513-999C-9584	Sequence 9584, Ap
C 688	41	3.2	29453	3	US-09-949-016-12941	Sequence 12941, A	761	40	3.1	307	3	US-09-621-976-12887	Sequence 12887, A
C 689	41	3.2	29453	3	US-09-949-016-12942	Sequence 12942, A	762	40	3.1	509	3	US-09-621-976-12966	Sequence 12966, A
C 690	41	3.2	33152	3	US-09-949-016-16719	Sequence 16719, A	763	40	3.1	601	3	US-09-949-016-25694	Sequence 25694, A
C 691	41	3.2	34422	3	US-09-949-016-16701	Sequence 16701, A	764	40	3.1	601	3	US-09-949-016-28122	Sequence 28122, A
C 692	41	3.2	34422	3	US-09-949-016-16705	Sequence 16705, A	765	40	3.1	601	3	US-09-949-016-28122	Sequence 28122, A
C 693	41	3.2	37155	3	US-09-949-016-16945	Sequence 16945, A	766	40	3.1	601	3	US-09-949-016-42563	Sequence 42563, A
C 694	41	3.2	39498	3	US-09-949-016-12410	Sequence 12410, A	767	40	3.1	601	3	US-09-949-016-61497	Sequence 61497, A
C 695	41	3.2	39498	3	US-09-949-016-16505	Sequence 16505, A	768	40	3.1	601	3	US-09-949-016-63298	Sequence 63298, A
C 696	41	3.2	43690	3	US-09-949-016-13904	Sequence 13904, A	769	40	3.1	601	3	US-09-949-016-63359	Sequence 63359, A
C 697	41	3.2	44064	3	US-09-949-016-12015	Sequence 12015, A	770	40	3.1	601	3	US-09-949-016-63360	Sequence 63360, A
C 698	41	3.2	44072	3	US-09-949-016-15757	Sequence 15757, A	771	40	3.1	601	3	US-09-949-016-66043	Sequence 66043, A
C 699	41	3.2	46319	3	US-09-949-016-12526	Sequence 12526, A	772	40	3.1	601	3	US-09-949-016-75929	Sequence 75929, A
C 700	41	3.2	46323	3	US-09-949-016-13267	Sequence 13267, A	773	40	3.1	601	3	US-09-949-016-91302	Sequence 91302, A
C 701	41	3.2	46725	3	US-09-949-016-15680	Sequence 15680, A	774	40	3.1	601	3	US-09-949-016-91303	Sequence 91303, A
C 702	41	3.2	49848	3	US-09-949-016-15575	Sequence 15575, A	775	40	3.1	601	3	US-09-949-016-91304	Sequence 91304, A
C 703	41	3.2	54463	3	US-09-949-016-14781	Sequence 14781, A	776	40	3.1	601	3	US-09-949-016-91305	Sequence 91305, A
C 704	41	3.2	55114	3	US-09-949-016-16792	Sequence 16792, A	777	40	3.1	601	3	Sequence 105615,	
C 705	41	3.2	56655	3	US-09-949-016-14026	Sequence 14026, A	778	40	3.1	601	3	Sequence 115238,	
C 706	41	3.2	57932	3	US-09-949-002-619	Sequence 619, App	779	40	3.1	601	3	Sequence 121015,	
C 707	41	3.2	57933	3	US-09-949-002-822	Sequence 822, App	780	40	3.1	601	3	Sequence 122692,	
C 708	41	3.2	60990	3	US-09-949-016-14080	Sequence 14080, A	781	40	3.1	601	3	Sequence 125260,	
C 709	41	3.2	62908	3	US-09-949-016-17554	Sequence 17554, A	782	40	3.1	601	3	Sequence 150122,	
C 710	41	3.2	63804	3	US-09-949-016-15200	Sequence 15200, A	783	40	3.1	601	3	Sequence 159913,	
C 711	41	3.2	69752	3	US-09-949-016-14094	Sequence 14094, A	784	40	3.1	601	3	Sequence 159934,	
C 712	41	3.2	70323	3	US-09-949-016-17594	Sequence 17594, A	785	40	3.1	601	3	Sequence 173666,	
C 713	41	3.2	74545	3	US-09-949-002-606	Sequence 606, App	786	40	3.1	601	3	Sequence 176721,	
C 714	41	3.2	76610	3	US-09-949-016-15521	Sequence 15521, A	787	40	3.1	601	3	Sequence 176721,	
C 715	41	3.2	83210	3	US-09-949-016-14209	Sequence 14209, A	788	40	3.1	601	3	Sequence 193596,	
C 716	41	3.2	87629	3	US-09-949-016-15262	Sequence 15262, A	789	40	3.1	601	3	Sequence 196208,	
C 717	41	3.2	87629	3	US-09-949-016-15263	Sequence 15263, A	790	40	3.1	601	3	Sequence 202742,	
C 718	41	3.2	87629	3	US-09-949-016-15264	Sequence 15264, A	791	40	3.1	601	3	Sequence 202743,	
C 719	41	3.2	87629	3	US-09-949-016-15265	Sequence 15265, A	792	40	3.1	1916	3	Sequence 446, App	
C 720	41	3.2	87629	3	US-09-949-016-15266	Sequence 15266, A	793	40	3.1	1916	3	Sequence 101, App	
C 721	41	3.2	87629	3	US-09-949-016-15267	Sequence 15267, A	794	40	3.1	4285	3	Sequence 1, Appli	
C 722	41	3.2	98689	3	US-09-949-016-13089	Sequence 13089, A	795	40	3.1	9110	3	Sequence 13642, A	
C 723	41	3.2	98302	3	US-09-949-016-12234	Sequence 12234, A	796	40	3.1	9113	3	Sequence 14224, A	
C 724	41	3.2	111454	3	US-09-949-016-14196	Sequence 14196, A	797	40	3.1	13948	3	Sequence 14224, A	
C 725	41	3.2	111459	3	US-09-949-016-12337	Sequence 14196, A	798	40	3.1	14246	3	Sequence 13023, A	
C 726	41	3.2	111677	3	US-09-949-016-16946	Sequence 12337, A	799	40	3.1	14664	3	Sequence 13023, A	
C 727	41	3.2	112507	3	US-09-949-016-12420	Sequence 14240, A	800	40	3.1	16056	3	Sequence 4, Appli	
C 728	41	3.2	112507	3	US-09-949-016-12794	Sequence 14240, A	801	40	3.1	16056	3	Sequence 16211, A	
C 729	41	3.2	112508	3	US-09-949-016-16589	Sequence 12794, A	802	40	3.1	17590	3	Sequence 16212, A	
C 730	41	3.2	112508	3	US-09-949-016-16589	Sequence 16589, A	803	40	3.1	17590	3	Sequence 1, Appli	
C 731	41	3.2	117001	3	US-09-949-016-15684	Sequence 16590, A	804	40	3.1	17972	3	Sequence 17214, A	
C 732	41	3.2	125902	3	US-09-949-016-13715	Sequence 15684, A	805	40	3.1	18319	3	Sequence 17446, A	
C 733	41	3.2	128516	3	US-09-949-016-13501	Sequence 13715, A	806	40	3.1	18319	3	Sequence 15113, A	
C 734	41	3.2	130298	3	US-09-949-016-16664	Sequence 13501, A	807	40	3.1	19389	3	Sequence 12309, A	
C 735	41	3.2	131860	3	US-09-949-002-730	Sequence 13501, A	808	40	3.1	19389	3	Sequence 13533, A	
C 736	41	3.2	133157	3	US-09-949-016-12541	Sequence 730, App	809	40	3.1	19979	3	Sequence 14240, A	
C 737	41	3.2	150409	3	US-09-949-016-12290	Sequence 12290, A	810	40	3.1	19980	3	Sequence 17215, A	
C 738	41	3.2	150409	3	US-09-949-016-12938	Sequence 12938, A	811	40	3.1	22218	3	Sequence 12894, A	
C 739	41	3.2	156942	3	US-09-949-016-12227	Sequence 12227, A	812	40	3.1	22218	3	Sequence 14300, A	
C 740	41	3.2	156950	3	US-09-949-016-15946	Sequence 15946, A	813	40	3.1	23193	3	Sequence 14758, A	
C 741	41	3.2	174170	3	US-09-949-016-14810	Sequence 14810, A	814	40	3.1	24497	3	Sequence 11823, A	
C 742	41	3.2	174170	3	US-09-949-016-14811	Sequence 14811, A	815	40	3.1	26134	3	Sequence 14253, A	
C 743	41	3.2	174318	3	US-09-949-016-11880	Sequence 14811, A	816	40	3.1	26167	3	Sequence 15285, A	
C 744	41	3.2	174318	3	US-09-949-016-11881	Sequence 11880, A	817	40	3.1	26167	3	Sequence 1, Appli	
C 745	41	3.2	205044	3	US-09-949-016-15851	Sequence 14812, A	818	40	3.1	27916	3	Sequence 15202, A	
C 746	41	3.2	205044	3	US-09-949-016-15852	Sequence 14813, A	819	40	3.1	28595	3	Sequence 16482, A	
C 747	41	3.2	205044	3	US-09-949-016-15853	Sequence 15851, A	820	40	3.1	28595	3	Sequence 15740, A	
C 748	41	3.2	223471	3	US-09-949-016-12724	Sequence 15852, A	821	40	3.1	32042	3	Sequence 44, Appli	
C 749	41	3.2	223471	3	US-09-949-016-12724	Sequence 15853, A	822	40	3.1	32042	3	Sequence 63, Appli	
C 750	41	3.2	223471	3	US-09-949-016-12725	Sequence 12387, A	823	40	3.1	32104	3	Sequence 14722, A	
C 751	41	3.2	223471	3	US-09-949-016-12725	Sequence 12724, A	824	40	3.1	32104	3	Sequence 3, Appli	
C 752	41	3.2	260286	3	US-09-949-016-17037	Sequence 12725, A	825	40	3.1	36651	3	Sequence 3, Appli	
C 753	41	3.2	260293	3	US-09-949-016-12106	Sequence 12726, A	826	40	3.1	36651	3	Sequence 3, Appli	

827	40	3.1	37712	3	US-09-949-016-16704	Sequence 16704, A	900	40	3.1	254778	3	US-09-949-016-12417	Sequence 12417, A
828	40	3.1	38374	4	US-09-880-107-3463	Sequence 3463, App	C 902	40	3.1	254964	3	US-09-949-016-12583	Sequence 12583, A
C 829	40	3.1	39553	3	US-09-949-002-810	Sequence 810, App	C 901	40	3.1	254964	3	US-09-949-016-17392	Sequence 17392, A
830	40	3.1	39982	3	US-09-820-924-3	Sequence 3, Appli	903	40	3.1	268449	3	US-09-949-016-17244	Sequence 17244, A
831	40	3.1	39982	3	US-10-369-626-3	Sequence 3, Appli	C 904	40	3.1	275110	3	US-09-949-016-12706	Sequence 12706, A
832	40	3.1	41318	3	US-09-949-016-16225	Sequence 16225, A	C 905	40	3.1	275110	3	US-09-949-016-16070	Sequence 16070, A
C 833	40	3.1	43343	3	US-09-949-016-14911	Sequence 14911, A	C 906	40	3.1	294836	3	US-09-949-016-15974	Sequence 15974, A
834	40	3.1	44342	3	US-09-949-016-12661	Sequence 12661, A	C 907	40	3.1	312957	3	US-09-949-001-31	Sequence 31, Appl
835	40	3.1	47181	3	US-09-949-016-16131	Sequence 16131, A	C 908	40	3.1	312972	3	US-09-949-001-34	Sequence 34, Appl
836	40	3.1	47181	3	US-09-949-016-16132	Sequence 16132, A	C 909	40	3.1	462589	3	US-09-949-016-12900	Sequence 12900, A
837	40	3.1	47181	3	US-09-949-016-16133	Sequence 16133, A	C 910	40	3.1	476044	3	US-09-949-016-12412	Sequence 12412, A
C 838	40	3.1	50810	3	US-09-949-016-16039	Sequence 16039, A	C 911	40	3.1	678533	3	US-09-949-016-14578	Sequence 14578, A
839	40	3.1	50950	3	US-09-949-016-16659	Sequence 16659, A	C 912	40	3.1	678533	3	US-09-949-016-14577	Sequence 14577, A
840	40	3.1	51043	3	US-09-949-016-12739	Sequence 12739, A	913	40	3.1	786431	3	US-09-751-389-3	Sequence 3, Appl
841	40	3.1	51046	3	US-09-949-016-13946	Sequence 13946, A	914	39	3.0	263	3	US-09-621-976-12054	Sequence 12054, A
C 842	40	3.1	51671	3	US-09-949-016-12068	Sequence 12068, A	C 915	39	3.0	293	3	US-09-621-976-12021	Sequence 12021, A
C 843	40	3.1	51671	3	US-09-949-016-15962	Sequence 15962, A	C 916	39	3.0	300	4	US-09-237-648-1551	Sequence 1551, Ap
844	40	3.1	51822	3	US-09-949-016-15233	Sequence 15233, A	917	39	3.0	302	3	US-09-621-976-12333	Sequence 12333, A
C 845	40	3.1	53806	3	US-09-949-016-12572	Sequence 12572, A	C 918	39	3.0	305	3	US-09-621-976-11672	Sequence 11672, A
C 846	40	3.1	54286	3	US-09-949-002-837	Sequence 837, App	C 919	39	3.0	309	3	US-09-621-976-11582	Sequence 11582, A
C 847	40	3.1	54649	3	US-09-949-016-15867	Sequence 15867, A	920	39	3.0	314	3	US-09-621-976-11901	Sequence 11901, A
848	40	3.1	57978	3	US-09-949-016-16667	Sequence 16667, A	921	39	3.0	322	3	US-09-621-976-11620	Sequence 11620, A
C 849	40	3.1	58111	3	US-09-949-002-673	Sequence 673, App	C 922	39	3.0	329	3	US-09-621-976-13502	Sequence 13502, A
C 850	40	3.1	60465	3	US-09-949-016-15595	Sequence 15595, A	C 923	39	3.0	416	3	US-09-621-976-11032	Sequence 11032, A
C 851	40	3.1	63783	3	US-09-949-016-13576	Sequence 13576, A	C 924	39	3.0	472	3	US-09-621-976-8819	Sequence 8819, Ap
C 852	40	3.1	69052	3	US-09-949-002-642	Sequence 642, App	C 925	39	3.0	476	3	US-09-621-976-11105	Sequence 11105, A
853	40	3.1	69062	3	US-09-949-016-13608	Sequence 13608, A	C 926	39	3.0	601	3	US-09-949-016-25766	Sequence 25766, A
854	40	3.1	69062	3	US-09-949-016-13609	Sequence 13609, A	C 927	39	3.0	601	3	US-09-949-016-27232	Sequence 27232, A
855	40	3.1	69687	3	US-09-949-016-12890	Sequence 12890, A	C 928	39	3.0	601	3	US-09-949-016-34976	Sequence 34976, A
856	40	3.1	76472	3	US-09-949-016-15896	Sequence 15896, A	929	39	3.0	601	3	US-09-949-016-41602	Sequence 41602, A
C 857	40	3.1	77036	3	US-09-949-016-16156	Sequence 16156, A	C 930	39	3.0	601	3	US-09-949-016-48651	Sequence 48651, A
858	40	3.1	78720	3	US-09-949-016-12710	Sequence 12710, A	C 931	39	3.0	601	3	US-09-949-016-48652	Sequence 48652, A
859	40	3.1	78720	3	US-09-949-016-17283	Sequence 17283, A	C 932	39	3.0	601	3	US-09-949-016-48737	Sequence 48737, A
C 860	40	3.1	79634	3	US-09-949-016-15642	Sequence 15642, A	C 933	39	3.0	601	3	US-09-949-016-69933	Sequence 69933, A
C 861	40	3.1	79988	3	US-09-949-016-12274	Sequence 12274, A	934	39	3.0	601	3	US-09-949-016-69994	Sequence 69994, A
C 862	40	3.1	79989	3	US-09-949-016-16254	Sequence 16254, A	C 935	39	3.0	601	3	US-09-949-016-71550	Sequence 71550, A
C 863	40	3.1	81701	3	US-09-949-016-14891	Sequence 14891, A	936	39	3.0	601	3	US-09-949-016-71594	Sequence 71594, A
864	40	3.1	84132	3	US-09-949-016-16241	Sequence 16241, A	937	39	3.0	601	3	US-09-949-016-74433	Sequence 74433, A
C 865	40	3.1	87562	3	US-09-949-016-13685	Sequence 13685, A	C 938	39	3.0	601	3	US-09-949-016-74434	Sequence 74434, A
C 866	40	3.1	87629	3	US-09-949-016-15262	Sequence 15262, A	C 939	39	3.0	601	3	US-09-949-016-76233	Sequence 76233, A
C 867	40	3.1	87629	3	US-09-949-016-15263	Sequence 15263, A	C 940	39	3.0	601	3	US-09-949-016-78971	Sequence 78971, A
C 868	40	3.1	87629	3	US-09-949-016-15264	Sequence 15264, A	C 941	39	3.0	601	3	US-09-949-016-78972	Sequence 78972, A
C 869	40	3.1	87629	3	US-09-949-016-15265	Sequence 15265, A	942	39	3.0	601	3	US-09-949-016-82425	Sequence 82425, A
C 870	40	3.1	89892	3	US-09-949-016-13667	Sequence 13667, A	943	39	3.0	601	3	US-09-949-016-82426	Sequence 82426, A
871	40	3.1	92276	3	US-09-949-016-12166	Sequence 12166, A	C 944	39	3.0	601	3	US-09-949-016-85305	Sequence 85305, A
C 872	40	3.1	94855	3	US-09-949-016-12264	Sequence 12264, A	C 945	39	3.0	601	3	US-09-949-016-86476	Sequence 86476, A
C 873	40	3.1	100463	3	US-09-949-016-12511	Sequence 12511, A	946	39	3.0	601	3	US-09-949-016-86517	Sequence 86517, A
C 874	40	3.1	100468	3	US-09-949-016-13725	Sequence 13725, A	947	39	3.0	601	3	US-09-949-016-86518	Sequence 86518, A
C 875	40	3.1	101558	3	US-09-949-016-12243	Sequence 12243, A	948	39	3.0	601	3	US-09-949-016-89126	Sequence 89126, A
C 876	40	3.1	102053	3	US-09-949-016-13025	Sequence 13025, A	C 949	39	3.0	601	3	US-09-949-016-104036	Sequence 104036, A
C 877	40	3.1	110096	4	US-09-880-107-1542	Sequence 1342, Ap	C 950	39	3.0	601	3	US-09-949-016-112425	Sequence 112425, A
C 878	40	3.1	113042	3	US-09-949-016-12343	Sequence 12343, A	C 951	39	3.0	601	3	US-09-949-016-112426	Sequence 112426, A
C 879	40	3.1	113042	3	US-09-949-016-15246	Sequence 15246, A	C 952	39	3.0	601	3	US-09-949-016-112427	Sequence 112427, A
C 880	40	3.1	117391	3	US-09-949-016-13945	Sequence 13945, A	C 953	39	3.0	601	3	US-09-949-016-113184	Sequence 113184, A
881	40	3.1	118382	3	US-09-949-016-15996	Sequence 15996, A	C 954	39	3.0	601	3	US-09-949-016-113454	Sequence 113454, A
C 882	40	3.1	118382	3	US-09-949-016-15997	Sequence 15997, A	C 955	39	3.0	601	3	US-09-949-016-119381	Sequence 119381, A
C 883	40	3.1	133063	3	US-09-949-016-16293	Sequence 16293, A	C 956	39	3.0	601	3	US-09-949-016-130264	Sequence 130264, A
884	40	3.1	133358	3	US-09-949-016-16964	Sequence 16964, A	957	39	3.0	601	3	US-09-949-016-131288	Sequence 131288, A
885	40	3.1	133360	3	US-09-949-016-12651	Sequence 12651, A	C 958	39	3.0	601	3	US-09-949-016-131289	Sequence 131289, A
C 886	40	3.1	139150	3	US-09-949-016-17398	Sequence 17398, A	959	39	3.0	601	3	US-09-949-016-131557	Sequence 131557, A
C 887	40	3.1	139577	3	US-09-949-016-12879	Sequence 12879, A	C 960	39	3.0	601	3	US-09-949-016-131558	Sequence 131558, A
C 888	40	3.1	143322	3	US-09-949-016-15316	Sequence 15316, A	961	39	3.0	601	3	US-09-949-016-131559	Sequence 131559, A
C 889	40	3.1	148609	3	US-09-949-016-12860	Sequence 12860, A	C 962	39	3.0	601	3	US-09-949-016-131560	Sequence 131560, A
C 890	40	3.1	148609	3	US-09-949-016-16787	Sequence 16787, A	963	39	3.0	601	3	US-09-949-016-136436	Sequence 136436, A
C 891	40	3.1	149543	3	US-09-949-016-15947	Sequence 15947, A	964	39	3.0	601	3	US-09-949-016-136437	Sequence 136437, A
C 892	40	3.1	150780	3	US-09-949-016-14711	Sequence 14711, A	965	39	3.0	601	3	US-09-949-016-140306	Sequence 140306, A
893	40	3.1	173787	3	US-09-949-016-12542	Sequence 12542, A	C 966	39	3.0	601	3	US-09-949-016-140307	Sequence 140307, A
894	40	3.1	173791	3	US-09-949-016-17302	Sequence 17302, A	C 967	39	3.0	601	3	US-09-949-016-140308	Sequence 140308, A
C 895	40	3.1	177293	3	US-09-949-016-16513	Sequence 16513, A	968	39	3.0	601	3	US-09-949-016-140309	Sequence 140309, A
C 896	40	3.1	187580	3	US-09-949-016-13266	Sequence 13266, A	969	39	3.0	601	3	US-09-949-016-141039	Sequence 141039, A
C 897	40	3.1	206433	3	US-09-949-016-13527	Sequence 13527, A	970	39	3.0	601	3	US-09-949-016-141040	Sequence 141040, A
898	40	3.1	223452	3	US-09-949-016-12968	Sequence 12968, A	971	39	3.0	601	3	US-09-949-016-141041	Sequence 141041, A
899	40	3.1	235452	3	US-09-949-016-13675	Sequence 13675, A	972	39	3.0	601	3	US-09-949-016-141043	Sequence 141043, A

39	3.0	601	3	US-09-949-016-141044	Sequence 141044,	1046	39	3.0	25419	3	US-09-949-016-15476	Sequence 15476, A
39	3.0	601	3	US-09-949-016-141045	Sequence 141045,	1047	39	3.0	25419	3	US-09-949-016-15477	Sequence 15477, A
39	3.0	601	3	US-09-949-016-143034	Sequence 143034,	1048	39	3.0	25966	3	US-09-949-002-632	Sequence 632, App
39	3.0	601	3	US-09-949-016-143035	Sequence 143035,	1049	39	3.0	25966	3	US-09-949-002-813	Sequence 813, App
39	3.0	601	3	US-09-949-016-154026	Sequence 154026,	c1050	39	3.0	26335	3	US-09-949-016-17602	Sequence 17602, A
39	3.0	601	3	US-09-949-016-154374	Sequence 154374,	1051	39	3.0	26611	3	US-09-949-016-16484	Sequence 16484, A
39	3.0	601	3	US-09-949-016-154956	Sequence 154956,	c1052	39	3.0	27377	3	US-09-816-248-18	Sequence 18, Appl
39	3.0	601	3	US-09-949-016-154957	Sequence 154957,	c1053	39	3.0	28433	3	US-09-949-016-11812	Sequence 11812, A
39	3.0	601	3	US-09-949-016-154957	Sequence 154957,	c1054	39	3.0	28433	3	US-09-949-016-12712	Sequence 12712, A
39	3.0	601	3	US-09-949-016-156929	Sequence 156929,	c1055	39	3.0	28843	3	US-09-949-016-17158	Sequence 17158, A
39	3.0	601	3	US-09-949-016-160756	Sequence 160756,	c1056	39	3.0	28843	3	US-09-949-016-17159	Sequence 17159, A
39	3.0	601	3	US-09-949-016-163070	Sequence 163070,	1057	39	3.0	31391	3	US-09-949-016-17200	Sequence 17200, A
39	3.0	601	3	US-09-949-016-163071	Sequence 163071,	c1058	39	3.0	31469	3	US-09-949-016-13722	Sequence 13722, A
39	3.0	601	3	US-09-949-016-170001	Sequence 170001,	1059	39	3.0	32414	3	US-09-949-016-16443	Sequence 16443, A
39	3.0	601	3	US-09-949-016-170002	Sequence 170002,	c1060	39	3.0	32594	3	US-09-949-016-12219	Sequence 12219, A
39	3.0	601	3	US-09-949-016-174222	Sequence 174222,	c1061	39	3.0	32594	3	US-09-949-016-12219	Sequence 12219, A
39	3.0	601	3	US-09-949-016-185610	Sequence 185610,	c1062	39	3.0	32594	3	US-09-949-016-12219	Sequence 12219, A
39	3.0	601	3	US-09-949-016-187595	Sequence 187595,	1063	39	3.0	33885	3	US-09-949-016-16081	Sequence 16081, A
39	3.0	601	3	US-09-949-016-187595	Sequence 187595,	c1064	39	3.0	34539	3	US-09-949-016-12226	Sequence 12226, A
39	3.0	601	3	US-09-949-016-189394	Sequence 189394,	1065	39	3.0	34540	3	US-09-949-016-13156	Sequence 13156, A
39	3.0	601	3	US-09-949-016-189395	Sequence 189395,	c1066	39	3.0	36023	3	US-09-949-016-15577	Sequence 15577, A
39	3.0	601	3	US-09-949-016-189396	Sequence 189396,	c1067	39	3.0	36181	3	US-09-949-016-12961	Sequence 12961, A
39	3.0	601	3	US-09-949-016-189397	Sequence 189397,	c1068	39	3.0	38009	3	US-09-949-016-13617	Sequence 13617, A
39	3.0	601	3	US-09-949-016-189398	Sequence 189398,	c1069	39	3.0	38343	3	US-09-949-016-15714	Sequence 15714, A
39	3.0	601	3	US-09-949-016-189399	Sequence 189399,	1070	39	3.0	38657	3	US-09-949-016-14267	Sequence 14267, A
39	3.0	601	3	US-09-949-016-201581	Sequence 201581,	1071	39	3.0	38844	3	US-09-734-675-3	Sequence 3, Appl1
39	3.0	601	3	US-09-949-001-549	Sequence 549, App	1072	39	3.0	38844	3	US-10-060-333-3	Sequence 3, Appl1
39	3.0	601	3	US-09-949-002-2135	Sequence 2135, Ap	c1073	39	3.0	38983	3	US-09-949-016-15700	Sequence 15700, A
39	3.0	601	3	US-09-949-002-5384	Sequence 5384, Ap	1074	39	3.0	40505	3	US-09-949-016-13439	Sequence 13439, A
39	3.0	601	3	US-09-949-002-5385	Sequence 5385, Ap	1075	39	3.0	41617	3	US-09-949-016-14356	Sequence 14356, A
39	3.0	601	3	US-09-949-002-8498	Sequence 8498, Ap	c1081	39	3.0	41618	3	US-09-949-016-14681	Sequence 14681, A
39	3.0	775	4	US-09-297-648-3721	Sequence 3721, Ap	c1082	39	3.0	42250	3	US-09-949-016-17171	Sequence 17171, A
39	3.0	1834	3	US-08-836-7348-3	Sequence 3, Appl1	1077	39	3.0	42846	3	US-09-949-016-14117	Sequence 14117, A
39	3.0	2387	3	US-09-375-318-38	Sequence 38, Appl	1078	39	3.0	42875	3	US-09-949-016-11965	Sequence 11965, A
39	3.0	2613	3	US-10-104-047-1908	Sequence 1908, Ap	c1079	39	3.0	43366	3	US-09-949-016-14185	Sequence 14185, A
39	3.0	2898	4	US-10-094-749-1082	Sequence 1082, Ap	1080	39	3.0	43507	3	US-09-949-016-13297	Sequence 13297, A
39	3.0	4411	3	US-09-949-016-14053	Sequence 14053, A	1081	39	3.0	43562	3	US-09-949-016-16222	Sequence 16222, A
39	3.0	5944	3	US-09-949-016-15134	Sequence 15134, A	c1082	39	3.0	43563	3	US-09-949-016-16294	Sequence 16294, A
39	3.0	5954	3	US-09-949-016-15237	Sequence 15237, A	c1083	39	3.0	44430	3	US-09-949-016-12468	Sequence 12468, A
39	3.0	8112	3	US-09-949-016-16470	Sequence 16470, A	c1084	39	3.0	44431	3	US-09-949-016-15882	Sequence 15882, A
39	3.0	9299	3	US-09-949-016-14415	Sequence 14415, A	1086	39	3.0	44836	3	US-09-949-016-14867	Sequence 14867, A
39	3.0	9740	3	US-09-949-016-15933	Sequence 15933, A	c1087	39	3.0	45546	3	US-09-146-053-6	Sequence 6, Appl1
39	3.0	10024	4	US-09-880-107-2430	Sequence 2430, Ap	1088	39	3.0	46340	3	US-09-984-429-344	Sequence 344, App
39	3.0	10317	3	US-09-949-016-11897	Sequence 11897, A	1089	39	3.0	46340	3	US-09-719-554-66	Sequence 66, Appl
39	3.0	10434	3	US-09-949-016-12258	Sequence 12258, A	c1089	39	3.0	46985	3	US-09-949-016-13848	Sequence 13848, A
39	3.0	10435	3	US-09-949-016-14654	Sequence 14654, A	1091	39	3.0	47064	3	US-09-949-016-13380	Sequence 13380, A
39	3.0	11665	3	US-09-949-016-12446	Sequence 12446, A	c1091	39	3.0	47347	3	US-09-949-016-14130	Sequence 14130, A
39	3.0	11665	3	US-09-949-016-16500	Sequence 16500, A	1093	39	3.0	47375	3	US-09-949-016-15420	Sequence 15420, A
39	3.0	12655	3	US-09-949-016-16388	Sequence 16388, A	c1093	39	3.0	47858	3	US-09-949-016-14965	Sequence 14965, A
39	3.0	12707	3	US-09-949-016-16928	Sequence 16928, A	1094	39	3.0	48108	3	US-09-949-016-12555	Sequence 12555, A
39	3.0	14082	3	US-09-949-016-11898	Sequence 11898, A	1095	39	3.0	48108	3	US-09-949-016-16942	Sequence 16942, A
39	3.0	14087	3	US-09-949-016-14783	Sequence 14783, A	1096	39	3.0	48219	3	US-09-949-016-16158	Sequence 16158, A
39	3.0	15415	3	US-09-949-016-13931	Sequence 13931, A	c1096	39	3.0	48691	3	US-09-949-016-16308	Sequence 16308, A
39	3.0	15415	3	US-09-949-016-13931	Sequence 13932, A	c1098	39	3.0	50836	3	US-09-949-016-16722	Sequence 16722, A
39	3.0	16712	3	US-09-949-016-16022	Sequence 16022, A	c1099	39	3.0	51403	3	US-09-949-016-15057	Sequence 15057, A
39	3.0	16885	3	US-09-949-016-17297	Sequence 17297, A	c1100	39	3.0	51905	3	US-09-949-003-667	Sequence 667, App
39	3.0	16890	3	US-09-949-016-12190	Sequence 12190, A	c1101	39	3.0	51905	3	US-09-949-002-781	Sequence 781, App
39	3.0	17023	3	US-09-949-016-12056	Sequence 12056, A	1102	39	3.0	51928	3	US-09-949-016-13184	Sequence 13184, A
39	3.0	17023	3	US-09-949-016-14431	Sequence 14431, A	c1103	39	3.0	52874	3	US-09-949-016-14868	Sequence 14868, A
39	3.0	17073	5	US-09-543-679A-2565	Sequence 2565, Ap	1104	39	3.0	53789	3	US-09-949-016-12137	Sequence 12137, A
39	3.0	17488	3	US-09-949-016-15574	Sequence 15574, A	c1105	39	3.0	53789	3	US-09-949-016-13955	Sequence 13955, A
39	3.0	18620	3	US-09-949-016-13010	Sequence 13010, A	c1106	39	3.0	54420	3	US-09-949-016-15422	Sequence 15422, A
39	3.0	18970	3	US-09-949-016-15319	Sequence 15319, A	c1107	39	3.0	54531	3	US-09-949-016-16267	Sequence 16267, A
39	3.0	19451	3	US-09-949-016-13695	Sequence 13695, A	c1108	39	3.0	57392	3	US-09-949-016-12070	Sequence 12070, A
39	3.0	19451	3	US-09-949-016-13695	Sequence 13695, A	c1109	39	3.0	57402	3	US-09-949-016-13293	Sequence 13293, A
39	3.0	19883	5	US-09-543-679A-2566	Sequence 2566, Ap	1110	39	3.0	57559	3	US-09-949-016-13077	Sequence 13077, A
39	3.0	22010	3	US-09-949-016-15360	Sequence 15360, A	1111	39	3.0	57560	3	US-09-949-016-12536	Sequence 12536, A
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39	3.0	22143	3	US-09-949-016-15983	Sequence 15983, A	c1113	39	3.0	59252	3	US-09-949-016-12150	Sequence 12150, A
39	3.0	23015	3	US-09-949-002-726	Sequence 726, App	c1114	39	3.0	59252	3	US-09-949-016-15374	Sequence 15374, A
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RESULT 2
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; Sequence 63, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63

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; ORGANISM: Homo sapiens									
US-09-907-794A-63									
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Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Qy	121	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180						
Db	121	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180						
Qy	181	CCCAAGAGCCAAAGTAGTACAGCAGTAGTAGTACCAAGAGGCTATTTTAGCCTGCAA	240						
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Qy	241	AACCCCAAGAGAGACTGTTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTC	300						
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US-09-905-125A-63

; Sequence 63, Application US/09905125A

; Patent No. 6664376

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,125A

; CURRENT FILING DATE: 2001-07-12

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090


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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
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; PRIOR FILING DATE: 1999-07-28
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; PRIOR FILING DATE: 1999-09-08
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-63

Query Match      100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      481  AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTGTGGT 540
QY      541  AGAGCTACGATGTCAAGACAAAGAGGAAATCCAGCTCTCTGAATACACATGTTTAAAGGA 600
DB      541  AGAGCTACGATGTCAAGACAAAGAGGAAATCCAGCTCTCTGAATACACATGTTTAAAGGA 600
QY      601  TGGCATCCGTTTGTCTAGAAAATCCAGACTTGGCTCCAAAGCAACCAAGCTCATACAC 660
DB      601  TGGCATCCGTTTGTCTAGAAAATCCAGACTTGGCTCCAAAGCAACCAAGCTCATACAC 660
QY      661  AATGAATACAAAACCTGGAACCTGCAATTTAATCTGTTTCCAAACTGGACACTGGAGA 720
DB      661  AATGAATACAAAACCTGGAACCTGCAATTTAATCTGTTTCCAAACTGGACACTGGAGA 720
QY      721  ATATTCTGTGAAGCCCGCAATTTCTGTGGATATCGCAGGTGCTCTGGGAAACGAATGCA 780
DB      721  ATATTCTGTGAAGCCCGCAATTTCTGTGGATATCGCAGGTGCTCTGGGAAACGAATGCA 780
QY      781  AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTAGTTGTGGCTTAGTGAT 840
DB      781  AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTAGTTGTGGCTTAGTGAT 840
QY      841  TTCGGTTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAC 900
DB      841  TTCGGTTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAC 900
QY      901  CTCTTTCAGAGAGTAAATTTCTTCACTAAAGCCAGCAATAGAGTGAAAATGTGCAGTG 960
DB      901  CTCTTTCAGAGAGTAAATTTCTTCACTAAAGCCAGCAATAGAGTGAAAATGTGCAGTG 960
QY      961  GCTCAGCGCTGTAATCCAGCACTTTTGAAGCGCGCGCGGGCGGATCAGAGTCAAGGA 1020
DB      961  GCTCAGCGCTGTAATCCAGCACTTTTGAAGCGCGCGGGCGGATCAGAGTCAAGGA 1020
QY      1021  GTTCTAGACCGCTCGCCCAATATGTTGAACCCCATCTCTACTTAATAACAAAATTAG 1080
DB      1021  GTTCTAGACCGCTCGCCCAATATGTTGAACCCCATCTCTACTTAATAACAAAATTAG 1080
QY      1081  CTGGGCAATGGTGGCATGTGCTCGAGTTCAGCTGCTTGGGAGACAGGAGAAATCAGTTGA 1140
DB      1081  CTGGGCAATGGTGGCATGTGCTCGAGTTCAGCTGCTTGGGAGACAGGAGAAATCAGTTGA 1140
QY      1141  ACCCGGAGCGGAGGTTGCGAGTGTGAGATCAGCCCACTGCGAGTCCAGCTCGGGTAA 1200
DB      1141  ACCCGGAGCGGAGGTTGCGAGTGTGAGATCAGCCCACTGCGAGTCCAGCTCGGGTAA 1200
QY      1201  CAGAGCAAGTTCCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1260
DB      1201  CAGAGCAAGTTCCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1260
QY      1261  TGTAGAAATCTTCAATAAATAATAGCTTGATATTC 1295
DB      1261  TGTAGAAATCTTCAATAAATAATAGCTTGATATTC 1295
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/ Sequence 63, Application US/09906700
/ Patent No. 6723535
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Aeshkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ ACIDS Encoding the Same
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/906,700
/ CURRENT FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 63
/ LENGTH: 1295
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-906-700-63

Query Match      100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCAGAGTTCAAGGGCCCGCCGCTCTCTGCGTCTCTGCGCGGACCCCTCGACCTCCT 60
DB      1  CCAGAGTTCAAGGGCCCGCCGCTCTCTGCGTCTCTGCGCGGACCCCTCGACCTCCT 60
QY      61  CAGAGCAGCCGGCTGCGCCCGCGGAAGATGCGGAGGAGCGCCACCGCTCTCTCT 120
DB      61  CAGAGCAGCCGGCTGCGCCCGCGGAAGATGCGGAGGAGCGCCACCGCTCTCTCT 120
QY      121  GCTGCTGCTGCGCTACCTGGTGGTGGCTGCTATCATAGGCTATGGGTTTCTGC 180
DB      121  GCTGCTGCTGCGCTACCTGGTGGTGGCTGCTATCATAGGCTATGGGTTTCTGC 180
QY      181  CCCAAAGACCAACAGTAGTCACAGCAGTAGTACCAAGAGGCTATTTTAGCCCTGCAA 240
DB      181  CCCAAAGACCAACAGTAGTCACAGCAGTAGTACCAAGAGGCTATTTTAGCCCTGCAA 240
QY      241  AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGGAAAGAACTGGGTGCGAGTGTCTC 300
DB      241  AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGGAAAGAACTGGGTGCGAGTGTCTC 300
QY      301  CTTTGTCTACTATCAACAGACTCTTCAGAGTATTTTAAATAATCGAGCTGAGATGATAGA 360
DB      301  CTTTGTCTACTATCAACAGACTCTTCAGAGTATTTTAAATAATCGAGCTGAGATGATAGA 360
QY      361  TTTCAATATCCGGATCAAAAATGTGACAAAGAGTGTGCGGGAAATATCGTTGTCAAGT 420
DB      361  TTTCAATATCCGGATCAAAAATGTGACAAAGAGTGTGCGGGAAATATCGTTGTCAAGT 420
QY      421  TAGTGCCCATCTGAGCAAGGCGCAAACTCTGGAAGAGGATACAGTCACTCTGGAAGTATT 480
DB      421  TAGTGCCCATCTGAGCAAGGCGCAAACTCTGGAAGAGGATACAGTCACTCTGGAAGTATT 480
QY      481  AGTGGCTCAGCAGTTCATCATGTGAGTACCTCTCTGCTCTGAGTGGAACTGTGGT 540
DB      481  AGTGGCTCAGCAGTTCATCATGTGAGTACCTCTCTGCTCTGAGTGGAACTGTGGT 540
QY      541  AGAGCTACGATCTCAAGACAAAGAGGGAATCCAGCTCTCTGAATACACATGTTTAAAGA 600
DB      541  AGAGCTACGATCTCAAGACAAAGAGGGAATCCAGCTCTCTGAATACACATGTTTAAAGA 600
QY      601  TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATAAC 660
DB      601  TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATAAC 660
QY      661  AATGAATACAAAACCTGGAACTCTGCAATTTTAAATACTGTTCCTGGAACCTGGAGA 720
DB      661  AATGAATACAAAACCTGGAACTCTGCAATTTTAAATACTGTTCCTGGAACCTGGAGA 720
QY      721  ATATTCTGTGAAGCCCGCAATTTCTGTTGGATATCGCAGGTGTCTTGGGAACGAATGCA 780
DB      721  ATATTCTGTGAAGCCCGCAATTTCTGTTGGATATCGCAGGTGTCTTGGGAACGAATGCA 780
QY      781  AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGCTAGTGTGGCTTCTAGTGTAT 840
DB      781  AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGCTAGTGTGGCTTCTAGTGTAT 840
QY      841  TTCGGTTTGTGGCTTGTGATGCTATGCTCAGAGGAAGGCTACTTTTCAAAGAAAC 900
DB      841  TTCGGTTTGTGGCTTGTGATGCTATGCTCAGAGGAAGGCTACTTTTCAAAGAAAC 900
QY      901  CTCCTTCCAGAGAGTAAATCTTCTCATCTAAAGCCACAAATGAGTGAATAATGTGAGTG 960
DB      901  CTCCTTCCAGAGAGTAAATCTTCTCATCTAAAGCCACAAATGAGTGAATAATGTGAGTG 960
QY      961  GCTCAGCCTGTAATCCAGCACTTTTGGAAAGCCCGCGGCGGATCACAGGTGAGG 1020
DB      961  GCTCAGCCTGTAATCCAGCACTTTTGGAAAGCCCGCGGCGGATCACAGGTGAGG 1020
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Qy 1021 GTTCTAGACCAAGTGGCCCAATATGGTGAACCCCACTCTTACTAAATAACAAAAATTAG 1080
Db 1021 GTTCTAGACCAAGTGGCCCAATATGGTGAACCCCACTCTTACTAAATAACAAAAATTAG 1080
Qy 1081 CTGGGCATGTGGCATGTGCTCGAGTTCAGCTGCTTGGGAGACAGGAGAACTCACTTGA 1140
Db 1081 CTGGGCATGTGGCATGTGCTCGAGTTCAGCTGCTTGGGAGACAGGAGAACTCACTTGA 1140
Qy 1141 ACCCGGAGGCGGAGTTGCAGTGCAGCTGAGATCACGCCCACTGCAGTCCAGCCTGGGTAA 1200
Db 1141 ACCCGGAGGCGGAGTTGCAGTGCAGCTGAGATCACGCCCACTGCAGTCCAGCCTGGGTAA 1200
Qy 1201 CAGACGAAGATTCATCTCAAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 1260
Db 1201 CAGACGAAGATTCATCTCAAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 1260
Qy 1261 TGTAGAATTCCTCAATAAATATAGCTTGATATTC 1295
Db 1261 TGTAGAATTCCTCAATAAATATAGCTTGATATTC 1295

RESULT 6

US-09-903-603A-63
; Sequence 63, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grøttisen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903.603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-903-603A-63
Query Match 100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCAGAAAGTTCAAGGGCCCCCGGCTCTCTCGCTCTCTCGCGGGAGACCCCTCGACCTCCT 60
Db 1 CCAGAAAGTTCAAGGGCCCCCGGCTCTCTCGCTCTCTCGCGGGAGACCCCTCGACCTCCT 60
Qy 61 CAGAGCAGCGGCTGCGCGCCCGGGAAGATGGCGAGGAGCGCGCCACCGCTCCTCCT 120
Db 61 CAGAGCAGCGGCTGCGCGCCCGGGAAGATGGCGAGGAGCGCGCCACCGCTCCTCCT 120
Qy 121 GCTGCTGCTGCGCTACCTGCTGCTGCGCTATCAAGGCTATCAAGGCTATGGTCTTCGC 180
Db 121 GCTGCTGCTGCGCTACCTGCTGCTGCGCTATCAAGGCTATGGTCTTCGC 180
Qy 181 CCAGAAAGACCAAGTAGTCAAGCAGTAGTAGTACCAAGAGGCTATTTTAGCCTGCAA 240
Db 181 CCAGAAAGACCAAGTAGTCAAGCAGTAGTAGTACCAAGAGGCTATTTTAGCCTGCAA 240
Qy 241 AACCCCAAGAGAGCTGTTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTC 300
Db 241 AACCCCAAGAGAGCTGTTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTC 300
Qy 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA 360
Db 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA 360
Qy 361 TTTCAATATCCGGATCAAAAATGTGACAGAAAGTGTGCGGGGAAAATATCTTGTGAAGT 420
Db 361 TTTCAATATCCGGATCAAAAATGTGACAGAAAGTGTGCGGGGAAAATATCTTGTGAAGT 420
Qy 421 TAGTGGCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAGTATT 480
Db 421 TAGTGGCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAGTATT 480
Qy 481 AGTGGCTCCAGCAGTTCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGAAGTGTGGT 540
Db 481 AGTGGCTCCAGCAGTTCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGAAGTGTGGT 540
Qy 541 AGAGCTACGATGTCAAGACAAAAGAGGAAATCCAGCTCTCTGAATACACATGTTTAAAGGA 600
Db 541 AGAGCTACGATGTCAAGACAAAAGAGGAAATCCAGCTCTCTGAATACACATGTTTAAAGGA 600
Qy 601 TGGCATCCGTTTGGTAGAAAATCCAGACTTGGCTCCCAAGCACCACAGCTCATACAC 660
Db 601 TGGCATCCGTTTGGTAGAAAATCCAGACTTGGCTCCCAAGCACCACAGCTCATACAC 660
Qy 661 AATGAATACAAAAGACTGGAATCTGCAATTTAATACTGTTTCCAAAATCGGACACTGGAGA 720

Db 661 ATGATACAAAACCTGGAACCTGCAATTTAATATCTGTTCCAACTGGACACTGGAGA 720
Qy 721 ATATTCCTGTGAAGCCCGCAATCTGTGGATATCGCAGGTGCTCGGGAACGAATGCA 780
Db 721 ATATTCCTGTGAAGCCCGCAATCTGTGGATATCGCAGGTGCTCGGGAACGAATGCA 780
Qy 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTAGTTGTGGCCCTTAGTGAT 840
Db 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTAGTTGTGGCCCTTAGTGAT 840
Qy 841 TTCGTTTGTGGCTTGTGTATGCTATGCTCAGAGAAAGGCTACTTTTCAAAGAAAC 900
Db 841 TTCGTTTGTGGCTTGTGTATGCTATGCTCAGAGAAAGGCTACTTTTCAAAGAAAC 900
Qy 901 CTCCTTCCAGAGAGTAATCTTTCATCTAAAGCCAGCAATAGAGTGAATAATGTGCAGTG 960
Db 901 CTCCTTCCAGAGAGTAATCTTTCATCTAAAGCCAGCAATAGAGTGAATAATGTGCAGTG 960
Qy 961 GCTCAGCCTGTAAATCCAGCACTTTTGAAGCGCGCGCGGCGGATCAGAGGTCAAGGA 1020
Db 961 GCTCAGCCTGTAAATCCAGCACTTTTGAAGCGCGCGCGGCGGATCAGAGGTCAAGGA 1020
Qy 1021 GTTCTAGACCAAGCTGSCCAATATGTTGAACCCCATCTCTACTAAATACAAAATTAG 1080
Db 1021 GTTCTAGACCAAGCTGSCCAATATGTTGAACCCCATCTCTACTAAATACAAAATTAG 1080
Qy 1081 CTGGGATGTTGGCATGTGCTGTCAGTTCAGTCTGGGAGACAGGAGAAATCACTTGA 1140
Db 1081 CTGGGATGTTGGCATGTGCTGTCAGTTCAGTCTGGGAGACAGGAGAAATCACTTGA 1140
Qy 1141 ACCGGGAGCGAGGTGTCAGTGAGTACGCGCATCTGCAGTCCAGTCCAGCCTCGGTA 1200
Db 1141 ACCGGGAGCGAGGTGTCAGTGAGTACGCGCATCTGCAGTCCAGTCCAGCCTCGGTA 1200
Qy 1201 CAGAGCAAGATTCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
Db 1201 CAGAGCAAGATTCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
Qy 1261 TGTAGATTCCTTACAATAATATAGCTTGATATTC 1295
Db 1261 TGTAGATTCCTTACAATAATATAGCTTGATATTC 1295

RESULT 7
US-09-904-920A-63
; Sequence 63, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-920A-63

Query Match 100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAGAGTTCAAGGGCCCCCGCCCTCTCGCGCTCTCTCGCGGGACCTCGACCTCT 60
Db 1 CCCAGAGTTCAAGGGCCCCCGCCCTCTCTCGCGCTCTCTCGCGGGACCTCGACCTCT 60
Qy 61 CAGACAGCCGCTGCGCCCGCGGGAAGATGCGAGGAGGAGCCGCGACCTCTCTCT 120
Db 61 CAGACAGCCGCTGCGCCCGCGGGAAGATGCGAGGAGGAGCCGCGACCTCTCTCT 120
Qy 121 GCTGCTGCTGCGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GCTGCTGCTGCGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Qy 181 CCAAAAGACCAACAAAGTAGTCACAGCAGTAGTAGTAGTACCAAGAGGCTATTTTAGCCCTGCAA 240
Db 181 CCAAAAGACCAACAAAGTAGTCACAGCAGTAGTAGTAGTACCAAGAGGCTATTTTAGCCCTGCAA 240
Qy 241 AACCCAAAGAGACTGTTTCTCAGATTAGATTGGAAGAACTGGGTGCGAGGTGCTC 300
Db 241 AACCCAAAGAGACTGTTTCTCAGATTAGATTGGAAGAACTGGGTGCGAGGTGCTC 300
Qy 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATAGA 360
Db 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATAGA 360

Db 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA 360
Qy 361 TTTCAATATCCGATCAAAATGTGACAGAAGTGATGCGGGGAAATATCTGTTGAGT 420
Db 361 TTTCAATATCCGATCAAAATGTGACAGAAGTGATGCGGGGAAATATCTGTTGAGT 420
Qy 421 TAGTGCCCATCTGAGCAAGGCCAAAACCTGGAAAGAGATACAGTCACTCTGGGAAGTATT 480
Db 421 TAGTGCCCATCTGAGCAAGGCCAAAACCTGGAAAGAGATACAGTCACTCTGGGAAGTATT 480
Qy 481 AGTGGCTCCAGCAGTTCATCATGTGAGTACCTCTTCTGCTCTGAGTGAACCTGGT 540
Db 481 AGTGGCTCCAGCAGTTCATCATGTGAGTACCTCTTCTGCTCTGAGTGAACCTGGT 540
Qy 541 AGAGCTACGATGTCAAGCAAAAGAGGAAATCCAGCTCCCTGAATACACATGTTTAAAGGA 600
Db 541 AGAGCTACGATGTCAAGCAAAAGAGGAAATCCAGCTCCCTGAATACACATGTTTAAAGGA 600
Qy 601 TGGCATCCGTTTGTCTAGAAAATCCAGACTTTGGCTCCCAAGCACCAACAGCTCATACAC 660
Db 601 TGGCATCCGTTTGTCTAGAAAATCCAGACTTTGGCTCCCAAGCACCAACAGCTCATACAC 660
Qy 661 AATGAATACAAAATCTGGAATCTGCAATTTAATCTGTTTCCAACTGGACACTGAGGA 720
Db 661 AATGAATACAAAATCTGGAATCTGCAATTTAATCTGTTTCCAACTGGACACTGAGGA 720
Qy 721 ATATTCTGTGAAGCCGCAATCTGTTGGATATCGCAGGTGCTCGGAAACGAATGCA 780
Db 721 ATATTCTGTGAAGCCGCAATCTGTTGGATATCGCAGGTGCTCGGAAACGAATGCA 780
Qy 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT 840
Db 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT 840
Qy 841 TTCGGTTTGTGGCCTTGGTGATGCTATGCTCAGAGAAAGGCTACTTTTCAAAAGAAC 900
Db 841 TTCGGTTTGTGGCCTTGGTGATGCTATGCTCAGAGAAAGGCTACTTTTCAAAAGAAC 900
Qy 901 CTCCTTCCAGAGAGTAAATCTTCTAATGAAGCCAGCAATGAGTGAATGTCAGTG 960
Db 901 CTCCTTCCAGAGAGTAAATCTTCTAATGAAGCCAGCAATGAGTGAATGTCAGTG 960
Qy 961 GCTCAGCCCTGTAATCCAGCACTTTGGAAGCCGCGCGGCGGATCAGAGTCAAGGA 1020
Db 961 GCTCAGCCCTGTAATCCAGCACTTTGGAAGCCGCGCGGCGGATCAGAGTCAAGGA 1020
Qy 1021 GTTCTAGACCACTGCGCCAAATATGGTGAACCCCATCTCTTCTAATAAATCAAAAATTAG 1080
Db 1021 GTTCTAGACCACTGCGCCAAATATGGTGAACCCCATCTCTTCTAATAAATCAAAAATTAG 1080
Qy 1081 CTGGGCATGTGGCATGTGCTGAGTTCAGTTCAGCTGCTTGGGAGACAGAGATCACTTGA 1140
Db 1081 CTGGGCATGTGGCATGTGCTGAGTTCAGTTCAGCTGCTTGGGAGACAGAGATCACTTGA 1140
Qy 1141 ACCCGGAGGCGGAGTTGAGTGCAGTGCAGTCAAGTCAAGCTGAGTCCAGCTGGGTAA 1200
Db 1141 ACCCGGAGGCGGAGTTGAGTGCAGTGCAGTCAAGTCAAGCTGAGTCCAGCTGGGTAA 1200
Qy 1201 CAGAGCAAGATTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
Db 1201 CAGAGCAAGATTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
Qy 1261 TGTGAATCTTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1295
Db 1261 TGTGAATCTTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1295

RESULT 8

US-09-909-064-63
; Sequence 63, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A. Paul J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCES: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-064-63

Query Match 100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCCAGAAAGTTTCAAGGGCCCCGGGCTCTCTGCGCTCTCTGCGCCGGGACCCCTCGACCTCCT	60
Db	1	CCCAGAAAGTTTCAAGGGCCCCGGGCTCTCTGCGCTCTCTGCGCCGGGACCCCTCGACCTCCT	60
Qy	61	CAGAGCAGCGGTGCGCGCCCGGGAAAGATGGCGAGGAGAGCGCGCACCGCTCTCTCCT	120
Db	61	CAGAGCAGCGGTGCGCGCCCGGGAAAGATGGCGAGGAGAGCGCGCACCGCTCTCTCCT	120
Qy	121	GCTGCTGCTCGCTTACCTGCTGCTGCGCTTGGGCTATCATAAAGCCCTATGGGTTTTCGTC	180
Db	121	GCTGCTGCTCGCTTACCTGCTGCTGCGCTTGGGCTATCATAAAGCCCTATGGGTTTTCGTC	180
Qy	181	CCCAAAAGACCAACAGTAGTATCAGCAGTAGAGTACCAAGAGGCTATTTTAGCTGCGAA	240
Db	181	CCCAAAAGACCAACAGTAGTATCAGCAGTAGAGTACCAAGAGGCTATTTTAGCTGCGAA	240
Qy	241	AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGAAGAAACTGGGTCGGAGTGCTC	300
Db	241	AACCCCAAGAGACTGTTTCTCCAGATTAGAGTGAAGAAACTGGGTCGGAGTGCTC	300
Qy	301	CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA	360
Db	301	CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA	360
Qy	361	TTTCAATATCCGGATCAAAAATGTGCAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT	420
Db	361	TTTCAATATCCGGATCAAAAATGTGCAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT	420
Qy	421	TAGTGCCTCATCTGAGCAAGGCCAAAACCTGGAAAGAGATACAGTCACTCTGGAAGTATT	480
Db	421	TAGTGCCTCATCTGAGCAAGGCCAAAACCTGGAAAGAGATACAGTCACTCTGGAAGTATT	480
Qy	481	AGTGGCTCCAGCAGTTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGCT	540
Db	481	AGTGGCTCCAGCAGTTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGCT	540
Qy	541	AGACTACGATGTCAAGCAAGAAGGGAAATCCAGCTCCCTGAATACACATGCTTTAAGGA	600
Db	541	AGACTACGATGTCAAGCAAGAAGGGAAATCCAGCTCCCTGAATACACATGCTTTAAGGA	600
Qy	601	TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGCAACCAAGCTCATACAC	660
Db	601	TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGCAACCAAGCTCATACAC	660
Qy	661	AATGAATACAAAACCTGGAACCTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGA	720
Db	661	AATGAATACAAAACCTGGAACCTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGA	720
Qy	721	ATATTCCTGTGAAGCCGCAATCTGTGTGAATATCGCAGGTGTCCTCGGAAAACGAATGCA	780
Db	721	ATATTCCTGTGAAGCCGCAATCTGTGTGAATATCGCAGGTGTCCTCGGAAAACGAATGCA	780
Qy	781	AGTAGATGATCTCAACATAAGTGCATCATAGCAGCCGTAGTAGTTGTGCGCTTAGTGAT	840
Db	781	AGTAGATGATCTCAACATAAGTGCATCATAGCAGCCGTAGTAGTTGTGCGCTTAGTGAT	840
Qy	841	TTCCGTTTGTGGCCCTTGGTGATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC	900
Db	841	TTCCGTTTGTGGCCCTTGGTGATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC	900
Qy	901	CTCCTTCCAGAAGTAGTAATCTTCATCTAAAGCCACGACAAATGAGTCGAAATGTGCAGTG	960
Db	901	CTCCTTCCAGAAGTAGTAATCTTCATCTAAAGCCACGACAAATGAGTCGAAATGTGCAGTG	960
Qy	961	GCTCAGCCCTGTAAATCCAGCACTTTTGGAAAGCCGCGCGCGGATCAGAGGTCAAGGA	1020
Db	961	GCTCAGCCCTGTAAATCCAGCACTTTTGGAAAGCCGCGCGCGGATCAGAGGTCAAGGA	1020
Qy	1021	GTTCTAGACAGTCTGGCCAAATATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAG	1080
Db	1021	GTTCTAGACAGTCTGGCCAAATATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAG	1080

[illegible]

CURRENT APPLICATION NUMBER: US/09/906,618		US-09-906-618-63	
CURRENT FILING DATE: 2001-07-16		SEQ ID NO 63	
PRIOR APPLICATION NUMBER: PCT/US00/04414		LENGTH: 1295	
PRIOR FILING DATE: 2000-02-22		TYPE: DNA	
PRIOR APPLICATION NUMBER: US 60/143,048		ORGANISM: Homo sapiens	
PRIOR FILING DATE: 1999-07-07		US-09-906-618-63	
PRIOR APPLICATION NUMBER: US 60/145,698		Query Match	
PRIOR FILING DATE: 1999-07-26		Best Local Similarity 100.0%; Score 1295; DB 3; Length 1295;	
PRIOR APPLICATION NUMBER: US 60/146,222		Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PRIOR FILING DATE: 1999-07-28		Query	
PRIOR APPLICATION NUMBER: PCT/US99/20594		Db	
PRIOR FILING DATE: 1999-09-08		Query	
PRIOR APPLICATION NUMBER: PCT/US99/20944		Db	
PRIOR FILING DATE: 1999-09-13		Query	
PRIOR APPLICATION NUMBER: PCT/US99/21090		Db	
PRIOR FILING DATE: 1999-09-15		Query	
PRIOR APPLICATION NUMBER: PCT/US99/21547		Db	
PRIOR FILING DATE: 1999-09-15		Query	
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PRIOR APPLICATION NUMBER: PCT/US99/28214		Db	
PRIOR FILING DATE: 1999-11-29		Query	
PRIOR APPLICATION NUMBER: PCT/US99/28313		Db	
PRIOR FILING DATE: 1999-11-30		Query	
PRIOR APPLICATION NUMBER: PCT/US99/28564		Db	
PRIOR FILING DATE: 1999-12-02		Query	
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PRIOR FILING DATE: 1999-12-16		Query	
PRIOR APPLICATION NUMBER: PCT/US99/30911		Db	
PRIOR FILING DATE: 1999-12-20		Query	
PRIOR APPLICATION NUMBER: PCT/US99/30999		Db	
PRIOR FILING DATE: 1999-12-20		Query	
PRIOR APPLICATION NUMBER: PCT/US00/00219		Db	
PRIOR FILING DATE: 2000-01-05		Query	
NUMBER OF SEQ ID NOS: 423		Db	
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 63
LENGTH: 1295
TYPE: DNA
ORGANISM: Homo sapiens
US-09-906-646-63

Query Match 100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAAGATTCAAGGGCCCGGCTCTCTCGCTCTCTGCGCGGACCCCTCGACCTCCT 60
DB 1 CCCAAGATTCAAGGGCCCGGCTCTCTCGCTCTCTGCGCGGACCCCTCGACCTCCT 60

QY 61 CAGACAGCGGCTGCGCGCCCGGGAAGATGGCAGAGAGAGCGCCACCGCTCTCTCT 120
DB 61 CAGACAGCGGCTGCGCGCCCGGGAAGATGGCAGAGAGAGCGCCACCGCTCTCTCT 120

QY 121 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

QY 181 CCCAAAGACCAACAGTAGTACAGCAGTAGTACAGCAGTAGTACAGCAGTAGTACAGC 240
DB 181 CCCAAAGACCAACAGTAGTACAGCAGTAGTACAGCAGTAGTACAGCAGTAGTACAGC 240

QY 241 AACCCCAAGAAGACTGTTTCTCCAGATTAGAGTGGAGAAJACTGGGTGCGAGTGTCTC 300
DB 241 AACCCCAAGAAGACTGTTTCTCCAGATTAGAGTGGAGAAJACTGGGTGCGAGTGTCTC 300

QY 301 CTTTGCTACTATCAACAGACTCTTCAAGTGATTTTAAATTCGAGCTGAGATGATAGA 360

RESULT 13
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; Sequence 63, Application US/09904462
; Patent No. 687807
; GENERAL INFORMATION:

Db 301 CTTTGCTACTATCAACAGACTCTTCAAGTGATTTTAAATTCGAGCTGAGATGATAGA 360
QY 361 TTTCAATATCCGATCAAAAATGTGCAAGAGTGTGCGGGAAATATCGTTGTGAAGT 420
Db 361 TTTCAATATCCGATCAAAAATGTGCAAGAGTGTGCGGGAAATATCGTTGTGAAGT 420
QY 421 TAGTGGCCCATCTGAGCAGGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT 480
Db 421 TAGTGGCCCATCTGAGCAGGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT 480
QY 481 AGTGGCTCCAGCAGTTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGT 540
Db 481 AGTGGCTCCAGCAGTTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGT 540
QY 541 AGAGCTACGATGTCAAGACAAAAGAGGGAATCCAGCTCTCTGAATACACATGTTTAAAGGA 600
Db 541 AGAGCTACGATGTCAAGACAAAAGAGGGAATCCAGCTCTCTGAATACACATGTTTAAAGGA 600
QY 601 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGCACCACAGCTCATACAC 660
Db 601 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGCACCACAGCTCATACAC 660
QY 661 AATGAATACAAAACCTGGAACCTCTGCAATTTAATCTGTTTCCAACTCGACACTGCGAGA 720
Db 661 AATGAATACAAAACCTGGAACCTCTGCAATTTAATCTGTTTCCAACTCGACACTGCGAGA 720
QY 721 ATATTCCTGTGAAGCCCGCAATTTCTGTTGGATATCGCAGGTGTCTGGGAAACGAATGCA 780
Db 721 ATATTCCTGTGAAGCCCGCAATTTCTGTTGGATATCGCAGGTGTCTGGGAAACGAATGCA 780
QY 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCCTTAGTGAT 840
Db 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCCTTAGTGAT 840
QY 841 TTCCGTTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAAC 900
Db 841 TTCCGTTTGTGGCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAAGAAAC 900
QY 901 CTCCTTCCAGAAGAGTAATTTCTTCATCTAAAGCCACGACAAATGAGTGAAGATGTGCAGTG 960
Db 901 CTCCTTCCAGAAGAGTAATTTCTTCATCTAAAGCCACGACAAATGAGTGAAGATGTGCAGTG 960
QY 961 GCTCAGCCCTTAATCCAGACACTTTTGGAGCCCGCGGCGGATCAGAGGTCAGGA 1020
Db 961 GCTCAGCCCTTAATCCAGACACTTTTGGAGCCCGCGGCGGATCAGAGGTCAGGA 1020
QY 1021 GTTCTAGACAGCTTGGCCCAATATGTTGAAACCCCATCTCTACTAAATATCAAAAATTAG 1080
Db 1021 GTTCTAGACAGCTTGGCCCAATATGTTGAAACCCCATCTCTACTAAATATCAAAAATTAG 1080
QY 1081 CTGGGCATGGTGGCATGTGCTGCGAGTCCAGTGTCTGGGAGACAGGAGAAATCACTTGA 1140
Db 1081 CTGGGCATGGTGGCATGTGCTGCGAGTCCAGTGTCTGGGAGACAGGAGAAATCACTTGA 1140
QY 1141 ACCCGGAGCGGAGGTTGCGAGTGGATCAGCCACTGCGAGTCCAGCCCTGGGTAA 1200
Db 1141 ACCCGGAGCGGAGGTTGCGAGTGGATCAGCCACTGCGAGTCCAGCCCTGGGTAA 1200
QY 1201 CAGAGCAAGATTCCCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
Db 1201 CAGAGCAAGATTCCCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
QY 1261 TGTAGAAATTTTACAAATAAATATAGCTTGATATTC 1295
Db 1261 TGTAGAAATTTTACAAATAAATATAGCTTGATATTC 1295


```

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,462
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-462-63

Query Match      100.0%; Score 1295; DB 3; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  CCAGAAAGTTCAAGGGGCGCGGCTCTCTGGGCTCTCTGGCGCTCTGGCGCGGGAGACCCCTCGACCTCTCT 60

Qy      61  CAGAGCAGCGGCTGCGCGCGCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCTCTCTCT 120
Db      61  CAGAGCAGCGGCTGCGCGCGCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCTCTCTCTCT 120

Qy     121  GCTGCTCTGCGCTACCTGGTGGTGGCTGCGCTGCGCTATCATAGGCTATATGGTCTCTGTC 180
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Db     181  CCAGAAAGACCAAGTAGTACAGCAGTAGATACCAAGAGGCTATTTTAGCTGCA 240

Qy     241  AACCCCAAGAGACTGTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTC 300
Db     241  AACCCCAAGAGACTGTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTC 300

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Qy     661  AATGAATACAAAACCTGGAATCTGCAATTTAATACTGTTTCCAACTGGACACTGGAGA 720
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Qy	541	AGAGCTACGATGTCAAGCAAAAGAGGAATCCAGCTCCTGGAATACACATGGTTTAAGGA	600
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Qy	661	AATGAATACAAAACCTGGAACTCTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGA	720
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Qy	721	ATATTCTGTGAAGCCCGCAATTCTGTGGATATCGCAGGTGTCTGGGAAACGAATGCA	780
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Qy	781	AGTAGATGATCTCAACATAGTGGCATCATAGCAGCGTAGTAGTTGTGGCCCTTAGTGAT	840
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SUMMARIES

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c 606	61	4.7	1330	12	US-10-301-480-95003	Sequence 95003, A
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C 623	58	4.5	569	12	US-10-301-480-224444	Sequence 224444,	C 696	51	3.9	201	9	US-10-741-600-41705	Sequence 41705, A
C 624	58	4.5	569	12	US-10-301-480-224446	Sequence 224446,	C 697	51	3.9	605	4	US-09-925-065A-918409	Sequence 918409,
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C 645	56	4.3	135005	9	US-10-723-860-2320	Sequence 2320, Ap	C 718	51	3.9	73063	11	US-10-330-773-704	Sequence 704, App
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C 655	54	4.2	889	12	US-10-301-480-84583	Sequence 84583, A	C 728	50	3.9	112	7	US-10-227-577-1574	Sequence 1574, Ap
C 656	54	4.2	889	12	US-10-301-480-84584	Sequence 84584, A	C 729	50	3.9	112	7	US-10-227-577-1575	Sequence 1575, Ap
C 657	54	4.2	889	12	US-10-301-480-697992	Sequence 697992,	C 730	50	3.9	201	9	US-10-719-993-14307	Sequence 14307, A
C 658	54	4.2	889	12	US-10-301-480-697993	Sequence 697993,	C 731	50	3.9	364	3	US-09-918-995-8878	Sequence 8878, Ap
C 659	53	4.1	465	3	US-09-918-995-15855	Sequence 15855, A	C 732	50	3.9	427	9	US-10-674-124A-23623	Sequence 23623, A
C 660	53	4.1	483	3	US-09-918-995-1619	Sequence 1619, Ap	C 733	50	3.9	434	9	US-10-357-930-50333	Sequence 50333, A
C 661	53	4.1	6644	7	US-10-308-460-14	Sequence 55470, A	C 734	50	3.9	498	4	US-09-925-065A-674396	Sequence 674396,
C 662	52	4.0	539	10	US-10-995-561-55470	Sequence 55470, A	C 735	50	3.9	498	5	US-09-925-065A-674396	Sequence 674396,
C 663	52	4.0	539	5	US-09-925-065A-355882	Sequence 355882,	C 736	50	3.9	501	6	US-10-027-632-130916	Sequence 130916,
C 664	52	4.0	539	5	US-09-925-065A-355882	Sequence 355882,	C 737	50	3.9	501	7	US-10-027-632-130916	Sequence 130916,
C 665	52	4.0	544	12	US-10-301-480-427361	Sequence 427361,	C 738	50	3.9	566	4	US-09-925-065A-929733	Sequence 929733,
C 666	52	4.0	544	12	US-10-301-480-1040770	Sequence 1040770,	C 739	50	3.9	566	4	US-09-925-065A-939565	Sequence 939565,
C 667	52	4.0	595	5	US-09-925-065A-232924	Sequence 232924,	C 740	50	3.9	566	5	US-09-925-065A-929733	Sequence 929733,
C 668	52	4.0	595	5	US-09-925-065A-232924	Sequence 232924,	C 741	50	3.9	566	5	US-09-925-065A-929733	Sequence 929733,
C 669	52	4.0	740	6	US-10-027-632-169689	Sequence 169689,	C 742	50	3.9	566	5	US-09-925-065A-939565	Sequence 939565,
C 670	52	4.0	740	6	US-10-027-632-169690	Sequence 169690,	C 743	50	3.9	566	5	US-09-925-065A-939565	Sequence 939565,
C 671	52	4.0	740	7	US-10-027-632-169689	Sequence 169689,	C 744	50	3.9	570	5	US-09-925-065A-930825	Sequence 930825,
C 672	52	4.0	822	4	US-09-925-065A-726512	Sequence 726512,	C 745	50	3.9	570	5	US-09-925-065A-930825	Sequence 930825,
C 673	52	4.0	822	4	US-09-925-065A-726512	Sequence 726512,	C 746	50	3.9	588	12	US-10-301-480-374665	Sequence 374665,
C 674	52	4.0	822	5	US-09-925-065A-726512	Sequence 726512,	C 747	50	3.9	588	12	US-10-301-480-988074	Sequence 988074,
C 675	52	4.0	1341	4	US-09-925-065A-547257	Sequence 547257,	C 748	50	3.9	607	4	US-09-925-065A-877474	Sequence 877474,
C 676	52	4.0	1341	5	US-09-925-065A-547257	Sequence 547257,	C 749	50	3.9	607	4	US-09-925-065A-877475	Sequence 877475,
C 677	52	4.0	1341	12	US-10-301-480-525207	Sequence 525207,	C 750	50	3.9	607	4	US-09-925-065A-906290	Sequence 906290,
C 678	52	4.0	1341	12	US-10-301-480-1138616	Sequence 1138616,	C 751	50	3.9	607	5	US-09-925-065A-877474	Sequence 877474,
C 679	52	4.0	2258	4	US-09-925-065A-685536	Sequence 685536,	C 752	50	3.9	607	5	US-09-925-065A-877475	Sequence 877475,
C 680	52	4.0	2258	4	US-09-925-065A-685536	Sequence 685536,	C 753	50	3.9	607	5	US-09-925-065A-906290	Sequence 906290,
C 681	52	4.0	21010	3	US-09-764-891-8576	Sequence 8576, Ap	C 754	50	3.9	624	4	US-09-925-065A-955973	Sequence 955973,
C 682	52	4.0	21024	3	US-09-764-891-8577	Sequence 8577, Ap	C 755	50	3.9	624	5	US-09-925-065A-955973	Sequence 955973,

c 756	50	3.9	633	4	US-09-925-065A-935565	Sequence 935565,	c 829	50	3.9	65608	3	US-09-954-531-180	Sequence 180, App
c 757	50	3.9	633	4	US-09-925-065A-953019	Sequence 953019,	c 830	50	3.9	65608	10	US-10-843-641A-1247	Sequence 1247, Ap
c 758	50	3.9	633	5	US-09-925-065A-935565	Sequence 935565,	c 831	50	3.9	65608	10	US-10-843-641A-2751	Sequence 2751, Ap
c 759	50	3.9	633	5	US-09-925-065A-953019	Sequence 953019,	c 832	50	3.9	65608	10	US-10-843-641A-6005	Sequence 6005, Ap
c 760	50	3.9	646	4	US-09-925-065A-908933	Sequence 908933,	c 833	50	3.9	92199	16	US-11-114-798-50	Sequence 50, Appl
c 761	50	3.9	646	4	US-09-925-065A-908934	Sequence 908934,	c 834	50	3.9	110608	9	US-10-775-169-193	Sequence 193, App
c 762	50	3.9	646	5	US-09-925-065A-908933	Sequence 908933,	c 835	50	3.9	110608	10	US-10-775-169-193	Sequence 193, App
c 763	50	3.9	646	5	US-09-925-065A-908934	Sequence 908934,	c 836	50	3.9	115935	9	US-10-775-169-241	Sequence 241, App
c 764	50	3.9	702	6	US-10-027-632-161735	Sequence 161735,	c 837	50	3.9	115935	10	US-10-775-169-241	Sequence 241, App
c 765	50	3.9	702	7	US-10-027-632-161735	Sequence 161735,	c 838	50	3.9	132279	10	US-10-756-149-3596	Sequence 3596, Ap
c 766	50	3.9	841	12	US-10-301-480-542833	Sequence 542833,	c 839	50	3.9	139214	6	US-10-087-192-2038	Sequence 2038, Ap
c 767	50	3.9	841	12	US-10-301-480-1156242	Sequence 1156242,	c 840	50	3.9	139214	9	US-10-331-053-56	Sequence 56, Appl
c 768	50	3.9	911	4	US-09-925-065A-716014	Sequence 716014,	c 841	50	3.9	150298	10	US-10-981-277-52	Sequence 52, Appl
c 769	50	3.9	911	5	US-09-925-065A-716014	Sequence 716014,	c 842	50	3.9	150298	10	US-10-981-277-52	Sequence 52, Appl
c 770	50	3.9	997	12	US-10-301-480-605653	Sequence 605653,	c 843	50	3.9	150525	10	US-10-981-277-36	Sequence 3, Appl
c 771	50	3.9	997	12	US-10-301-480-605653	Sequence 605653,	c 844	50	3.9	163350	10	US-10-469-052-3	Sequence 53, Appl
c 772	50	3.9	1048	4	US-09-925-065A-1219062	Sequence 1219062,	c 845	50	3.9	164910	10	US-10-981-277-53	Sequence 35, Appl
c 773	50	3.9	1048	4	US-09-925-065A-37591	Sequence 37591, A	c 846	50	3.9	166536	10	US-10-981-277-53	Sequence 35, Appl
c 774	50	3.9	1048	4	US-09-925-065A-37592	Sequence 37592, A	c 847	50	3.9	171732	15	US-11-121-086-98	Sequence 98, Appl
c 775	50	3.9	1048	4	US-09-925-065A-37592	Sequence 37592, A	c 848	50	3.9	191150	12	US-10-517-905-19	Sequence 19, Appl
c 776	50	3.9	1048	4	US-09-925-065A-37594	Sequence 37594, A	c 849	50	3.9	196151	10	US-10-981-277-51	Sequence 51, Appl
c 777	50	3.9	1048	4	US-09-925-065A-37594	Sequence 37594, A	c 850	50	3.9	207600	15	US-11-112-908-31	Sequence 31, Appl
c 778	50	3.9	1048	5	US-09-925-065A-37595	Sequence 37595, A	c 851	50	3.9	215308	15	US-11-121-086-77	Sequence 77, Appl
c 779	50	3.9	1048	5	US-09-925-065A-37590	Sequence 37590, A	c 852	50	3.9	238417	9	US-10-461-862-98	Sequence 98, Appl
c 780	50	3.9	1048	5	US-09-925-065A-37591	Sequence 37591, A	c 853	50	3.9	252907	9	US-10-417-375-66	Sequence 66, Appl
c 781	50	3.9	1048	5	US-09-925-065A-37592	Sequence 37592, A	c 854	50	3.9	318488	16	US-11-114-798-58	Sequence 58, Appl
c 782	50	3.9	1048	5	US-09-925-065A-37594	Sequence 37594, A	c 855	50	3.9	333702	6	US-10-087-192-292	Sequence 292, App
c 783	50	3.9	1048	5	US-09-925-065A-37595	Sequence 37595, A	c 856	49	3.8	393999	9	US-10-719-993-6787	Sequence 6787, Ap
c 784	50	3.9	1048	12	US-10-301-480-138828	Sequence 138828,	c 857	49	3.8	282	9	US-10-674-124A-9184	Sequence 9184, Ap
c 785	50	3.9	1048	12	US-10-301-480-138828	Sequence 138828,	c 858	49	3.8	432	9	US-10-357-930-57737	Sequence 57737, A
c 786	50	3.9	1048	12	US-10-301-480-138830	Sequence 138830,	c 859	49	3.8	454	12	US-10-301-480-20970	Sequence 20970, A
c 787	50	3.9	1048	12	US-10-301-480-138831	Sequence 138831,	c 860	49	3.8	454	12	US-10-301-480-634379	Sequence 634379, A
c 788	50	3.9	1048	12	US-10-301-480-138832	Sequence 138832,	c 861	49	3.8	466	6	US-10-027-632-92981	Sequence 92981, A
c 789	50	3.9	1048	12	US-10-301-480-138832	Sequence 138832,	c 862	49	3.8	466	6	US-10-027-632-92982	Sequence 92982, A
c 790	50	3.9	1048	12	US-10-301-480-752237	Sequence 752237,	c 863	49	3.8	466	7	US-10-027-632-92982	Sequence 92982, A
c 791	50	3.9	1048	12	US-10-301-480-752238	Sequence 752238,	c 864	49	3.8	468	6	US-10-027-632-307672	Sequence 307672,
c 792	50	3.9	1048	12	US-10-301-480-752239	Sequence 752239,	c 865	49	3.8	468	6	US-10-027-632-307672	Sequence 307672,
c 793	50	3.9	1048	12	US-10-301-480-752240	Sequence 752240,	c 866	49	3.8	468	7	US-10-027-632-307672	Sequence 307672,
c 794	50	3.9	1048	12	US-10-301-480-752241	Sequence 752241,	c 867	49	3.8	468	7	US-10-027-632-307673	Sequence 307673,
c 795	50	3.9	1048	12	US-10-301-480-752242	Sequence 752242,	c 868	49	3.8	472	8	US-10-242-535A-29966	Sequence 29966, A
c 796	50	3.9	1170	4	US-09-925-065A-297981	Sequence 297981,	c 869	49	3.8	472	8	US-10-085-783A-29966	Sequence 29966, A
c 797	50	3.9	1170	5	US-09-925-065A-297981	Sequence 297981,	c 870	49	3.8	519	4	US-09-925-065A-89325	Sequence 89325, A
c 798	50	3.9	1202	4	US-09-925-065A-26821	Sequence 26821, A	c 871	49	3.8	519	5	US-09-925-065A-89325	Sequence 89325, A
c 799	50	3.9	1202	4	US-09-925-065A-26822	Sequence 26822, A	c 872	49	3.8	519	12	US-10-301-480-190566	Sequence 190566,
c 800	50	3.9	1202	5	US-09-925-065A-26821	Sequence 26821, A	c 873	49	3.8	519	12	US-10-301-480-803975	Sequence 803975,
c 801	50	3.9	1202	5	US-09-925-065A-26822	Sequence 26822, A	c 874	49	3.8	567	4	US-09-925-065A-602639	Sequence 602639,
c 802	50	3.9	1202	12	US-10-301-480-128058	Sequence 128058,	c 875	49	3.8	567	5	US-09-925-065A-602639	Sequence 602639,
c 803	50	3.9	1202	12	US-10-301-480-128059	Sequence 128059,	c 876	49	3.8	577	4	US-09-925-065A-921845	Sequence 921845,
c 804	50	3.9	1202	12	US-10-301-480-741467	Sequence 741467,	c 877	49	3.8	577	5	US-09-925-065A-921845	Sequence 921845,
c 805	50	3.9	1202	12	US-10-301-480-741468	Sequence 741468,	c 878	49	3.8	581	4	US-09-925-065A-479824	Sequence 479824,
c 806	50	3.9	1683	4	US-09-925-065A-70243	Sequence 70243, A	c 879	49	3.8	581	5	US-09-925-065A-479824	Sequence 479824,
c 807	50	3.9	1683	5	US-09-925-065A-70243	Sequence 70243, A	c 880	49	3.8	617	4	US-09-925-065A-604899	Sequence 604899,
c 808	50	3.9	1683	12	US-10-301-480-171482	Sequence 171482,	c 881	49	3.8	617	5	US-09-925-065A-604899	Sequence 604899,
c 809	50	3.9	1683	12	US-10-301-480-784891	Sequence 784891,	c 882	49	3.8	644	4	US-09-925-065A-76464	Sequence 76464, A
c 810	50	3.9	2380	5	US-09-925-065A-723952	Sequence 723952,	c 883	49	3.8	644	4	US-09-925-065A-76465	Sequence 76465, A
c 811	50	3.9	2380	5	US-09-925-065A-723952	Sequence 723952,	c 884	49	3.8	644	5	US-09-925-065A-76465	Sequence 76465, A
c 812	50	3.9	3313	6	US-10-027-632-115843	Sequence 115843,	c 885	49	3.8	644	5	US-09-925-065A-76465	Sequence 76465, A
c 813	50	3.9	3313	6	US-10-027-632-115843	Sequence 115843,	c 886	49	3.8	644	12	US-10-301-480-177703	Sequence 177703,
c 814	50	3.9	3655	6	US-10-027-632-259680	Sequence 259680,	c 887	49	3.8	644	12	US-10-301-480-177704	Sequence 177704,
c 815	50	3.9	3655	7	US-10-027-632-259680	Sequence 259680,	c 888	49	3.8	644	12	US-10-301-480-791112	Sequence 791112,
c 816	50	3.9	3655	12	US-10-301-480-94488	Sequence 94488, A	c 889	49	3.8	644	12	US-10-301-480-791113	Sequence 791113,
c 817	50	3.9	3655	12	US-10-301-480-707897	Sequence 707897,	c 890	49	3.8	646	6	US-10-027-632-273304	Sequence 273304,
c 818	50	3.9	18722	8	US-10-377-749A-1	Sequence 1,	c 891	49	3.8	646	7	US-10-027-632-273304	Sequence 273304,
c 819	50	3.9	33112	8	US-10-429-873A-3	Sequence 3, Appli	c 892	49	3.8	646	7	US-09-925-065A-934233	Sequence 934233,
c 820	50	3.9	33112	13	US-11-134-465-3	Sequence 3, Appli	c 893	49	3.8	648	4	US-09-925-065A-934233	Sequence 934233,
c 821	50	3.9	37225	10	US-10-756-149-4170	Sequence 4170, Ap	c 894	49	3.8	648	5	US-09-925-065A-934233	Sequence 934233,
c 822	50	3.9	38045	10	US-10-493-759-6	Sequence 6, Appli	c 895	49	3.8	648	5	US-09-925-065A-934234	Sequence 934234,
c 823	50	3.9	38045	10	US-10-493-759-6	Sequence 6, Appli	c 896	49	3.8	648	6	US-10-027-632-143036	Sequence 143036,
c 824	50	3.9	46193	9	US-10-719-993-6789	Sequence 6789, Ap	c 897	49	3.8	648	7	US-10-027-632-143036	Sequence 143036,
c 825	50	3.9	52510	6	US-10-087-192-1006	Sequence 1006, Ap	c 898	49	3.8	652	10	US-10-779-543-19679	Sequence 19679, A
c 826	50	3.9	60940	8	US-10-052-482-88	Sequence 88, Appl	c 899	49	3.8	653	4	US-09-925-065A-695143	Sequence 695143,
c 827	50	3.9	65608	3	US-09-962-436-292	Sequence 292, App	c 900	49	3.8	653	5	US-09-925-065A-695143	Sequence 695143,
c 828	50	3.9	65608	3	US-09-962-832-119	Sequence 119, App	c 901	49	3.8	657	4	US-09-925-065A-477123	Sequence 477123,

C 902	49	3.8	657	4	US-09-925-065A-477124	Sequence 477124,	1044	48	3.7	48	8	US-10-767-904-30	Sequence 30, Appl
C 903	49	3.8	657	4	US-09-925-065A-477125	Sequence 477125,	1045	48	3.7	48	9	US-10-771-187-67	Sequence 67, Appl
C 904	49	3.8	657	5	US-09-925-065A-477123	Sequence 477123,	1046	48	3.7	48	9	US-10-767-374-30	Sequence 30, Appl
C 905	49	3.8	657	5	US-09-925-065A-477124	Sequence 477124,	1047	48	3.7	48	9	US-10-785-607-30	Sequence 30, Appl
C 906	49	3.8	657	5	US-09-925-065A-477125	Sequence 477125,	1048	48	3.7	48	10	US-10-963-467-67	Sequence 67, Appl
C 907	49	3.8	672	4	US-09-925-065A-901122	Sequence 901122, A	1049	48	3.7	48	10	US-10-978-255-67	Sequence 67, Appl
C 908	49	3.8	672	5	US-09-925-065A-90122	Sequence 90122, A	1050	48	3.7	48	10	US-10-970-823-67	Sequence 67, Appl
C 909	49	3.8	672	12	US-10-301-480-191363	Sequence 191363,	c1051	48	3.7	201	8	US-10-741-601-6129	Sequence 6129, Ap
C 910	49	3.8	672	12	US-10-301-480-804772	Sequence 804772,	c1052	48	3.7	201	9	US-10-741-600-67902	Sequence 67902, A
C 911	49	3.8	704	6	US-10-027-632-132625	Sequence 132625,	1053	48	3.7	201	10	US-10-995-561-75501	Sequence 75501, A
C 912	49	3.8	704	7	US-10-027-632-132625	Sequence 132625,	1054	48	3.7	433	10	US-10-779-543-17440	Sequence 17440, A
C 913	49	3.8	711	6	US-10-027-632-25186	Sequence 25186, A	1055	48	3.7	541	12	US-10-301-480-574754	Sequence 574754,
C 914	49	3.8	711	6	US-10-027-632-25186	Sequence 25186, A	1056	48	3.7	541	12	US-10-301-480-574754	Sequence 574754,
C 915	49	3.8	711	7	US-10-027-632-25186	Sequence 25186, A	c1057	48	3.7	549	6	US-10-027-632-169700	Sequence 169700,
C 916	49	3.8	711	7	US-10-027-632-25186	Sequence 25186, A	c1058	48	3.7	549	6	US-10-027-632-169700	Sequence 169700,
C 917	49	3.8	772	4	US-09-925-065A-921133	Sequence 921133,	c1059	48	3.7	549	7	US-10-027-632-169701	Sequence 169701,
C 918	49	3.8	772	5	US-09-925-065A-921133	Sequence 921133,	c1060	48	3.7	549	7	US-10-027-632-169701	Sequence 169701,
C 919	49	3.8	992	12	US-10-301-480-596796	Sequence 596796,	c1061	48	3.7	569	4	US-09-925-065A-87941	Sequence 87941, A
C 920	49	3.8	992	12	US-10-301-480-1210205	Sequence 1210205,	c1062	48	3.7	569	5	US-09-925-065A-87941	Sequence 87941, A
C 921	49	3.8	1372	4	US-09-925-065A-4121	Sequence 4121, Ap	c1063	48	3.7	569	12	US-10-301-480-809182	Sequence 809182,
C 922	49	3.8	1372	4	US-09-925-065A-4122	Sequence 4122, Ap	c1064	48	3.7	569	12	US-10-301-480-809182	Sequence 809182,
C 923	49	3.8	1372	4	US-09-925-065A-4123	Sequence 4123, Ap	1065	48	3.7	575	12	US-09-925-065A-74613	Sequence 74613, A
C 924	49	3.8	1372	4	US-09-925-065A-4124	Sequence 4124, Ap	1066	48	3.7	575	5	US-09-925-065A-74613	Sequence 74613, A
C 925	49	3.8	1372	5	US-09-925-065A-4124	Sequence 4124, Ap	1067	48	3.7	575	12	US-10-301-480-175852	Sequence 175852,
C 926	49	3.8	1372	5	US-09-925-065A-4122	Sequence 4122, Ap	1068	48	3.7	575	12	US-10-301-480-789261	Sequence 789261,
C 927	49	3.8	1372	5	US-09-925-065A-4123	Sequence 4123, Ap	1069	48	3.7	595	4	US-09-925-065A-4237	Sequence 4237, Ap
C 928	49	3.8	1372	5	US-09-925-065A-4124	Sequence 4124, Ap	1070	48	3.7	595	4	US-09-925-065A-4237	Sequence 4237, Ap
C 929	49	3.8	1372	12	US-10-301-480-105358	Sequence 105358,	1071	48	3.7	595	12	US-10-301-480-105474	Sequence 105474,
C 930	49	3.8	1372	12	US-10-301-480-105358	Sequence 105358,	1072	48	3.7	595	12	US-10-301-480-105474	Sequence 105474,
C 931	49	3.8	1372	12	US-10-301-480-105360	Sequence 105360,	c1073	48	3.7	619	12	US-10-301-480-565667	Sequence 565667,
C 932	49	3.8	1372	12	US-10-301-480-105361	Sequence 105361,	c1074	48	3.7	619	12	US-10-301-480-1179076	Sequence 1179076,
C 933	49	3.8	1372	12	US-10-301-480-105360	Sequence 105360,	c1075	48	3.7	620	4	US-09-925-065A-36439	Sequence 36439, A
C 934	49	3.8	1372	12	US-10-301-480-105360	Sequence 105360,	c1076	48	3.7	620	5	US-09-925-065A-36439	Sequence 36439, A
C 935	49	3.8	1372	12	US-10-301-480-105360	Sequence 105360,	c1077	48	3.7	620	12	US-10-301-480-137677	Sequence 137677,
C 936	49	3.8	1372	12	US-10-301-480-105360	Sequence 105360,	c1078	48	3.7	620	12	US-10-301-480-137677	Sequence 137677,
C 937	49	3.8	1841	3	US-09-798-889-40	Sequence 718770,	1079	48	3.7	628	12	US-10-301-480-562157	Sequence 562157,
C 938	49	3.8	1841	3	US-09-798-889-40	Sequence 718770,	1080	48	3.7	628	12	US-10-301-480-562157	Sequence 562157,
C 939	49	3.8	3004	7	US-10-633-680-40	Sequence 40, Appl	1081	48	3.7	641	4	US-09-925-065A-427368	Sequence 427368,
C 940	49	3.8	3004	16	US-11-072-513-99	Sequence 99, Appl	1082	48	3.7	641	4	US-09-925-065A-427369	Sequence 427369,
C 941	49	3.8	25138	9	US-10-832-777-18	Sequence 18, Appl	1083	48	3.7	641	4	US-09-925-065A-427370	Sequence 427370,
C 942	49	3.8	25138	9	US-10-832-777-18	Sequence 18, Appl	1084	48	3.7	641	5	US-09-925-065A-427368	Sequence 427368,
C 943	49	3.8	56181	11	US-10-330-6228-18	Sequence 18, Appl	1085	48	3.7	641	5	US-09-925-065A-427369	Sequence 427369,
C 944	49	3.8	56181	11	US-10-330-6228-18	Sequence 18, Appl	1086	48	3.7	641	5	US-09-925-065A-427370	Sequence 427370,
C 945	49	3.8	62001	8	US-10-316-459-13	Sequence 13, Appl	1087	48	3.7	644	12	US-10-301-480-490709	Sequence 490709,
C 946	49	3.8	81001	3	US-10-052-482-124	Sequence 124, Appl	1088	48	3.7	644	12	US-10-301-480-490710	Sequence 490710,
C 947	49	3.8	81001	3	US-09-751-877-1	Sequence 1, Appl	1089	48	3.7	644	12	US-10-301-480-490710	Sequence 490710,
C 948	49	3.8	81001	3	US-09-842-364-1	Sequence 1, Appl	1090	48	3.7	644	12	US-10-301-480-1104118	Sequence 1104118,
C 949	49	3.8	81001	8	US-09-751-877-1	Sequence 1, Appl	c1091	48	3.7	649	4	US-09-925-065A-430814	Sequence 430814,
C 950	49	3.8	81001	9	US-10-121-034-1	Sequence 1, Appl	c1092	48	3.7	649	5	US-09-925-065A-430814	Sequence 430814,
C 951	49	3.8	105219	6	US-10-087-192-658	Sequence 658, App	c1093	48	3.7	724	4	US-09-925-065A-948472	Sequence 948472,
C 952	49	3.8	108316	7	US-10-292-798-1789	Sequence 1789, Ap	c1094	48	3.7	724	5	US-09-925-065A-948472	Sequence 948472,
C 953	49	3.8	108317	7	US-10-017-161-2143	Sequence 2143, Ap	1095	48	3.7	919	12	US-10-301-480-612363	Sequence 612363,
C 954	49	3.8	139214	6	US-10-087-192-2038	Sequence 2038, Ap	1096	48	3.7	919	12	US-10-301-480-612363	Sequence 612363,
C 955	49	3.8	141079	9	US-10-331-053-56	Sequence 56, Appl	1097	48	3.7	998	12	US-10-301-480-1225772	Sequence 1225772,
C 956	49	3.8	155937	9	US-10-723-860-2208	Sequence 2208, Ap	1098	48	3.7	998	12	US-10-301-480-591915	Sequence 591915,
C 957	49	3.8	188971	9	US-10-235-192A-27	Sequence 27, Appl	c1099	48	3.7	2088	6	US-10-027-632-98072	Sequence 98072, A
C 958	49	3.8	230101	9	US-10-719-993-6829	Sequence 6829, Ap	c1100	48	3.7	2088	7	US-10-027-632-98072	Sequence 98072, A
C 959	48	3.7	48	3	US-09-905-291A-67	Sequence 67, Appl	c1101	48	3.7	10256	6	US-10-092-154-1182	Sequence 1182, Ap
C 960	48	3.7	48	3	US-09-953-499-30	Sequence 30, Appl	c1102	48	3.7	10256	6	US-10-092-154-1182	Sequence 1182, Ap
C 961	48	3.7	48	7	US-10-265-542-30	Sequence 30, Appl	c1103	48	3.7	10339	3	US-09-764-891-6747	Sequence 6747, Ap
C 962	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1104	48	3.7	10339	6	US-10-091-572-597	Sequence 597, App
C 963	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1105	48	3.7	10339	6	US-10-091-572-597	Sequence 597, App
C 964	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1106	48	3.7	23606	9	US-10-741-600-17944	Sequence 17944, A
C 965	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	1107	48	3.7	23606	10	US-10-995-561-13465	Sequence 13465, A
C 966	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1108	48	3.7	29921	6	US-10-083-853-1	Sequence 1, Appli
C 967	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1109	48	3.7	29921	6	US-10-083-853-1	Sequence 1, Appli
C 968	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1110	48	3.7	75839	6	US-10-087-192-166	Sequence 166, App
C 969	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1111	48	3.7	75839	6	US-10-087-192-166	Sequence 166, App
C 970	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1112	48	3.7	77777	8	US-10-318-389-4	Sequence 4, Appli
C 971	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1113	48	3.7	77777	8	US-10-318-389-4	Sequence 4, Appli
C 972	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1114	48	3.7	79134	15	US-11-124-368A-2924	Sequence 2924, Ap
C 973	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1115	48	3.7	79134	15	US-11-124-368A-2924	Sequence 2924, Ap
C 974	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1116	48	3.7	124990	9	US-10-684-422-156	Sequence 156, App
C 975	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1117	48	3.7	124990	9	US-10-684-422-156	Sequence 156, App
C 976	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1118	48	3.7	172543	15	US-11-121-086-6	Sequence 6, Appli
C 977	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1119	48	3.7	172543	15	US-11-121-086-6	Sequence 6, Appli
C 978	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1120	48	3.7	174424	3	US-09-967-768A-314	Sequence 314, App
C 979	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1121	48	3.7	174424	3	US-09-967-768A-314	Sequence 314, App
C 980	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1122	48	3.7	174424	3	US-09-967-768A-314	Sequence 314, App
C 981	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1123	48	3.7	174424	3	US-09-967-768A-314	Sequence 314, App
C 982	48	3.7	48	7	US-10-449-656-67	Sequence 67, Appl	c1124	48	3.7	174424	3	US-09-967	

c1117	48	3.7	181343	9	US-10-723-860-2392	Sequence 2392, Ap	c1190	47	3.6	20951	3	US-09-805-455-3	Sequence 3, Appli
c1118	48	3.7	181343	10	US-10-756-149-2215	Sequence 2215, Ap	c1191	47	3.6	20951	8	US-10-678-140-3	Sequence 3, Appli
c1119	48	3.7	198161	9	US-10-775-169-52	Sequence 52, Appl	c1192	47	3.6	25899	8	US-10-322-696-10	Sequence 10, Appl
c1120	48	3.7	198161	9	US-10-723-860-165	Sequence 165, App	c1193	47	3.6	38918	7	US-10-017-161-2049	Sequence 2049, Ap
c1121	48	3.7	198161	9	US-10-775-169-52	Sequence 52, Appl	c1194	47	3.6	38918	7	US-10-292-798-1695	Sequence 1695, Ap
c1122	48	3.7	220895	9	US-10-775-169-88	Sequence 88, Appl	c1195	47	3.6	38918	9	US-10-741-600-17637	Sequence 17637, A
c1123	48	3.7	220895	10	US-10-756-149-723	Sequence 723, App	c1196	47	3.6	61103	6	US-10-087-192-58	Sequence 58, Appl
c1124	48	3.7	220895	10	US-10-775-169-88	Sequence 88, Appl	c1197	47	3.6	98716	10	US-10-995-561-13331	Sequence 13331, A
c1125	48	3.7	235070	6	US-10-087-192-1990	Sequence 1990, Ap	c1198	47	3.6	100000	16	US-11-124-367A-5086	Sequence 5086, Ap
c1126	48	3.7	253861	8	US-10-741-601-5611	Sequence 5611, Ap	c1199	47	3.6	106707	8	US-10-694-685-8	Sequence 8, Appli
c1127	48	3.7	261817	6	US-10-087-192-2002	Sequence 2002, Ap	c1200	47	3.6	112604	9	US-10-723-860-970	Sequence 970, App
c1128	48	3.7	295772	11	US-10-330-773-410	Sequence 410, App	c1201	47	3.6	122279	10	US-10-756-143-3596	Sequence 3596, Ap
c1129	47	3.6	201	9	US-10-741-600-53547	Sequence 53547, A	c1202	47	3.6	172111	15	US-11-121-086-28	Sequence 28, Appl
c1130	47	3.6	201	16	US-11-124-367A-20793	Sequence 20793, A	c1203	47	3.6	175416	15	US-11-121-086-43	Sequence 43, Appl
c1131	47	3.6	201	16	US-11-124-367A-21120	Sequence 21120, A	c1204	47	3.6	201900	10	US-10-995-561-13303	Sequence 13303, A
c1132	47	3.6	220	8	US-10-242-535A-23836	Sequence 23836, A	c1205	47	3.6	220895	9	US-10-775-169-88	Sequence 88, Appl
c1133	47	3.6	220	8	US-10-085-783A-23836	Sequence 23836, A	c1206	47	3.6	220895	10	US-10-756-149-723	Sequence 723, App
c1134	47	3.6	325	9	US-10-357-930-49834	Sequence 49834, A	c1207	47	3.6	220895	10	US-10-775-169-88	Sequence 88, Appl
c1135	47	3.6	352	9	US-10-357-930-49747	Sequence 49747, A	c1208	47	3.6	246940	8	US-10-322-696-58	Sequence 58, Appl
c1136	47	3.6	421	9	US-10-357-930-19958	Sequence 19958, A	c1209	46	3.6	492	12	US-10-301-480-355475	Sequence 355475,
c1137	47	3.6	446	12	US-10-301-480-501360	Sequence 501360,	c1210	46	3.6	492	12	US-10-301-480-968884	Sequence 968884,
c1138	47	3.6	446	12	US-10-301-480-1114769	Sequence 1114769,	c1211	46	3.6	496	3	US-09-918-995-13741	Sequence 13741, A
c1139	47	3.6	450	4	US-09-925-065A-440384	Sequence 440384,	c1212	46	3.6	500	4	US-09-925-065A-278457	Sequence 278457,
c1140	47	3.6	450	5	US-09-925-065A-440384	Sequence 440384,	c1213	46	3.6	500	5	US-09-925-065A-278457	Sequence 278457,
c1141	47	3.6	531	9	US-10-357-930-20047	Sequence 20047, A	c1214	46	3.6	551	9	US-10-357-930-48229	Sequence 48229, A
c1142	47	3.6	556	4	US-09-925-065A-29720	Sequence 29720, A	c1215	46	3.6	559	6	US-10-027-632-46721	Sequence 46721, A
c1143	47	3.6	556	5	US-09-925-065A-29720	Sequence 29720, A	c1216	46	3.6	559	6	US-10-027-632-46722	Sequence 46722, A
c1144	47	3.6	556	12	US-10-301-480-130958	Sequence 130958,	c1217	46	3.6	559	7	US-10-027-632-46721	Sequence 46721, A
c1145	47	3.6	556	12	US-10-301-480-744367	Sequence 744367,	c1218	46	3.6	599	7	US-10-027-632-46722	Sequence 46722, A
c1146	47	3.6	572	12	US-10-301-480-432441	Sequence 432441,	c1219	46	3.6	608	12	US-10-301-480-6997	Sequence 6997, Ap
c1147	47	3.6	572	12	US-10-301-480-1045850	Sequence 1045850,	c1220	46	3.6	608	12	US-10-301-480-620406	Sequence 620406,
c1148	47	3.6	582	4	US-09-925-065A-361424	Sequence 361424,	c1221	46	3.6	610	12	US-10-301-480-6996	Sequence 6996, Ap
c1149	47	3.6	582	5	US-09-925-065A-361424	Sequence 361424,	c1222	46	3.6	610	12	US-10-301-480-620405	Sequence 620405,
c1150	47	3.6	594	4	US-09-925-065A-694808	Sequence 694808,	c1223	46	3.6	613	4	US-09-925-065A-75015	Sequence 75015, A
c1151	47	3.6	594	5	US-09-925-065A-694808	Sequence 694808,	c1224	46	3.6	613	5	US-09-925-065A-75015	Sequence 75015, A
c1152	47	3.6	638	4	US-09-925-065A-256	Sequence 256, App	c1225	46	3.6	613	9	US-10-357-930-18416	Sequence 18416, A
c1153	47	3.6	638	5	US-09-925-065A-256	Sequence 256, App	c1226	46	3.6	613	12	US-10-301-480-176254	Sequence 176254,
c1154	47	3.6	638	12	US-10-301-480-101493	Sequence 101493,	c1227	46	3.6	613	12	US-10-301-480-789663	Sequence 789663,
c1155	47	3.6	638	12	US-10-301-480-714902	Sequence 714902,	c1228	46	3.6	613	12	US-10-301-480-586567	Sequence 586567,
c1156	47	3.6	681	4	US-09-925-065A-943974	Sequence 943974,	c1229	46	3.6	626	12	US-10-301-480-1199976	Sequence 1199976,
c1157	47	3.6	681	5	US-09-925-065A-943974	Sequence 943974,	c1230	46	3.6	626	6	US-10-027-632-64820	Sequence 64820, A
c1158	47	3.6	708	6	US-10-027-632-104213	Sequence 104213,	c1231	46	3.6	626	6	US-10-027-632-64821	Sequence 64821, A
c1159	47	3.6	708	6	US-10-027-632-325148	Sequence 325148,	c1232	46	3.6	626	7	US-10-027-632-64820	Sequence 64820, A
c1160	47	3.6	708	7	US-10-027-632-104213	Sequence 104213,	c1233	46	3.6	626	7	US-10-027-632-64821	Sequence 64821, A
c1161	47	3.6	708	7	US-10-027-632-325148	Sequence 325148,	c1234	46	3.6	631	6	US-10-027-632-107978	Sequence 107978,
c1162	47	3.6	808	6	US-10-027-632-132993	Sequence 132993,	c1235	46	3.6	631	6	US-10-027-632-107978	Sequence 107978,
c1163	47	3.6	808	7	US-10-027-632-132993	Sequence 132993,	c1236	46	3.6	631	7	US-10-027-632-107978	Sequence 107978,
c1164	47	3.6	988	12	US-10-301-480-605593	Sequence 605593,	c1237	46	3.6	631	7	US-10-027-632-107978	Sequence 107978,
c1165	47	3.6	988	12	US-10-301-480-1219002	Sequence 1219002,	c1238	46	3.6	636	4	US-09-925-065A-626160	Sequence 626160,
c1166	47	3.6	991	12	US-10-301-480-611422	Sequence 611422,	c1239	46	3.6	636	5	US-09-925-065A-626160	Sequence 626160,
c1167	47	3.6	991	12	US-10-301-480-1224831	Sequence 1224831,	c1240	46	3.6	636	5	US-09-925-065A-626160	Sequence 626160,
c1168	47	3.6	1000	12	US-10-301-480-565312	Sequence 565312,	c1241	46	3.6	689	7	US-10-027-632-165978	Sequence 165978,
c1169	47	3.6	1000	12	US-10-301-480-1178721	Sequence 1178721,	c1242	46	3.6	689	7	US-10-027-632-165978	Sequence 165978,
c1170	47	3.6	1210	4	US-09-925-065A-721762	Sequence 721762,	c1243	46	3.6	910	12	US-10-301-480-535531	Sequence 535531,
c1171	47	3.6	1210	5	US-09-925-065A-721762	Sequence 721762,	c1244	46	3.6	988	12	US-10-301-480-608089	Sequence 608089,
c1172	47	3.6	1244	12	US-10-301-480-34865	Sequence 34865, A	c1245	46	3.6	998	12	US-10-301-480-1221498	Sequence 1221498,
c1173	47	3.6	1244	12	US-10-301-480-648274	Sequence 648274,	c1246	46	3.6	1160	3	US-09-764-891-5684	Sequence 5684, Ap
c1174	47	3.6	1258	6	US-10-027-632-123686	Sequence 123686,	c1247	46	3.6	1160	3	US-09-764-891-5684	Sequence 5684, Ap
c1175	47	3.6	1258	6	US-10-027-632-123686	Sequence 123687,	c1248	46	3.6	2841	10	US-10-956-157-4363	Sequence 4363, Ap
c1176	47	3.6	1258	7	US-10-027-632-123686	Sequence 123687,	c1249	46	3.6	2841	10	US-10-094-749-1158	Sequence 1158, Ap
c1177	47	3.6	1258	7	US-10-027-632-123687	Sequence 123687,	c1250	46	3.6	3011	6	US-10-103-313-630	Sequence 38, App
c1178	47	3.6	1435	4	US-09-925-065A-681496	Sequence 681496,	c1251	46	3.6	6798	10	US-10-737-082-38	Sequence 38, Appl
c1179	47	3.6	1435	5	US-09-925-065A-681496	Sequence 681496,	c1252	46	3.6	6798	10	US-10-765-790-38	Sequence 38, Appl
c1180	47	3.6	1605	4	US-09-925-065A-715615	Sequence 715615,	c1253	46	3.6	7734	3	US-09-764-868-1317	Sequence 1317, Ap
c1181	47	3.6	1605	4	US-09-925-065A-715615	Sequence 715615,	c1254	46	3.6	26928	3	US-09-880-107-2278	Sequence 2278, Ap
c1182	47	3.6	1605	5	US-09-925-065A-715615	Sequence 715615,	c1255	46	3.6	26928	3	US-10-020-141-7	Sequence 7, Appli
c1183	47	3.6	1605	5	US-09-925-065A-715615	Sequence 715615,	c1256	46	3.6	26928	6	US-10-017-631-1	Sequence 34, Appl
c1184	47	3.6	1605	5	US-09-925-065A-715615	Sequence 715615,	c1257	46	3.6	26928	8	US-10-235-192A-34	Sequence 34, Appl
c1185	47	3.6	1690	9	US-10-741-600-886	Sequence 886, App	c1258	46	3.6	33037	7	US-10-087-192-1114	Sequence 1114, App
c1186	47	3.6	5780	3	US-09-764-891-8702	Sequence 8702, Ap	c1259	46	3.6	32093	7	US-10-085-117-256	Sequence 256, App
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c1188	47	3.6	6906	9	US-10-781-581-184	Sequence 184, App	c1261	46	3.6	53641	10	US-10-995-561-13238	Sequence 13238, A
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3514.227 Million cell updates/sec

Title: US-10-785-221-8

Perfect score: 1295

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 224314 seqs, 35277956 residues

Word size : 1

Total number of hits satisfying chosen parameters: 448564

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Database : Published Applications NA New:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	4.7	14468	7	US-11-181-115-7
2	46	3.6	4651	7	US-11-181-115-7
3	36	2.8	3178	6	US-10-505-928-277
4	36	2.8	6163	6	US-10-524-021-9
5	36	2.8	138941	6	US-10-489-730-10
6	34	2.6	2534	7	US-11-145-307A-58
7	34	2.6	4500	6	US-10-511-937-533
8	34	2.6	6807	6	US-10-511-937-2858
9	34	2.6	70665	6	US-10-505-928-596
10	34	2.6	138941	6	US-10-489-730-10
11	34	2.6	394191	6	US-10-506-549-3
12	34	2.6	394191	6	US-10-506-549-3
13	34	2.6	394191	6	US-10-506-549-3
14	33	2.5	416	7	US-11-301-554-971
15	33	2.5	964	7	US-11-246-999-91
16	33	2.5	2295	7	US-11-246-999-15
17	33	2.5	2605	6	US-10-505-928-649
18	33	2.5	3144	6	US-10-511-937-467
19	32	2.5	5198	6	US-10-505-928-342
20	32	2.5	5198	6	US-10-505-928-342
21	31	2.4	545	6	US-10-473-173-146
22	31	2.4	807	6	US-11-246-999-22
23	31	2.4	1145	6	US-10-511-937-377
24	31	2.4	1237	6	US-10-511-937-430
25	31	2.4	1535	7	US-11-106-014-11
26	31	2.4	1629	6	US-10-511-937-444
27	31	2.4	2280	7	US-11-301-554-321
28	31	2.4	2280	7	US-11-301-554-321
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c 312	15	1.2	661	7	US-11-301-554-219	Sequence 219, App	395	15	1.2	2763	7	US-11-217-529-716	Sequence 716, App
c 313	15	1.2	679	6	US-10-509-131-2	Sequence 2, Appli	c 397	15	1.2	2846	7	US-11-101-316-37	Sequence 37, Appl
c 314	15	1.2	687	7	US-11-242-317-38	Sequence 38, Appl	398	15	1.2	2988	7	US-11-217-529-80377	Sequence 80377, A
c 315	15	1.2	697	6	US-10-488-619-1995	Sequence 1995, Ap	c 399	15	1.2	3129	6	US-10-511-937-588	Sequence 588, App
c 316	15	1.2	717	6	US-10-488-619-2149	Sequence 2149, Ap	400	15	1.2	3213	7	US-11-217-529-1576	Sequence 1576, Ap
c 317	15	1.2	735	7	US-11-217-529-81697	Sequence 81697, A	c 401	15	1.2	3249	7	US-11-217-529-1719	Sequence 1719, Ap
c 318	15	1.2	765	6	US-10-488-619-2151	Sequence 2151, Ap	402	15	1.2	3301	6	US-10-370-959-10	Sequence 10, Appl
c 319	15	1.2	783	6	US-10-488-619-1777	Sequence 1777, Ap	403	15	1.2	3315	6	US-10-505-928-554	Sequence 554, App
c 320	15	1.2	783	7	US-11-217-529-800	Sequence 800, App	c 405	15	1.2	3356	7	US-11-242-111-2	Sequence 2, Appli
c 321	15	1.2	784	7	US-11-301-554-1866	Sequence 1866, Ap	c 406	15	1.2	3396	6	US-10-505-928-346	Sequence 346, App
c 322	15	1.2	785	7	US-11-301-554-1868	Sequence 1868, Ap	c 407	15	1.2	3444	7	US-11-217-529-3058	Sequence 3058, Ap
c 323	15	1.2	786	7	US-11-217-529-77025	Sequence 77025, A	c 408	15	1.2	3444	7	US-11-217-529-5473	Sequence 5473, Ap
c 324	15	1.2	789	7	US-11-301-554-1867	Sequence 1867, Ap	409	15	1.2	3513	7	US-11-217-529-865	Sequence 865, App
c 325	15	1.2	790	7	US-11-301-554-1865	Sequence 1865, Ap	410	15	1.2	3597	6	US-10-505-928-651	Sequence 651, App
c 326	15	1.2	818	7	US-11-145-307A-157	Sequence 157, App	411	15	1.2	3597	6	US-10-511-937-2802	Sequence 2802, Ap
c 327	15	1.2	820	6	US-10-488-619-2550	Sequence 2550, Ap	c 412	15	1.2	3869	6	US-10-511-937-2853	Sequence 2853, Ap
c 328	15	1.2	826	6	US-10-488-619-2114	Sequence 2114, Ap	413	15	1.2	3930	7	US-11-217-529-76026	Sequence 76026, A
c 329	15	1.2	858	6	US-10-488-619-2147	Sequence 2147, Ap	414	15	1.2	4059	7	US-11-106-014-47	Sequence 47, Appl
c 330	15	1.2	884	7	US-11-101-316-135	Sequence 135, App	415	15	1.2	4080	7	US-11-217-529-77077	Sequence 77077, A
c 331	15	1.2	894	7	US-11-217-529-1982	Sequence 1982, Ap	c 416	15	1.2	4446	6	US-10-511-937-2840	Sequence 2840, Ap
c 332	15	1.2	900	7	US-11-217-529-139	Sequence 139, App	c 417	15	1.2	4465	6	US-10-505-928-528	Sequence 528, App
c 333	15	1.2	916	6	US-10-511-937-2921	Sequence 2921, Ap	c 418	15	1.2	4465	6	US-10-511-937-460	Sequence 460, App
c 335	15	1.2	955	6	US-10-488-619-3026	Sequence 3026, Ap	419	15	1.2	4773	6	US-10-511-455-1	Sequence 1, Appli
c 337	15	1.2	975	7	US-11-203-609-1	Sequence 1, Appli	420	15	1.2	5307	6	US-10-505-928-824	Sequence 824, App
c 338	15	1.2	1000	7	US-11-233-726-10	Sequence 10, Appl	c 421	15	1.2	6243	6	US-10-518-039-2	Sequence 2, Appli
c 339	15	1.2	1026	7	US-11-217-529-76877	Sequence 76877, A	c 422	15	1.2	6317	6	US-10-511-937-387	Sequence 387, App
c 340	15	1.2	1028	6	US-10-511-937-508	Sequence 508, App	c 423	15	1.2	6450	6	US-10-505-928-750	Sequence 750, App
c 341	15	1.2	1077	7	US-11-217-529-82679	Sequence 82679, A	c 424	15	1.2	6843	6	US-10-518-039-1	Sequence 1, Appli
c 343	15	1.2	1125	6	US-10-505-928-454	Sequence 454, App	425	15	1.2	8196	7	US-11-024-544A-55	Sequence 55, Appl
c 344	15	1.2	1125	6	US-10-511-937-431	Sequence 431, App	426	15	1.2	8196	7	US-11-190-750-32	Sequence 32, Appl
c 345	15	1.2	1212	7	US-11-217-529-78198	Sequence 78198, A	427	15	1.2	8196	7	US-11-264-784-156	Sequence 156, App
c 346	15	1.2	1212	7	US-11-217-529-79560	Sequence 79560, A	c 428	15	1.2	8370	7	US-11-217-529-777	Sequence 77, Appl
c 347	15	1.2	1230	7	US-11-217-529-76131	Sequence 76131, A	429	15	1.2	8502	7	US-11-264-784-120	Sequence 120, App
c 348	15	1.2	1236	7	US-11-217-529-75992	Sequence 75992, A	c 430	15	1.2	8810	7	US-11-258-704-40	Sequence 40, Appl
c 349	15	1.2	1269	7	US-11-217-529-3899	Sequence 3899, Ap	c 431	15	1.2	8819	7	US-11-358-704-41	Sequence 41, Appl
c 350	15	1.2	1314	7	US-11-217-529-4372	Sequence 4372, Ap	432	15	1.2	8953	7	US-11-185-301-10	Sequence 10, Appl
c 352	15	1.2	1321	7	US-11-217-529-79217	Sequence 79217, A	c 433	15	1.2	8953	7	US-11-264-784-113	Sequence 113, App
c 353	15	1.2	1341	7	US-11-249-111-38	Sequence 38, Appl	c 434	15	1.2	10945	7	US-11-024-544A-121	Sequence 121, App
c 354	15	1.2	1386	7	US-11-217-529-3766	Sequence 3766, Ap	c 435	15	1.2	10945	7	US-11-024-545-49	Sequence 49, Appl
c 355	15	1.2	1389	7	US-11-217-529-76684	Sequence 76684, A	c 436	15	1.2	10945	7	US-11-185-301-37	Sequence 37, Appl
c 356	15	1.2	1398	7	US-11-301-554-322	Sequence 322, App	c 437	15	1.2	10945	7	US-11-190-750-104	Sequence 104, App
c 357	15	1.2	1404	7	US-11-217-529-5866	Sequence 5866, Ap	c 438	15	1.2	10945	7	US-11-251-466-23	Sequence 23, Appl

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C 440	15	1.2	11435	7	US-11-264-784-126	Sequence 126, App	C 513	14	1.1	488	6	US-10-473-173-332	Sequence 332, App
C 441	15	1.2	12690	7	US-11-024-544-124	Sequence 124, App	C 514	14	1.1	488	6	US-10-488-619-1497	Sequence 1497, App
C 442	15	1.2	12690	7	US-11-024-545-52	Sequence 52, Appl	C 515	14	1.1	491	7	US-11-301-554-1227	Sequence 1227, App
C 443	15	1.2	12690	7	US-11-190-750-107	Sequence 107, App	C 516	14	1.1	498	6	US-10-488-619-982	Sequence 982, App
C 444	15	1.2	12690	7	US-11-251-466-26	Sequence 26, Appl	C 517	14	1.1	505	6	US-10-473-173-242	Sequence 242, App
C 445	15	1.2	12690	7	US-11-254-173-42	Sequence 42, Appl	C 518	14	1.1	510	7	US-11-217-529-6158	Sequence 6158, App
C 446	15	1.2	12690	7	US-11-264-784-128	Sequence 128, App	C 519	14	1.1	511	7	US-11-301-554-1138	Sequence 1138, App
C 447	15	1.2	13034	7	US-11-254-173-37	Sequence 37, Appl	C 520	14	1.1	528	7	US-11-217-529-1556	Sequence 1556, App
C 448	15	1.2	13034	7	US-11-264-784-116	Sequence 116, App	C 521	14	1.1	529	6	US-10-473-173-323	Sequence 323, App
C 449	15	1.2	16325	7	US-11-264-784-127	Sequence 127, App	C 522	14	1.1	543	6	US-10-488-619-2662	Sequence 2662, App
C 450	14	1.1	20	7	US-11-316-132-24	Sequence 24, Appl	C 523	14	1.1	555	6	US-10-488-619-787	Sequence 787, App
C 451	14	1.1	24	7	US-11-257-502-93	Sequence 93, Appl	C 524	14	1.1	555	7	US-11-217-529-2282	Sequence 2282, App
C 452	14	1.1	25	7	US-11-217-529-7093	Sequence 7093, App	C 525	14	1.1	558	6	US-10-488-619-2238	Sequence 2238, App
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C 454	14	1.1	25	7	US-11-217-529-23982	Sequence 23982, A	C 527	14	1.1	567	7	US-11-217-529-78112	Sequence 78112, A
C 455	14	1.1	25	7	US-11-217-529-27551	Sequence 27551, A	C 528	14	1.1	570	7	US-11-217-529-173903	Sequence 173903, A
C 456	14	1.1	25	7	US-11-217-529-33403	Sequence 33403, A	C 529	14	1.1	583	6	US-10-488-619-1703	Sequence 1703, App
C 457	14	1.1	25	7	US-11-217-529-51090	Sequence 51090, A	C 530	14	1.1	592	7	US-11-106-014-31	Sequence 31, Appl
C 458	14	1.1	25	7	US-11-217-529-53861	Sequence 53861, A	C 531	14	1.1	594	6	US-10-488-619-1704	Sequence 1704, App
C 459	14	1.1	25	7	US-11-217-529-72094	Sequence 72094, A	C 532	14	1.1	594	7	US-11-217-529-78931	Sequence 78931, A
C 460	14	1.1	25	7	US-11-217-529-74454	Sequence 74454, A	C 533	14	1.1	595	6	US-10-488-619-1034	Sequence 1034, App
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C 462	14	1.1	25	7	US-11-217-529-102365	Sequence 102365, A	C 535	14	1.1	618	7	US-11-217-529-6116	Sequence 6116, App
C 463	14	1.1	25	7	US-11-217-529-110254	Sequence 110254, A	C 536	14	1.1	621	7	US-11-217-529-75580	Sequence 75580, A
C 464	14	1.1	25	7	US-11-217-529-126108	Sequence 126108, A	C 537	14	1.1	635	6	US-10-468-193-23	Sequence 23, Appl
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C 467	14	1.1	25	7	US-11-217-529-172243	Sequence 172243, A	C 540	14	1.1	637	7	US-11-217-529-79267	Sequence 79267, A
C 468	14	1.1	25	7	US-11-217-529-189183	Sequence 189183, A	C 541	14	1.1	639	7	US-11-217-529-78398	Sequence 78398, A
C 469	14	1.1	28	7	US-11-257-502-127	Sequence 127, App	C 542	14	1.1	640	6	US-10-488-619-1296	Sequence 1296, App
C 470	14	1.1	28	7	US-11-257-502-209	Sequence 209, App	C 543	14	1.1	646	6	US-10-488-619-2941	Sequence 2941, App
C 471	14	1.1	41	7	US-11-223-738-31	Sequence 31, Appl	C 544	14	1.1	647	6	US-10-525-126-141	Sequence 141, App
C 472	14	1.1	51	7	US-11-143-642-582	Sequence 582, App	C 545	14	1.1	654	6	US-10-488-619-1783	Sequence 1783, App
C 473	14	1.1	53	7	US-11-283-332A-4	Sequence 4, Appl	C 546	14	1.1	657	7	US-11-217-529-79500	Sequence 79500, A
C 474	14	1.1	94	7	US-10-445-444-2	Sequence 2, Appl	C 547	14	1.1	667	6	US-10-488-619-2667	Sequence 2667, App
C 475	14	1.1	100	6	US-10-511-455-42	Sequence 42, Appl	C 548	14	1.1	668	7	US-11-256-428-50	Sequence 50, Appl
C 476	14	1.1	105	7	US-11-217-529-77799	Sequence 77799, A	C 549	14	1.1	675	7	US-11-217-529-166962	Sequence 166962, A
C 477	14	1.1	132	7	US-11-217-529-174455	Sequence 174455, A	C 550	14	1.1	678	7	US-11-301-554-208	Sequence 208, App
C 478	14	1.1	195	7	US-11-217-529-3976	Sequence 3976, App	C 551	14	1.1	678	7	US-11-217-529-4205	Sequence 4205, App
C 479	14	1.1	249	7	US-11-301-554-1645	Sequence 1645, App	C 552	14	1.1	684	7	US-11-217-529-4757	Sequence 4757, App
C 480	14	1.1	249	7	US-11-217-529-166983	Sequence 166983, A	C 553	14	1.1	690	7	US-11-217-529-190972	Sequence 190972, A
C 481	14	1.1	291	7	US-11-283-332A-1	Sequence 1, Appl	C 554	14	1.1	696	6	US-10-488-619-2542	Sequence 2542, App
C 482	14	1.1	309	7	US-11-301-554-104	Sequence 104, App	C 555	14	1.1	708	7	US-11-217-529-76796	Sequence 76796, App
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C 484	14	1.1	318	6	US-10-488-619-598	Sequence 598, App	C 557	14	1.1	713	6	US-10-488-619-2333	Sequence 2333, A
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C 486	14	1.1	320	7	US-11-245-514-10	Sequence 10, Appl	C 559	14	1.1	733	6	US-10-488-619-2864	Sequence 2864, App
C 487	14	1.1	321	7	US-11-217-529-80939	Sequence 80939, A	C 560	14	1.1	744	7	US-11-217-529-295	Sequence 295, App
C 488	14	1.1	345	7	US-11-217-529-77003	Sequence 77003, A	C 561	14	1.1	752	6	US-10-488-619-2124	Sequence 2124, App
C 489	14	1.1	345	7	US-11-283-332A-32	Sequence 32, Appl	C 562	14	1.1	762	7	US-11-217-529-3526	Sequence 3526, App
C 490	14	1.1	360	7	US-11-254-679-16	Sequence 16, Appl	C 563	14	1.1	771	7	US-11-217-529-81029	Sequence 81029, A
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C 492	14	1.1	391	7	US-11-217-529-190879	Sequence 190879, A	C 565	14	1.1	789	7	US-11-217-529-5206	Sequence 5206, App
C 493	14	1.1	393	7	US-11-217-529-3977	Sequence 3977, App	C 566	14	1.1	798	7	US-11-145-307A-169	Sequence 169, App
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C 495	14	1.1	399	6	US-10-473-173-489	Sequence 485, App	C 568	14	1.1	806	6	US-10-488-619-1430	Sequence 1430, App
C 496	14	1.1	415	6	US-10-488-619-374	Sequence 374, App	C 569	14	1.1	818	6	US-10-488-619-2757	Sequence 2757, App
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C 498	14	1.1	427	7	US-11-301-554-854	Sequence 854, App	C 571	14	1.1	834	7	US-11-217-529-174327	Sequence 174327, A
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C 504	14	1.1	452	7	US-11-301-554-5	Sequence 5, Appl	C 577	14	1.1	887	7	US-11-249-111-53	Sequence 53, Appl
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C 507	14	1.1	465	6	US-10-488-619-674	Sequence 674, App	C 580	14	1.1	909	7	US-11-217-529-1523	Sequence 1523, App
C 508	14	1.1	471	7	US-11-217-529-3919	Sequence 3919, App	C 581	14	1.1	909	7	US-11-217-529-1999	Sequence 1999, App
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C 510	14	1.1	475	6	US-10-473-173-373	Sequence 373, App	C 583	14	1.1	933	7	US-11-217-529-76878	Sequence 76878, A
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586	14	1.1	993	6	US-10-473-173-04	Sequence 84, Appl	c 665	14	1.1	1636	7	US-11-101-316-77	Sequence 77, Appl
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591	14	1.1	1008	7	US-11-217-529-174182	Sequence 174182,	c 670	14	1.1	1666	6	US-10-511-937-407	Sequence 407, App
592	14	1.1	1011	6	US-10-525-126-121	Sequence 121, App	c 671	14	1.1	1667	6	US-10-505-928-419	Sequence 419, App
c 593	14	1.1	1014	7	US-11-217-529-2540	Sequence 2540, Ap	c 672	14	1.1	1668	6	US-11-217-529-80574	Sequence 80574, A
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598	14	1.1	1081	6	US-10-505-928-66	Sequence 66, Appl	c 677	14	1.1	1695	7	US-11-217-529-3778	Sequence 3778, Ap
c 599	14	1.1	1089	7	US-11-217-529-75789	Sequence 75789, A	c 678	14	1.1	1719	7	US-11-217-529-77733	Sequence 77733, Ap
c 600	14	1.1	1092	7	US-11-217-529-2226	Sequence 2226, Ap	c 679	14	1.1	1726	7	US-11-183-218-25	Sequence 25, Appl
c 601	14	1.1	1104	7	US-11-217-529-1636	Sequence 1636, Ap	c 680	14	1.1	1749	7	US-11-217-529-81937	Sequence 81937, A
c 602	14	1.1	1107	7	US-11-217-529-1036	Sequence 1036, Ap	c 681	14	1.1	1758	7	US-11-217-529-2344	Sequence 2344, Ap
c 603	14	1.1	1107	7	US-11-217-529-79219	Sequence 79219, A	c 682	14	1.1	1763	6	US-10-473-173-17	Sequence 17, Appl
c 604	14	1.1	1122	7	US-11-217-529-81650	Sequence 81650, A	c 684	14	1.1	1764	7	US-11-217-529-78239	Sequence 78239, A
c 605	14	1.1	1155	7	US-11-217-529-1064	Sequence 1064, Ap	c 685	14	1.1	1776	7	US-11-217-529-3257	Sequence 3257, Ap
c 607	14	1.1	1157	7	US-11-101-316-145	Sequence 145, App	c 687	14	1.1	1800	7	US-11-217-529-4484	Sequence 4484, Ap
c 608	14	1.1	1161	7	US-11-217-529-77853	Sequence 77853, A	c 688	14	1.1	1815	7	US-11-217-529-4155	Sequence 4155, Ap
c 609	14	1.1	1209	7	US-11-217-529-4631	Sequence 4631, Ap	c 689	14	1.1	1824	7	US-11-217-529-81785	Sequence 81785, A
c 610	14	1.1	1213	7	US-11-244-678-6	Sequence 6, Appli	c 690	14	1.1	1827	7	US-11-217-529-5619	Sequence 5619, Ap
c 611	14	1.1	1221	7	US-11-217-529-2573	Sequence 2573, Ap	c 691	14	1.1	1845	7	US-11-217-529-4399	Sequence 4399, Ap
c 612	14	1.1	1251	7	US-11-217-529-1148	Sequence 1148, Ap	c 692	14	1.1	1851	7	US-11-217-529-4063	Sequence 4063, Ap
c 613	14	1.1	1281	7	US-11-217-529-77971	Sequence 77971, A	c 693	14	1.1	1854	7	US-11-217-529-534	Sequence 534, App
c 614	14	1.1	1287	7	US-11-217-529-2755	Sequence 2755, Ap	c 694	14	1.1	1869	7	US-11-217-529-79617	Sequence 79617, A
c 615	14	1.1	1293	7	US-11-217-529-701	Sequence 701, App	c 695	14	1.1	1875	7	US-11-217-529-174200	Sequence 174200,
c 616	14	1.1	1308	7	US-11-217-529-2265	Sequence 2265, Ap	c 697	14	1.1	1882	7	US-11-101-316-133	Sequence 133, App
c 617	14	1.1	1308	7	US-11-217-529-166656	Sequence 166656,	c 699	14	1.1	1901	7	US-11-101-316-11	Sequence 11, Appl
c 618	14	1.1	1311	7	US-11-217-529-4258	Sequence 4258, Ap	c 700	14	1.1	1910	6	US-10-538-767-3	Sequence 3, Appli
c 619	14	1.1	1311	7	US-11-217-529-78434	Sequence 78434, A	c 702	14	1.1	1920	7	US-11-217-529-77403	Sequence 77403, A
c 620	14	1.1	1317	7	US-11-217-529-79612	Sequence 79612, A	c 703	14	1.1	1931	1	US-09-949-925-78	Sequence 78, Appl
c 621	14	1.1	1339	6	US-10-505-928-498	Sequence 498, App	c 704	14	1.1	1935	6	US-09-949-925-12	Sequence 12, Appl
c 622	14	1.1	1368	7	US-11-217-529-2691	Sequence 2691, Ap	c 705	14	1.1	1935	6	US-10-505-928-564	Sequence 564, App
c 623	14	1.1	1368	7	US-11-217-529-79906	Sequence 79906, A	c 706	14	1.1	1948	7	US-11-264-784-360	Sequence 360, App
c 624	14	1.1	1374	7	US-11-024-544A-114	Sequence 114, App	c 707	14	1.1	1953	6	US-11-217-529-1409	Sequence 1409, Ap
c 625	14	1.1	1374	7	US-11-024-545-42	Sequence 42, Appl	c 707	14	1.1	1953	6	US-10-504-120-9	Sequence 9, Appli
c 626	14	1.1	1374	7	US-11-185-301-30	Sequence 30, Appl	c 708	14	1.1	1998	6	US-10-370-959-41	Sequence 41, Appl
c 627	14	1.1	1374	7	US-11-190-750-97	Sequence 97, Appl	c 709	14	1.1	2007	7	US-11-217-529-76072	Sequence 76072, A
c 628	14	1.1	1374	7	US-11-251-466-16	Sequence 16, Appl	c 710	14	1.1	2022	7	US-11-217-529-78304	Sequence 78304, A
c 629	14	1.1	1374	7	US-11-254-173-30	Sequence 30, Appl	c 711	14	1.1	2025	7	US-11-217-529-76064	Sequence 76064, A
c 630	14	1.1	1374	7	US-11-264-784-1	Sequence 1, Appli	c 712	14	1.1	2038	7	US-11-217-529-79191	Sequence 79191, A
c 631	14	1.1	1374	7	US-11-264-784-3	Sequence 3, Appli	c 713	14	1.1	2038	6	US-10-511-937-2831	Sequence 2831, Ap
c 632	14	1.1	1389	7	US-11-217-529-78881	Sequence 78881, A	c 714	14	1.1	2043	7	US-11-217-529-77353	Sequence 77353, A
c 633	14	1.1	1392	7	US-11-217-529-174216	Sequence 174216,	c 715	14	1.1	2067	7	US-11-217-529-714	Sequence 714, App
c 634	14	1.1	1418	6	US-10-505-928-366	Sequence 366, App	c 716	14	1.1	2079	7	US-11-217-529-76446	Sequence 76446, A
c 636	14	1.1	1449	7	US-11-217-529-81835	Sequence 81835, A	c 717	14	1.1	2097	7	US-11-217-529-75567	Sequence 75567, A
c 637	14	1.1	1452	1	US-09-949-925-62	Sequence 62, Appl	c 718	14	1.1	2100	7	US-11-217-529-79086	Sequence 79086, A
c 638	14	1.1	1470	7	US-11-217-529-78020	Sequence 78020, A	c 719	14	1.1	2106	7	US-11-217-529-1078	Sequence 1078, Ap
c 639	14	1.1	1476	6	US-11-217-529-304	Sequence 304, App	c 720	14	1.1	2115	7	US-11-217-529-3350	Sequence 3350, Ap
c 640	14	1.1	1486	6	US-10-973-274-30	Sequence 30, Appl	c 721	14	1.1	2130	7	US-11-217-529-854	Sequence 854, App
c 641	14	1.1	1491	7	US-11-217-529-666	Sequence 666, App	c 722	14	1.1	2178	7	US-11-217-529-3773	Sequence 3773, Ap
c 642	14	1.1	1491	7	US-11-217-529-4988	Sequence 4988, Ap	c 723	14	1.1	2180	6	US-10-505-928-771	Sequence 771, App
c 643	14	1.1	1500	7	US-11-217-529-3960	Sequence 3960, Ap	c 724	14	1.1	2181	6	US-10-504-120-13	Sequence 13, Appl
c 644	14	1.1	1506	7	US-11-217-529-146	Sequence 146, App	c 725	14	1.1	2195	6	US-10-505-928-285	Sequence 285, App
c 645	14	1.1	1509	7	US-11-217-529-81126	Sequence 81126, A	c 726	14	1.1	2196	7	US-11-217-529-1032	Sequence 1032, Ap
c 646	14	1.1	1515	7	US-11-217-529-3477	Sequence 3477, Ap	c 727	14	1.1	2247	7	US-11-217-529-78971	Sequence 78971, A
c 647	14	1.1	1521	7	US-11-024-544A-137	Sequence 135, App	c 728	14	1.1	2251	6	US-10-946-650-77	Sequence 77, Appl
c 648	14	1.1	1521	7	US-11-190-750-118	Sequence 118, App	c 729	14	1.1	2362	7	US-11-217-529-75527	Sequence 75527, A
c 649	14	1.1	1521	7	US-11-264-784-4	Sequence 4, Appli	c 730	14	1.1	2319	7	US-11-217-529-78262	Sequence 78262, A
c 650	14	1.1	1530	7	US-11-217-529-2013	Sequence 2013, Ap	c 731	14	1.1	2376	7	US-11-217-529-3183	Sequence 3183, Ap
c 651	14	1.1	1536	7	US-11-217-529-76326	Sequence 76326, A	c 732	14	1.1	2398	7	US-11-315-766-25	Sequence 25, Appl
c 652	14	1.1	1560	7	US-11-217-529-173529	Sequence 173529,	c 733	14	1.1	2403	7	US-11-217-529-214	Sequence 214, App
c 653	14	1.1	1563	7	US-11-217-529-76323	Sequence 76323, A	c 734	14	1.1	2412	7	US-11-217-529-82371	Sequence 82371, A
c 654	14	1.1	1571	7	US-11-101-316-137	Sequence 137, App	c 735	14	1.1	2430	7	US-11-217-529-81269	Sequence 81269, A
c 655	14	1.1	1602	7	US-11-217-529-86	Sequence 86, Appl	c 736	14	1.1	2439	7	US-11-217-529-76352	Sequence 76352, A
c 656	14	1.1	1617	7	US-11-217-529-1954	Sequence 1954, Ap	c 737	14	1.1	2454	7	US-11-217-529-190867	Sequence 190867, A
c 657	14	1.1	1629	6	US-10-541-993-21	Sequence 21, Appl	c 738	14	1.1	2484	7	US-11-217-529-77095	Sequence 77095, A
c 658	14	1.1	1629	7	US-11-242-111-1	Sequence 1, Appli	c 739	14	1.1	2490	7	US-11-217-529-2926	Sequence 2926, Ap
c 659	14	1.1	1631	6	US-10-541-993-17	Sequence 17, Appl	c 740	14	1.1	2499	7	US-11-217-529-1666	Sequence 1666, Ap

C 741	14	1.1	2505	7	US-11-217-529-52	Sequence 52, Appl	C 818	14	1.1	5787	7	US-11-217-529-76923	Sequence 76923, A
C 742	14	1.1	2523	7	US-11-217-529-75363	Sequence 75363, A	C 819	14	1.1	5853	7	US-11-217-529-1030	Sequence 1030, Ap
743	14	1.1	2565	7	US-11-217-529-166155	Sequence 166155, A	C 820	14	1.1	5940	7	US-11-217-529-82606	Sequence 82606, A
744	14	1.1	2568	7	US-11-217-529-82245	Sequence 82245, A	C 821	14	1.1	5957	6	US-10-473-173-106	Sequence 106, App
C 745	14	1.1	2595	7	US-11-217-529-1628	Sequence 1628, Ap	C 822	14	1.1	6507	7	US-11-217-529-802	Sequence 802, App
747	14	1.1	2609	7	US-11-246-999-11	Sequence 11, Appl	C 823	14	1.1	6596	7	US-11-263-326-105	Sequence 105, App
748	14	1.1	2628	7	US-11-217-529-77724	Sequence 77724, A	C 824	14	1.1	6599	7	US-11-263-326-106	Sequence 106, App
749	14	1.1	2643	6	US-10-473-173-15	Sequence 15, Appl	C 825	14	1.1	6599	7	US-11-263-326-107	Sequence 107, App
750	14	1.1	2653	6	US-10-505-928-548	Sequence 548, App	C 826	14	1.1	6599	7	US-11-263-326-109	Sequence 109, App
751	14	1.1	2655	6	US-10-473-173-96	Sequence 96, Appl	C 827	14	1.1	7572	6	US-10-473-173-80	Sequence 80, Appl
C 752	14	1.1	2661	7	US-11-217-529-77121	Sequence 77121, A	C 828	14	1.1	8292	6	US-10-501-814-2	Sequence 2, Appl
C 753	14	1.1	2700	7	US-11-315-766-23	Sequence 23, Appl	C 829	14	1.1	8370	7	US-11-263-326-90	Sequence 90, Appl
C 754	14	1.1	2726	6	US-10-982-908-27	Sequence 27, Appl	C 830	14	1.1	8377	7	US-11-263-326-95	Sequence 95, Appl
755	14	1.1	2745	6	US-10-370-959-39	Sequence 39, Appl	C 831	14	1.1	8380	7	US-11-263-326-89	Sequence 89, Appl
757	14	1.1	2778	7	US-11-217-529-5649	Sequence 5649, Ap	C 832	14	1.1	8381	7	US-11-263-326-1	Sequence 1, Appl
C 758	14	1.1	2788	6	US-10-505-928-476	Sequence 476, App	C 833	14	1.1	8381	7	US-11-263-326-3	Sequence 3, Appl
C 759	14	1.1	2841	7	US-11-217-529-77067	Sequence 77067, A	C 834	14	1.1	8381	7	US-11-263-326-5	Sequence 5, Appl
C 760	14	1.1	2868	7	US-11-217-529-81168	Sequence 81168, A	C 835	14	1.1	8381	7	US-11-263-326-7	Sequence 7, Appl
C 761	14	1.1	2874	7	US-11-217-529-1151	Sequence 1151, Ap	C 836	14	1.1	8381	7	US-11-263-326-8	Sequence 8, Appl
C 762	14	1.1	2895	7	US-11-217-529-1996	Sequence 1996, Ap	C 837	14	1.1	8381	7	US-11-263-326-9	Sequence 9, Appl
C 763	14	1.1	2898	7	US-11-217-529-156	Sequence 156, App	C 838	14	1.1	8381	7	US-11-263-326-11	Sequence 11, Appl
C 764	14	1.1	2904	7	US-11-145-307A-161	Sequence 161, App	C 839	14	1.1	8381	7	US-11-263-326-91	Sequence 91, Appl
C 765	14	1.1	2905	6	US-10-505-928-295	Sequence 295, App	C 840	14	1.1	8381	7	US-11-263-326-92	Sequence 92, Appl
C 766	14	1.1	2942	7	US-11-170-482-17	Sequence 17, Appl	C 841	14	1.1	8381	7	US-11-263-326-93	Sequence 93, Appl
C 767	14	1.1	3015	7	US-11-217-529-76054	Sequence 76054, A	C 842	14	1.1	8381	7	US-11-263-326-96	Sequence 96, Appl
768	14	1.1	3048	6	US-10-511-455-49	Sequence 49, Appl	C 843	14	1.1	8381	7	US-11-263-326-97	Sequence 97, Appl
C 769	14	1.1	3096	7	US-11-217-529-82685	Sequence 82685, A	C 844	14	1.1	8381	7	US-11-263-326-108	Sequence 108, App
770	14	1.1	3105	7	US-11-217-529-77156	Sequence 77156, A	C 845	14	1.1	8381	7	US-11-263-326-136	Sequence 136, App
C 772	14	1.1	3252	7	US-11-217-529-76569	Sequence 76569, A	C 846	14	1.1	8381	7	US-11-263-326-137	Sequence 137, App
C 773	14	1.1	3252	7	US-11-217-529-76569	Sequence 76569, A	C 847	14	1.1	8381	7	US-11-263-326-138	Sequence 138, App
C 774	14	1.1	3300	7	US-11-217-529-3190	Sequence 3190, Ap	C 848	14	1.1	8381	7	US-11-263-326-139	Sequence 139, App
C 775	14	1.1	3362	6	US-10-511-937-2874	Sequence 2874, Ap	C 849	14	1.1	8381	7	US-11-263-326-140	Sequence 140, App
C 776	14	1.1	3387	7	US-11-217-529-78908	Sequence 78908, A	C 850	14	1.1	8381	7	US-11-263-326-141	Sequence 141, App
C 777	14	1.1	3411	6	US-10-473-173-61	Sequence 61, Appl	C 851	14	1.1	8381	7	US-11-263-326-142	Sequence 142, App
C 779	14	1.1	3411	7	US-11-217-529-82099	Sequence 82099, A	C 852	14	1.1	8381	7	US-11-263-326-143	Sequence 143, App
C 780	14	1.1	3484	7	US-11-181-115-34	Sequence 34, Appl	C 853	14	1.1	8381	7	US-11-263-326-144	Sequence 144, App
C 781	14	1.1	3501	7	US-11-217-529-80328	Sequence 80328, A	C 854	14	1.1	8462	7	US-11-263-326-145	Sequence 145, App
C 782	14	1.1	3503	6	US-10-505-928-609	Sequence 609, App	C 855	14	1.1	9362	7	US-11-297-317-18	Sequence 18, Appl
C 783	14	1.1	3536	7	US-11-251-465-15	Sequence 15, Appl	C 856	14	1.1	9400	7	US-11-297-317-17	Sequence 17, Appl
C 784	14	1.1	3551	7	US-11-145-307A-60	Sequence 60, Appl	C 857	14	1.1	10195	7	US-11-264-784-149	Sequence 149, App
C 785	14	1.1	3597	6	US-10-505-928-651	Sequence 651, App	C 858	14	1.1	10809	7	US-11-264-784-151	Sequence 151, App
C 786	14	1.1	3597	6	US-10-511-937-2802	Sequence 2802, Ap	C 859	14	1.1	11046	7	US-11-264-784-146	Sequence 146, App
C 787	14	1.1	3610	7	US-11-181-115-32	Sequence 32, Appl	C 860	14	1.1	12449	7	US-11-254-173-26	Sequence 12, Appl
C 788	14	1.1	3628	7	US-11-145-307A-15	Sequence 15, Appl	C 861	14	1.1	12449	7	US-11-264-784-114	Sequence 114, App
C 789	14	1.1	3633	7	US-11-217-529-110	Sequence 110, App	C 862	14	1.1	12649	7	US-11-024-548-38	Sequence 38, Appl
C 790	14	1.1	3675	7	US-11-217-529-583	Sequence 583, App	C 863	14	1.1	12649	7	US-11-185-301-27	Sequence 27, Appl
C 791	14	1.1	3675	7	US-11-217-529-79669	Sequence 79669, A	C 864	14	1.1	12649	7	US-11-190-750-93	Sequence 93, Appl
C 792	14	1.1	3771	7	US-11-217-529-4666	Sequence 4666, Ap	C 865	14	1.1	12649	7	US-11-251-466-12	Sequence 26, Appl
C 793	14	1.1	3780	6	US-10-511-937-2811	Sequence 2811, Ap	C 866	14	1.1	12649	7	US-11-254-173-26	Sequence 26, Appl
C 794	14	1.1	3900	7	US-11-217-529-5779	Sequence 5779, Ap	C 867	14	1.1	12649	7	US-11-264-784-144	Sequence 144, App
C 795	14	1.1	3969	6	US-10-982-908-15	Sequence 15, Appl	C 868	14	1.1	12783	7	US-11-217-529-4700	Sequence 4700, Ap
C 796	14	1.1	4005	7	US-11-217-529-3980	Sequence 3980, Ap	C 869	14	1.1	12918	6	US-10-501-834-4	Sequence 4, Appl
C 797	14	1.1	4011	7	US-11-106-014-91	Sequence 91, Appl	C 870	14	1.1	13128	7	US-11-118-524-1	Sequence 1, Appl
C 798	14	1.1	4056	7	US-11-217-529-76436	Sequence 76436, A	C 871	14	1.1	13971	6	US-10-501-834-3	Sequence 3, Appl
C 799	14	1.1	4082	7	US-11-217-529-3000	Sequence 3000, Ap	C 872	14	1.1	14864	7	US-11-254-173-58	Sequence 58, Appl
C 800	14	1.1	4291	6	US-10-509-131-42	Sequence 42, Appl	C 873	14	1.1	14864	7	US-11-264-784-134	Sequence 134, App
C 801	14	1.1	4299	7	US-11-301-924-17	Sequence 17, Appl	C 874	14	1.1	22118	7	US-11-284-877-16	Sequence 16, Appl
C 802	14	1.1	4305	7	US-11-217-529-77088	Sequence 77088, A	C 875	14	1.1	22118	7	US-11-284-877-16	Sequence 16, Appl
C 803	14	1.1	4368	7	US-11-217-529-80559	Sequence 80559, A	C 876	13	1.0	20	6	US-10-511-937-1329	Sequence 1329, Ap
C 804	14	1.1	4419	7	US-11-217-529-2484	Sequence 2484, Ap	C 877	13	1.0	20	7	US-11-283-528-27	Sequence 27, Appl
C 805	14	1.1	4458	7	US-11-217-529-190990	Sequence 190990	C 878	13	1.0	25	7	US-11-257-502-130	Sequence 130, App
C 806	14	1.1	4584	7	US-11-217-529-3073	Sequence 3073, Ap	C 879	13	1.0	25	7	US-11-217-529-8626	Sequence 8626, Ap
C 807	14	1.1	4624	7	US-11-223-945-44	Sequence 44, Appl	C 880	13	1.0	25	7	US-11-217-529-13543	Sequence 13543, A
C 808	14	1.1	4804	7	US-11-181-115-42	Sequence 42, Appl	C 881	13	1.0	25	7	US-11-217-529-14301	Sequence 14301, A
C 809	14	1.1	4882	6	US-10-511-937-2865	Sequence 2865, Ap	C 882	13	1.0	25	7	US-11-217-529-14655	Sequence 14655, A
C 810	14	1.1	4987	7	US-10-505-928-433	Sequence 433, App	C 883	13	1.0	25	7	US-11-217-529-17470	Sequence 17470, A
C 811	14	1.1	4987	7	US-11-351-465-4	Sequence 4, Appl	C 884	13	1.0	25	7	US-11-217-529-20882	Sequence 20882, A
C 812	14	1.1	5014	7	US-11-251-465-5	Sequence 5, Appl	C 885	13	1.0	25	7	US-11-217-529-24673	Sequence 24673, A
C 813	14	1.1	5028	7	US-11-217-529-5947	Sequence 5947, Ap	C 886	13	1.0	25	7	US-11-217-529-27262	Sequence 27262, A
C 814	14	1.1	5037	7	US-11-217-529-5248	Sequence 5248, Ap	C 887	13	1.0	25	7	US-11-217-529-32882	Sequence 32882, A
C 815	14	1.1	5130	7	US-11-217-529-80522	Sequence 80522, A	C 888	13	1.0	25	7	US-11-217-529-35420	Sequence 35420, A
816	14	1.1	5410	7	US-11-217-529-190959	Sequence 190959,	C 889	13	1.0	25	7	US-11-217-529-36781	Sequence 36781, A
C 817	14	1.1	5734	6	US-10-505-928-28	Sequence 28, Appl	C 890	13	1.0	25	7	US-11-217-529-38329	Sequence 38329, A

c 891	13	1.0	25	7	US-11-217-529-38365	Sequence 38365, A	964	13	1.0	25	7	US-11-217-529-194837	Sequence 194837,
c 892	13	1.0	25	7	US-11-217-529-40930	Sequence 40930, A	965	13	1.0	25	7	US-11-217-529-195550	Sequence 195550,
c 893	13	1.0	25	7	US-11-217-529-44007	Sequence 44007, A	966	13	1.0	33	6	US-10-511-937-2350	Sequence 2350, Ap
c 894	13	1.0	25	7	US-11-217-529-44588	Sequence 44588, A	967	13	1.0	34	7	US-11-242-317-51	Sequence 51, Appl
c 895	13	1.0	25	7	US-11-217-529-47090	Sequence 47090, A	968	13	1.0	30	6	US-10-511-937-26	Sequence 26, Appl
c 896	13	1.0	25	7	US-11-217-529-47678	Sequence 47678, A	969	13	1.0	50	6	US-10-511-937-2638	Sequence 2638, Ap
c 897	13	1.0	25	7	US-11-217-529-47679	Sequence 47679, A	970	13	1.0	51	7	US-11-143-642-134	Sequence 134, App
c 898	13	1.0	25	7	US-11-217-529-47684	Sequence 47684, A	971	13	1.0	51	7	US-11-143-642-878	Sequence 878, App
c 899	13	1.0	25	7	US-11-217-529-47685	Sequence 47685, A	972	13	1.0	51	7	US-11-143-642-1649	Sequence 1649, Ap
c 900	13	1.0	25	7	US-11-217-529-47686	Sequence 47686, A	973	13	1.0	78	7	US-11-267-871-404	Sequence 404, App
c 901	13	1.0	25	7	US-11-217-529-48565	Sequence 48565, A	974	13	1.0	78	7	US-11-267-871-404	Sequence 404, App
c 902	13	1.0	25	7	US-11-217-529-49715	Sequence 49715, A	975	13	1.0	99	7	US-11-217-529-82329	Sequence 82329, A
c 903	13	1.0	25	7	US-11-217-529-49724	Sequence 49724, A	976	13	1.0	108	7	US-11-217-529-5120	Sequence 5120, Ap
c 904	13	1.0	25	7	US-11-217-529-50071	Sequence 50071, A	977	13	1.0	111	7	US-11-301-554-1744	Sequence 1744, Ap
c 905	13	1.0	25	7	US-11-217-529-50914	Sequence 50914, A	978	13	1.0	117	7	US-11-217-529-81173	Sequence 81173, A
c 906	13	1.0	25	7	US-11-217-529-51733	Sequence 51733, A	979	13	1.0	126	7	US-11-217-529-174129	Sequence 174129,
c 907	13	1.0	25	7	US-11-217-529-65411	Sequence 65411, A	980	13	1.0	132	7	US-11-217-529-4289	Sequence 4289, Ap
c 908	13	1.0	25	7	US-11-217-529-69919	Sequence 69919, A	981	13	1.0	135	7	US-11-156-0144-30	Sequence 30, Appl
c 909	13	1.0	25	7	US-11-217-529-70857	Sequence 70857, A	982	13	1.0	141	7	US-11-217-529-3771	Sequence 3771, Ap
c 910	13	1.0	25	7	US-11-217-529-70863	Sequence 70863, A	983	13	1.0	142	6	US-10-488-619-283	Sequence 283, App
c 911	13	1.0	25	7	US-11-217-529-71239	Sequence 71239, A	984	13	1.0	147	7	US-11-217-529-174015	Sequence 174015,
c 912	13	1.0	25	7	US-11-217-529-83123	Sequence 83123, A	985	13	1.0	156	7	US-11-217-529-3495	Sequence 3495, Ap
c 913	13	1.0	25	7	US-11-217-529-85114	Sequence 85114, A	986	13	1.0	171	7	US-11-217-529-80134	Sequence 80134, A
c 914	13	1.0	25	7	US-11-217-529-85224	Sequence 85224, A	987	13	1.0	174	7	US-11-217-529-166980	Sequence 166980,
c 915	13	1.0	25	7	US-11-217-529-97619	Sequence 97619, A	988	13	1.0	174	7	US-11-217-529-174097	Sequence 174097,
c 916	13	1.0	25	7	US-11-217-529-100750	Sequence 100750, A	989	13	1.0	180	7	US-11-217-529-80358	Sequence 80358, A
c 917	13	1.0	25	7	US-11-217-529-103380	Sequence 103380, A	990	13	1.0	186	7	US-11-217-529-173154	Sequence 173154,
c 918	13	1.0	25	7	US-11-217-529-108021	Sequence 108021, A	991	13	1.0	186	7	US-11-217-529-173561	Sequence 173561,
c 919	13	1.0	25	7	US-11-217-529-108177	Sequence 108177, A	992	13	1.0	186	7	US-11-217-529-174145	Sequence 174145,
c 920	13	1.0	25	7	US-11-217-529-109039	Sequence 109039, A	993	13	1.0	198	7	US-11-217-529-82248	Sequence 82248, A
c 921	13	1.0	25	7	US-11-217-529-109041	Sequence 109041, A	994	13	1.0	200	6	US-10-473-173-110	Sequence 110, App
c 922	13	1.0	25	7	US-11-217-529-109046	Sequence 109046, A	995	13	1.0	201	7	US-11-217-529-5701	Sequence 5701, Ap
c 923	13	1.0	25	7	US-11-217-529-109056	Sequence 109056, A	996	13	1.0	210	7	US-11-217-529-173857	Sequence 173857,
c 924	13	1.0	25	7	US-11-217-529-109471	Sequence 109471, A	997	13	1.0	213	7	US-11-217-529-80695	Sequence 80625, A
c 925	13	1.0	25	7	US-11-217-529-11016	Sequence 11016, A	998	13	1.0	216	6	US-10-488-619-940	Sequence 940, App
c 926	13	1.0	25	7	US-11-217-529-111328	Sequence 111328, A	999	13	1.0	219	7	US-11-217-529-82626	Sequence 82626, A
c 927	13	1.0	25	7	US-11-217-529-121641	Sequence 121641, A	c1000	13	1.0	222	7	US-11-217-529-5870	Sequence 5870, Ap
c 928	13	1.0	25	7	US-11-217-529-130730	Sequence 130730, A	c1001	13	1.0	228	7	US-11-283-332A-15	Sequence 15, Appl
c 929	13	1.0	25	7	US-11-217-529-131631	Sequence 131631, A	c1002	13	1.0	231	7	US-11-217-529-174235	Sequence 174235,
c 930	13	1.0	25	7	US-11-217-529-134730	Sequence 134730, A	c1003	13	1.0	237	7	US-11-217-529-3500	Sequence 3500, Ap
c 931	13	1.0	25	7	US-11-217-529-135393	Sequence 135393, A	1004	13	1.0	240	7	US-11-217-529-5327	Sequence 5327, Ap
c 932	13	1.0	25	7	US-11-217-529-136309	Sequence 136309, A	1005	13	1.0	242	7	US-11-301-554-615	Sequence 615, App
c 933	13	1.0	25	7	US-11-217-529-136499	Sequence 136499, A	c1006	13	1.0	242	7	US-11-301-554-722	Sequence 722, App
c 934	13	1.0	25	7	US-11-217-529-139032	Sequence 139032, A	c1007	13	1.0	244	6	US-10-488-619-1090	Sequence 1090, Ap
c 935	13	1.0	25	7	US-11-217-529-140880	Sequence 140880, A	c1008	13	1.0	255	7	US-11-217-529-80953	Sequence 80953, A
c 936	13	1.0	25	7	US-11-217-529-143821	Sequence 143821, A	1009	13	1.0	258	7	US-11-246-999-100	Sequence 100, App
c 937	13	1.0	25	7	US-11-217-529-145646	Sequence 145646, A	1010	13	1.0	262	6	US-10-488-619-696	Sequence 696, App
c 938	13	1.0	25	7	US-11-217-529-148096	Sequence 148096, A	1011	13	1.0	264	7	US-11-217-529-166817	Sequence 166817,
c 939	13	1.0	25	7	US-11-217-529-149167	Sequence 149167, A	c1012	13	1.0	267	7	US-11-217-529-6082	Sequence 6082, Ap
c 940	13	1.0	25	7	US-11-217-529-152634	Sequence 152634, A	1013	13	1.0	267	7	US-11-217-529-80386	Sequence 80386, A
c 941	13	1.0	25	7	US-11-217-529-153613	Sequence 153613, A	1014	13	1.0	282	7	US-11-301-554-1734	Sequence 1734, Ap
c 942	13	1.0	25	7	US-11-217-529-159462	Sequence 159462, A	1015	13	1.0	282	7	US-11-217-529-79368	Sequence 79368, A
c 943	13	1.0	25	7	US-11-217-529-163707	Sequence 163707, A	c1016	13	1.0	285	7	US-11-217-529-4325	Sequence 4325, Ap
c 944	13	1.0	25	7	US-11-217-529-172465	Sequence 172465, A	1017	13	1.0	285	7	US-11-217-529-5835	Sequence 5835, Ap
c 945	13	1.0	25	7	US-11-217-529-174923	Sequence 174923, A	1018	13	1.0	288	7	US-11-217-529-173959	Sequence 173959,
c 946	13	1.0	25	7	US-11-217-529-179564	Sequence 179564, A	1019	13	1.0	303	7	US-11-217-529-82528	Sequence 82528, A
c 947	13	1.0	25	7	US-11-217-529-182619	Sequence 182619, A	c1020	13	1.0	309	7	US-11-217-529-5936	Sequence 5936, Ap
c 948	13	1.0	25	7	US-11-217-529-184340	Sequence 184340, A	c1021	13	1.0	309	7	US-11-217-529-78021	Sequence 78021, A
c 949	13	1.0	25	7	US-11-217-529-184353	Sequence 184353, A	c1022	13	1.0	315	6	US-10-488-619-794	Sequence 794, App
c 950	13	1.0	25	7	US-11-217-529-184357	Sequence 184357, A	c1023	13	1.0	315	7	US-11-217-529-79623	Sequence 79623, A
c 951	13	1.0	25	7	US-11-217-529-184358	Sequence 184358, A	1024	13	1.0	321	7	US-11-217-529-81579	Sequence 81579, A
c 952	13	1.0	25	7	US-11-217-529-184361	Sequence 184361, A	c1025	13	1.0	327	7	US-11-217-529-1459	Sequence 1459, Ap
c 953	13	1.0	25	7	US-11-217-529-185253	Sequence 185253, A	c1026	13	1.0	327	7	US-11-254-679-67	Sequence 67, Appl
c 954	13	1.0	25	7	US-11-217-529-185262	Sequence 185262, A	1027	13	1.0	330	7	US-11-217-529-190909	Sequence 190909,
c 955	13	1.0	25	7	US-11-217-529-185611	Sequence 185611, A	1029	13	1.0	333	7	US-11-301-554-250	Sequence 250, App
c 956	13	1.0	25	7	US-11-217-529-185775	Sequence 185775, A	c1030	13	1.0	333	7	US-11-101-316-147	Sequence 147, App
c 957	13	1.0	25	7	US-11-217-529-185777	Sequence 185777, A	1031	13	1.0	336	7	US-11-217-529-76950	Sequence 76950, A
c 958	13	1.0	25	7	US-11-217-529-186760	Sequence 186760, A	1032	13	1.0	336	7	US-11-217-529-82553	Sequence 82553, A
c 959	13	1.0	25	7	US-11-217-529-189686	Sequence 189686, A	c1033	13	1.0	338	6	US-11-301-554-247	Sequence 247, App
c 960	13	1.0	25	7	US-11-217-529-190114	Sequence 190114, A	c1034	13	1.0	346	7	US-10-488-619-988	Sequence 988, App
c 961	13	1.0	25	7	US-11-217-529-191593	Sequence 191593, A	c1035	13	1.0	347	7	US-11-222-810-1	Sequence 1, Appl
c 962	13	1.0	25	7	US-11-217-529-192269	Sequence 192269, A	c1036	13	1.0	347	7	US-11-222-810-3	Sequence 3, Appl
c 963	13	1.0	25	7	US-11-217-529-194836	Sequence 194836, A	1037	13	1.0	348	6	US-10-488-619-2352	Sequence 2352, Ap

c1038	1.0	13	1.0	348	6	US-10-946-650-30	Sequence 30, Appl	1112	13	1.0	502	7	US-11-301-554-1361	Sequence 1361, Ap
c1039	1.0	13	1.0	348	7	US-11-217-529-191144	Sequence 191144,	1113	13	1.0	510	6	US-10-488-619-41	Sequence 41, Appl
c1040	1.0	13	1.0	349	6	US-10-473-173-230	Sequence 230, App	1114	13	1.0	510	6	US-10-488-619-1678	Sequence 1678, Ap
c1041	1.0	13	1.0	351	6	US-10-488-619-234	Sequence 234, App	1115	13	1.0	514	6	US-10-488-619-1032	Sequence 1032, Ap
c1042	1.0	13	1.0	351	7	US-11-217-529-4322	Sequence 4322, App	1116	13	1.0	516	6	US-11-301-554-663	Sequence 663, App
c1043	1.0	13	1.0	351	7	US-11-217-529-5940	Sequence 5940, Ap	1117	13	1.0	518	6	US-10-473-173-62	Sequence 62, Appl
c1044	1.0	13	1.0	360	7	US-11-254-679-8	Sequence 8, Appli	1118	13	1.0	518	6	US-10-488-619-584	Sequence 584, App
c1045	1.0	13	1.0	361	6	US-10-488-619-2566	Sequence 2566, Ap	1119	13	1.0	518	6	US-10-488-619-1469	Sequence 1469, Ap
c1046	1.0	13	1.0	370	6	US-11-301-554-1117	Sequence 1117, Ap	1120	13	1.0	519	6	US-10-488-619-1899	Sequence 1899, Ap
c1047	1.0	13	1.0	372	7	US-11-217-529-77731	Sequence 77731, A	1121	13	1.0	522	6	US-10-488-619-2787	Sequence 2787, Ap
c1048	1.0	13	1.0	372	7	US-11-217-529-773812	Sequence 773812,	1122	13	1.0	522	7	US-11-217-529-79034	Sequence 79034, A
c1049	1.0	13	1.0	374	6	US-10-488-619-2353	Sequence 2353, Ap	1123	13	1.0	526	6	US-10-488-619-811	Sequence 811, App
c1050	1.0	13	1.0	377	7	US-11-301-554-1127	Sequence 1127, Ap	1124	13	1.0	527	7	US-10-488-619-1502	Sequence 1502, Ap
c1051	1.0	13	1.0	377	7	US-11-301-554-1136	Sequence 1136, Ap	1125	13	1.0	527	7	US-11-301-554-92	Sequence 92, Appl
c1052	1.0	13	1.0	381	6	US-11-217-529-80789	Sequence 80789, A	1126	13	1.0	528	6	US-10-488-619-686	Sequence 686, App
c1053	1.0	13	1.0	381	6	US-10-488-619-388	Sequence 388, App	1127	13	1.0	528	7	US-11-217-529-5699	Sequence 5699, Ap
c1054	1.0	13	1.0	384	7	US-11-217-529-77615	Sequence 77615, A	1128	13	1.0	528	7	US-11-217-529-173604	Sequence 173604,
c1055	1.0	13	1.0	386	7	US-11-301-554-1620	Sequence 1620, Ap	1129	13	1.0	528	7	US-11-217-529-190846	Sequence 190846,
c1056	1.0	13	1.0	387	7	US-11-217-529-75469	Sequence 75469, A	1130	13	1.0	529	7	US-11-301-554-88	Sequence 88, Appl
c1057	1.0	13	1.0	387	7	US-11-217-529-190818	Sequence 190818,	1131	13	1.0	533	6	US-10-488-619-2625	Sequence 2625, Ap
c1058	1.0	13	1.0	395	7	US-11-301-554-831	Sequence 831, App	1132	13	1.0	535	6	US-10-488-619-2618	Sequence 2618, Ap
c1059	1.0	13	1.0	396	7	US-11-217-529-1875	Sequence 1875, Ap	1133	13	1.0	535	6	US-10-488-619-2850	Sequence 2850, Ap
c1060	1.0	13	1.0	396	7	US-11-217-529-5988	Sequence 5988, Ap	1134	13	1.0	535	6	US-10-488-619-2852	Sequence 2852, Ap
c1061	1.0	13	1.0	399	7	US-11-217-529-5753	Sequence 5753, Ap	1135	13	1.0	537	7	US-11-217-529-77894	Sequence 77894, A
c1062	1.0	13	1.0	401	6	US-10-488-619-276	Sequence 276, App	1136	13	1.0	537	7	US-11-217-529-82362	Sequence 82362, A
c1063	1.0	13	1.0	401	7	US-11-301-554-1476	Sequence 1476, Ap	1137	13	1.0	537	7	US-11-217-529-82567	Sequence 82567, A
c1064	1.0	13	1.0	402	7	US-11-217-529-77866	Sequence 77866, A	1138	13	1.0	540	6	US-10-488-619-2626	Sequence 2626, Ap
c1065	1.0	13	1.0	405	7	US-11-217-529-6002	Sequence 6002, Ap	1139	13	1.0	541	6	US-10-473-173-199	Sequence 199, App
c1066	1.0	13	1.0	418	7	US-11-301-554-701	Sequence 701, App	1140	13	1.0	544	7	US-11-217-529-191210	Sequence 191210,
c1067	1.0	13	1.0	423	6	US-10-488-619-208	Sequence 208, App	1141	13	1.0	546	6	US-10-488-619-2524	Sequence 2524, Ap
c1068	1.0	13	1.0	423	7	US-11-217-529-3086	Sequence 3086, Ap	1142	13	1.0	548	6	US-10-488-619-1928	Sequence 1928, Ap
c1069	1.0	13	1.0	427	7	US-11-301-554-165	Sequence 165, App	1143	13	1.0	549	7	US-11-217-529-80494	Sequence 80494, A
c1070	1.0	13	1.0	429	7	US-11-217-529-75650	Sequence 75650, A	1144	13	1.0	549	7	US-11-217-529-173542	Sequence 173542,
c1071	1.0	13	1.0	429	7	US-11-217-529-166790	Sequence 166790,	1145	13	1.0	550	7	US-11-145-307A-178	Sequence 178, App
c1072	1.0	13	1.0	429	7	US-11-217-529-190987	Sequence 190987,	1146	13	1.0	552	6	US-10-488-619-1238	Sequence 1238, Ap
c1073	1.0	13	1.0	432	7	US-11-136-524-5	Sequence 5, Appli	1147	13	1.0	552	7	US-11-217-529-4853	Sequence 4853, Ap
c1074	1.0	13	1.0	435	6	US-10-488-619-588	Sequence 588, App	1148	13	1.0	555	7	US-11-217-529-2830	Sequence 2830, Ap
c1075	1.0	13	1.0	435	7	US-11-301-554-1649	Sequence 1649, App	1149	13	1.0	555	7	US-11-217-529-81045	Sequence 81045, A
c1076	1.0	13	1.0	435	7	US-11-217-529-75781	Sequence 75781, A	1150	13	1.0	557	7	US-11-301-554-196	Sequence 196, App
c1077	1.0	13	1.0	439	6	US-10-473-173-170	Sequence 170, App	1151	13	1.0	561	7	US-11-217-529-80140	Sequence 80140, A
c1078	1.0	13	1.0	449	6	US-10-473-173-445	Sequence 445, App	1152	13	1.0	562	6	US-10-488-619-260	Sequence 260, App
c1079	1.0	13	1.0	449	6	US-10-488-619-2285	Sequence 2285, Ap	1153	13	1.0	563	6	US-10-488-619-1289	Sequence 1289, Ap
c1080	1.0	13	1.0	480	6	US-10-473-173-246	Sequence 246, App	1154	13	1.0	564	6	US-10-488-619-2851	Sequence 2851, Ap
c1081	1.0	13	1.0	451	6	US-10-488-619-315	Sequence 315, App	1155	13	1.0	567	7	US-11-217-529-3483	Sequence 3483, Ap
c1082	1.0	13	1.0	454	6	US-10-488-619-479	Sequence 479, App	1156	13	1.0	567	7	US-11-217-529-81394	Sequence 81394, A
c1083	1.0	13	1.0	455	6	US-10-488-619-274	Sequence 274, App	1157	13	1.0	567	7	US-11-217-529-166684	Sequence 166684,
c1084	1.0	13	1.0	456	7	US-11-217-529-78473	Sequence 78473, A	1158	13	1.0	568	6	US-10-488-619-2487	Sequence 2487, Ap
c1085	1.0	13	1.0	459	6	US-10-511-937-2807	Sequence 2807, Ap	1159	13	1.0	570	6	US-10-488-619-2539	Sequence 2539, Ap
c1086	1.0	13	1.0	459	7	US-11-217-529-1756	Sequence 1756, Ap	1160	13	1.0	570	6	US-10-488-619-2541	Sequence 2541, Ap
c1087	1.0	13	1.0	459	7	US-11-217-529-77693	Sequence 77693, A	1161	13	1.0	572	6	US-10-511-937-3112	Sequence 3112, Ap
c1088	1.0	13	1.0	462	6	US-10-473-173-248	Sequence 248, App	1162	13	1.0	573	6	US-10-488-619-2639	Sequence 2639, Ap
c1089	1.0	13	1.0	462	7	US-11-217-529-4331	Sequence 4331, Ap	1163	13	1.0	575	6	US-10-488-619-1236	Sequence 1236, Ap
c1090	1.0	13	1.0	466	6	US-10-488-619-1086	Sequence 1086, Ap	1164	13	1.0	575	6	US-10-488-619-2377	Sequence 2377, Ap
c1091	1.0	13	1.0	466	7	US-11-301-554-61	Sequence 61, Appl	1165	13	1.0	579	6	US-11-217-529-78746	Sequence 78746, A
c1092	1.0	13	1.0	467	6	US-10-511-937-545	Sequence 545, App	1166	13	1.0	581	6	US-10-488-619-1325	Sequence 1325, Ap
c1093	1.0	13	1.0	467	6	US-10-488-619-1364	Sequence 1364, Ap	1167	13	1.0	581	6	US-10-488-619-1646	Sequence 1646, Ap
c1094	1.0	13	1.0	467	7	US-11-301-554-456	Sequence 456, App	1168	13	1.0	581	6	US-10-488-619-2947	Sequence 2947, Ap
c1095	1.0	13	1.0	473	7	US-11-301-554-717	Sequence 717, App	1169	13	1.0	581	7	US-11-301-951-1	Sequence 1, Appli
c1096	1.0	13	1.0	474	7	US-11-301-554-157	Sequence 157, App	1170	13	1.0	588	7	US-11-217-529-78204	Sequence 78204, A
c1097	1.0	13	1.0	481	6	US-10-488-619-784	Sequence 784, App	1171	13	1.0	589	6	US-10-488-619-1674	Sequence 1674, Ap
c1098	1.0	13	1.0	482	6	US-10-488-619-2330	Sequence 2330, Ap	1172	13	1.0	590	6	US-10-488-619-2461	Sequence 2461, Ap
c1099	1.0	13	1.0	483	7	US-11-217-529-174540	Sequence 174540,	1173	13	1.0	590	7	US-11-301-554-495	Sequence 495, App
c1100	1.0	13	1.0	485	7	US-11-101-316-43	Sequence 43, Appl	1174	13	1.0	591	7	US-11-217-529-76141	Sequence 76141, A
c1101	1.0	13	1.0	488	6	US-10-473-173-332	Sequence 332, App	1175	13	1.0	591	7	US-11-217-529-80208	Sequence 80208, A
c1102	1.0	13	1.0	491	6	US-10-488-619-2307	Sequence 2307, Ap	1176	13	1.0	591	7	US-11-217-529-80438	Sequence 80438, A
c1103	1.0	13	1.0	491	7	US-10-488-619-2519	Sequence 2519, Ap	1177	13	1.0	592	6	US-10-488-619-2376	Sequence 2376, Ap
c1104	1.0	13	1.0	494	6	US-11-301-554-1537	Sequence 1537, App	1178	13	1.0	594	7	US-11-217-529-840	Sequence 840, App
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c1106	1.0	13	1.0	494	7	US-11-101-316-29	Sequence 29, Appl	1180	13	1.0	595	6	US-10-473-173-447	Sequence 447, App
c1107	1.0	13	1.0	495	6	US-10-488-619-1677	Sequence 1677, Ap	1181	13	1.0	595	6	US-10-488-619-1611	Sequence 1611, Ap
c1108	1.0	13	1.0	495	7	US-11-217-529-1375	Sequence 1375, Ap	1182	13	1.0	597	6	US-10-488-619-64	Sequence 64, Appl
c1109	1.0	13	1.0	497	6	US-10-488-619-143	Sequence 143, App	1183	13	1.0	597	6	US-10-946-650-64	Sequence 7726, A
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1187	13	1.0	603	7	US-11-217-529-81899	Sequence 81899, A	c1260	13	1.0	748	6	US-10-525-126-116	Sequence 116, App
1188	13	1.0	605	6	US-10-488-619-1468	Sequence 1468, Ap	c1261	13	1.0	748	6	US-10-525-126-117	Sequence 117, App
1189	13	1.0	609	6	US-10-488-619-1284	Sequence 1284, Ap	c1262	13	1.0	750	6	US-11-217-529-78396	Sequence 78396, A
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1191	13	1.0	612	7	US-11-217-529-3219	Sequence 3219, Ap	c1264	13	1.0	753	7	US-11-217-529-77181	Sequence 77181, A
1192	13	1.0	612	7	US-11-217-529-3507	Sequence 3507, Ap	c1265	13	1.0	756	6	US-10-488-619-1460	Sequence 1460, Ap
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1194	13	1.0	617	6	US-10-541-993-73	Sequence 73, App	c1267	13	1.0	759	7	US-11-217-529-80508	Sequence 80508, A
1195	13	1.0	618	7	US-11-217-529-2538	Sequence 2538, Ap	c1268	13	1.0	762	7	US-11-217-529-80718	Sequence 80718, A
1196	13	1.0	621	7	US-11-217-529-536	Sequence 536, App	c1269	13	1.0	765	6	US-10-488-619-808	Sequence 808, App
1197	13	1.0	621	7	US-11-217-529-3966	Sequence 3966, Ap	c1271	13	1.0	766	6	US-10-488-619-2741	Sequence 2741, Ap
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1204	13	1.0	639	7	US-11-217-529-143	Sequence 143, App	c1278	13	1.0	777	7	US-11-217-529-270	Sequence 270, App
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1237	13	1.0	699	7	US-11-217-529-2389	Sequence 2389, Ap	c1311	13	1.0	848	6	US-10-473-173-105	Sequence 105, App
1238	13	1.0	699	7	US-11-217-529-2787	Sequence 2787, Ap	c1312	13	1.0	855	7	US-11-217-529-2895	Sequence 2895, Ap
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1246	13	1.0	718	6	US-10-488-619-1363	Sequence 1363, Ap	c1320	13	1.0	876	7	US-11-252-276-15	Sequence 15, Appl
1247	13	1.0	718	6	US-10-488-619-2466	Sequence 2466, Ap	c1321	13	1.0	876	7	US-11-217-529-174501	Sequence 174501, A
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1250	13	1.0	720	7	US-11-252-276-51	Sequence 51, Appl	c1324	13	1.0	886	6	US-10-542-038-11	Sequence 11, Appl
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1252	13	1.0	720	7	US-11-217-529-76122	Sequence 76122, A	c1326	13	1.0	889	7	US-11-252-276-11	Sequence 11, Appl
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1254	13	1.0	730	7	US-11-301-554-143	Sequence 143, App	c1328	13	1.0	894	7	US-11-217-529-77988	Sequence 77988, A
1255	13	1.0	732	7	US-11-217-529-1895	Sequence 1895, Ap	c1329	13	1.0	896	7	US-11-268-890-3	Sequence 3, Appl
1256	13	1.0	732	7	US-11-217-529-76993	Sequence 76993, A	c1330	13	1.0	900	7	US-11-217-529-3118	Sequence 3118, Ap
1257	13	1.0	738	7	US-11-217-529-5593	Sequence 5593, Ap	c1331	13	1.0	906	7	US-11-252-276-17	Sequence 17, Appl

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1333	13	1.0	909	7	US-11-217-529-397	Sequence 397, App	c1408	13	1.0	1068	7	US-11-024-545-7	Sequence 7, Appl
1334	13	1.0	915	7	US-11-217-529-77828	Sequence 77828, A	c1409	13	1.0	1068	7	US-11-190-750-75	Sequence 75, Appl
c1335	13	1.0	915	7	US-11-217-529-80911	Sequence 80911, A	c1410	13	1.0	1068	7	US-11-264-784-93	Sequence 93, Appl
1336	13	1.0	918	7	US-11-217-529-4363	Sequence 4363, Ap	1411	13	1.0	1071	7	US-11-217-529-5360	Sequence 5360, Ap
c1337	13	1.0	918	7	US-11-217-529-79626	Sequence 79626, A	c1412	13	1.0	1077	7	US-11-217-529-79208	Sequence 79208, A
1338	13	1.0	921	7	US-11-217-529-80825	Sequence 80825, A	1413	13	1.0	1080	7	US-11-217-529-2670	Sequence 2670, Ap
c1339	13	1.0	921	7	US-11-217-529-82317	Sequence 82317, A	c1414	13	1.0	1080	7	US-11-217-529-166756	Sequence 166756, A
c1340	13	1.0	930	7	US-11-217-529-77031	Sequence 77031, A	c1415	13	1.0	1083	7	US-11-217-529-4517	Sequence 4517, Ap
c1341	13	1.0	936	7	US-11-217-529-1067	Sequence 1067, Ap	c1416	13	1.0	1083	7	US-11-217-529-75687	Sequence 75687, A
c1342	13	1.0	936	7	US-11-217-529-1779	Sequence 1779, Ap	1417	13	1.0	1086	7	US-11-217-529-1630	Sequence 1630, Ap
c1343	13	1.0	936	7	US-11-217-529-75485	Sequence 75485, A	1418	13	1.0	1092	7	US-11-217-529-77591	Sequence 77591, A
c1344	13	1.0	939	7	US-11-217-529-3301	Sequence 3301, Ap	1419	13	1.0	1096	6	US-10-488-619-3024	Sequence 3024, Ap
c1345	13	1.0	939	7	US-11-217-529-80365	Sequence 80365, A	c1420	13	1.0	1101	7	US-11-217-529-2832	Sequence 2832, Ap
1346	13	1.0	939	7	US-11-217-529-82368	Sequence 82368, A	c1421	13	1.0	1101	7	US-11-217-529-75617	Sequence 75617, A
1347	13	1.0	945	7	US-11-145-307A-32	Sequence 32, Appl	1422	13	1.0	1119	7	US-11-217-529-76178	Sequence 76178, A
1348	13	1.0	945	7	US-11-217-529-78102	Sequence 78102, A	c1423	13	1.0	1124	6	US-10-511-937-465	Sequence 465, App
c1349	13	1.0	948	6	US-10-488-619-3034	Sequence 3034, Ap	c1424	13	1.0	1131	7	US-11-217-529-78672	Sequence 78672, A
c1350	13	1.0	948	7	US-11-252-276-25	Sequence 25, Appl	1425	13	1.0	1134	7	US-11-217-529-75818	Sequence 75818, A
c1351	13	1.0	954	6	US-10-370-959-114	Sequence 114, App	c1426	13	1.0	1134	7	US-11-217-529-77678	Sequence 77678, A
1352	13	1.0	959	6	US-10-488-619-9	Sequence 9, Appl	1427	13	1.0	1137	7	US-11-217-529-333	Sequence 333, App
c1353	13	1.0	963	7	US-11-217-529-5170	Sequence 5170, Ap	1428	13	1.0	1137	7	US-11-217-529-3726	Sequence 3726, Ap
c1354	13	1.0	963	7	US-11-217-529-80486	Sequence 80486, A	c1429	13	1.0	1149	7	US-11-217-529-2681	Sequence 2681, Ap
1355	13	1.0	969	7	US-11-217-529-78326	Sequence 78326, A	c1430	13	1.0	1149	7	US-11-217-529-80600	Sequence 80600, A
1356	13	1.0	975	6	US-10-546-109-19	Sequence 19, Appl	c1431	13	1.0	1155	7	US-11-217-529-78503	Sequence 78503, A
1357	13	1.0	975	6	US-10-546-109-23	Sequence 23, Appl	1432	13	1.0	1158	6	US-10-511-937-333	Sequence 393, App
c1358	13	1.0	975	7	US-11-217-529-2632	Sequence 2632, Ap	c1433	13	1.0	1158	7	US-11-217-529-967	Sequence 967, App
c1359	13	1.0	976	7	US-11-217-529-191118	Sequence 191118, A	1434	13	1.0	1158	7	US-11-217-529-2777	Sequence 2777, Ap
c1360	13	1.0	978	7	US-11-252-276-23	Sequence 23, Appl	c1435	13	1.0	1158	7	US-11-217-529-76720	Sequence 76720, A
c1361	13	1.0	978	7	US-11-217-529-258	Sequence 258, App	1436	13	1.0	1161	7	US-11-217-529-166519	Sequence 166519, A
1362	13	1.0	978	7	US-11-217-529-5417	Sequence 5417, App	1437	13	1.0	1167	7	US-11-113-081A-9	Sequence 9, Appl
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c1365	13	1.0	984	7	US-11-106-014-57	Sequence 57, Appl	1440	13	1.0	1170	7	US-11-217-529-1451	Sequence 1451, A
1366	13	1.0	984	7	US-11-217-529-2754	Sequence 2754, Ap	c1442	13	1.0	1176	7	US-11-217-529-79991	Sequence 79991, A
1367	13	1.0	984	7	US-11-217-529-79413	Sequence 79413, A	1444	13	1.0	1177	7	US-11-101-316-129	Sequence 129, App
1368	13	1.0	987	7	US-11-301-554-1899	Sequence 1899, Ap	c1445	13	1.0	1179	7	US-11-217-529-1455	Sequence 1455, Ap
c1369	13	1.0	987	7	US-11-217-529-171	Sequence 171, App	c1446	13	1.0	1182	7	US-11-217-529-1214	Sequence 1214, Ap
1370	13	1.0	990	7	US-11-217-529-77231	Sequence 77231, A	c1447	13	1.0	1182	7	US-11-217-529-3621	Sequence 3621, Ap
c1371	13	1.0	990	7	US-11-217-529-166819	Sequence 166819, A	1448	13	1.0	1185	7	US-11-264-784-109	Sequence 109, App
c1372	13	1.0	993	7	US-11-217-529-174050	Sequence 174050, A	c1449	13	1.0	1185	7	US-11-217-529-80746	Sequence 80746, A
1373	13	1.0	996	7	US-11-217-529-82325	Sequence 82325, A	c1450	13	1.0	1188	7	US-11-217-529-951	Sequence 951, App
c1374	13	1.0	1000	7	US-11-233-726-3	Sequence 3, Appl	c1451	13	1.0	1188	7	US-11-217-529-76688	Sequence 76688, A
c1375	13	1.0	1000	7	US-11-233-726-31	Sequence 31, Appl	c1452	13	1.0	1188	7	US-11-217-529-79751	Sequence 79751, A
1376	13	1.0	1003	6	US-10-525-126-90	Sequence 90, Appl	1453	13	1.0	1194	7	US-11-217-529-5729	Sequence 5729, Ap
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1379	13	1.0	1003	7	US-11-226-605-24	Sequence 24, Appl	c1456	13	1.0	1198	7	US-11-305-447-3	Sequence 3, Appl
c1380	13	1.0	1003	7	US-11-226-605-32	Sequence 32, Appl	c1457	13	1.0	1206	6	US-10-505-928-70	Sequence 70, Appl
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c1394	13	1.0	1035	7	US-11-217-529-166174	Sequence 166174, A	1471	13	1.0	1249	6	US-10-370-959-112	Sequence 112, App
1395	13	1.0	1038	7	US-11-217-529-81605	Sequence 81605, A	1472	13	1.0	1251	7	US-11-217-529-76985	Sequence 76985, A
c1396	13	1.0	1041	7	US-11-217-529-80889	Sequence 80889, A	c1473	13	1.0	1256	6	US-10-505-928-29	Sequence 29, Appl
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1400	13	1.0	1047	7	US-11-311-561-3	Sequence 3, Appl	1475	13	1.0	1257	7	US-11-101-316-121	Sequence 121, App
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c1406	13	1.0	1062	7	US-11-217-529-1077	Sequence 1077, Ap	c1482	13	1.0	1275	7	US-11-217-529-792	Sequence 792, App

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 Sequence 8110, A
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 Sequence 14, Appl
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 Job time : 27 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 17, 2006, 13:27:18 ; Search time 6458 Seconds
(without alignments)
4634.158 Million cell updates/sec

Title: US-10-785-221-9

Perfect score: 1605

Sequence: 1 MARRSRHRLLLLLRLYLVA.....TPVIPALWKAAGSRGQEF 312

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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Database :

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13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1605	100.0	1295 2	BD172280 Secreted
3	1605	100.0	1295 2	BD172599 Secreted

4	1605	100.0	1295 2	BD172918 Secreted
5	1605	100.0	1295 2	BD173237 Secreted
6	1605	100.0	1295 2	BD175271 Secretary
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8	1605	100.0	1295 2	CQ957936 Sequence
9	1605	100.0	1295 2	AR216160 Sequence
10	1605	100.0	1295 2	AR410649 Sequence
11	1605	100.0	1295 2	AR439013 Sequence
12	1605	100.0	1295 2	AR473033 Sequence
13	1605	100.0	1295 2	AR527019 Sequence
14	1605	100.0	1295 2	AR566052 Sequence
15	1605	100.0	1295 2	AR592070 Sequence
16	1605	100.0	1295 2	AR604344 Sequence
17	1605	100.0	1295 2	AR604930 Sequence
18	1605	100.0	1295 2	AR613595 Sequence
19	1605	100.0	1295 2	AR629922 Sequence
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27	1605	100.0	1295 2	AX098375 Sequence
28	1605	100.0	1295 2	AX464202 Sequence
29	1605	100.0	1295 2	AX697472 Sequence
30	1605	100.0	1295 5	AY358361 Homo sapi
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32	1475	91.9	1260 5	AF255910 Homo sapi
33	1475	91.9	1263 5	BC017779 Homo sapi
34	1475	91.9	1397 2	DD210216 Methods o
35	1475	91.9	1410 5	AY016009 Homo sapi
36	1468	91.5	1246 5	AY077698 Homo sapi
37	1465	91.3	1022 2	BD084186 28 human
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39	1465	91.3	1022 2	AR650426 Sequence
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46	1172	73.0	1082 6	AF255911 Mus muscu
47	1172	73.0	1349 6	BC028778 Mus muscu
48	1172	73.0	1551 6	MMU291757 Mus muscu
49	1144	71.3	1826 2	BD268817 Vascular
50	1144	71.3	1631 2	AX036060 Sequence
51	1143.5	71.2	800 2	CQ731715 Sequence
52	1048	65.3	920 7	BV180595 sqmml1044
53	1046	65.2	905 2	AX083641 Sequence
54	679	42.3	413 2	CQ957893 Sequence
55	679	42.3	413 2	CQ957955 Sequence
56	679	42.3	413 2	AR216173 Sequence
57	679	42.3	413 2	AR629935 Sequence
58	598.5	37.3	1630 11	AJ720503 Gallus ga
59	555	34.6	484 2	CQ684447 Sequence
60	510	31.8	343 6	BD071857 Secreted
61	484	30.2	1312 6	BC079429 Rattus no
62	479	29.8	1941 6	MMU300304 Mus muscu
63	479	29.8	1943 2	BD268816 Vascular
64	479	29.8	1943 2	AX036059 Sequence
65	479	29.8	1957 6	BC024357 Mus muscu
66	461.5	28.8	933 5	AF356518 Homo sapi
67	461.5	28.8	960 5	HSX344431 Homo sapi
68	461.5	28.8	1296 2	BD268818 Vascular
69	461.5	28.8	1296 2	AX036065 Sequence
70	461.5	28.8	1724 2	BD127272 Primer fo
71	461.5	28.8	1724 2	CQ782704 Sequence
72	461.5	28.8	1724 5	AK074769 Homo sapi
73	461.5	28.8	1740 5	AF448478 Homo sapi
74	461.5	28.8	3515 2	BD127896 Primer fo
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78	461.5	28.8	3554	2	AR439323	Sequence	151	404	25.2	1857	2	AR604389	Sequence
79	461.5	28.8	3554	2	AR473343	Sequence	152	404	25.2	1857	2	AR604975	Sequence
80	461.5	28.8	3554	2	AR527329	Sequence	153	404	25.2	1857	2	AR613640	Sequence
81	461.5	28.8	3554	2	AR566362	Sequence	154	404	25.2	1857	2	AR635811	Sequence
82	461.5	28.8	3554	2	AR592380	Sequence	155	404	25.2	1857	2	AR650540	Sequence
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87	461.5	28.8	3554	2	AR650805	Sequence	160	404	25.2	1857	2	AX098379	Sequence
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91	461.5	28.8	3554	2	AR771257	Sequence	164	404	25.2	1857	2	AX490946	Sequence
92	461.5	28.8	3554	2	AR771624	Sequence	165	404	25.2	1857	2	AX697527	Sequence
93	461.5	28.8	3554	2	AR773792	Sequence	166	404	25.2	1857	5	AY358896	Homo sapi
94	461.5	28.8	3554	2	AX454676	Sequence	167	404	25.2	1915	2	CQ963661	Sequence
95	461.5	28.8	3554	2	AX464404	Sequence	168	404	25.2	1918	2	CQ963691	Sequence
96	461.5	28.8	3554	2	AX491154	Sequence	169	404	25.2	2100	5	AF111713	Homo sapi
97	461.5	28.8	3554	2	AX697831	Sequence	170	404	25.2	2141	2	BD127538	Primer fo
98	461.5	28.8	3554	5	AY358335	Homo sapi	171	404	25.2	2141	2	CQ783224	Sequence
99	461.5	28.8	3626	5	BC012147	Homo sapi	172	404	25.2	2141	5	AK075152	Homo sapi
100	461.5	28.8	3662	5	BSA416101	Homo sapi	173	404	25.2	2152	5	AK026665	Homo sapi
101	461.5	28.8	4385	2	BD275994	62 Human	174	404	25.2	2166	5	BC001533	Homo sapi
102	461.5	28.8	4386	2	BD275944	62 Human	175	404	25.2	2187	5	AF191495	Homo sapi
103	461.5	28.8	4386	2	BD275995	62 Human	176	404	25.2	3389	2	CQ490392	Sequence
104	461.5	28.7	3507	5	BC010690	Homo sapi	177	404	25.2	3389	2	CQ496249	Sequence
105	458.5	28.6	3560	2	BD250062	48 human	178	404	25.2	3738	5	AF172398	Homo sapi
106	456.5	28.4	1956	2	BD248699	Immunoglo	179	404	25.2	3794	2	CQ981235	Sequence
107	451.5	28.1	1802	11	BC080901	Xenopus t	180	404	25.2	3794	2	CQ981360	Sequence
108	439.5	27.4	1795	11	BC082710	Xenopus l	181	402.5	25.1	1065	14	AF111714	Bos tauru
109	439.5	27.4	1803	11	BC054305	Xenopus l	182	402.5	25.1	1660	14	BT020812	Bos tauru
110	439.5	27.4	1808	11	BC108445	Xenopus l	183	402.5	25.1	2701	14	BC103325	Bos tauru
111	438	27.3	980	2	AX364850	Sequence	184	401.5	25.0	1110	11	BC081502	Sequence
112	431	26.9	1482	14	AB196140	Felis cat	185	394	24.5	900	2	A91702	Sequence 6
113	427	26.6	148196	5	BS000106	Pan trogi	186	394	24.5	900	2	BD023445	Junction
114	422	26.3	31839	5	AP000225	Homo sapi	187	394	24.5	903	6	CT010347	Mus muscu
115	422	26.3	100000	5	AP000087	Homo sapi	188	394	24.5	1374	2	A91700	Sequence 4
116	422	26.3	100000	5	AP000139	Homo sapi	189	394	24.5	1374	2	BD023443	Junction
117	422	26.3	340000	5	AP001694	Homo sapi	190	394	24.5	1851	6	BC021876	Mus muscu
118	419.5	26.1	1791	11	BC046720	Xenopus l	191	394	24.5	2029	6	MMU89915	Mus muscu
119	413	25.7	897	5	AB196141	Cercopith	192	382	23.8	1676	6	BC065309	Rattus no
120	405	25.2	1421	2	BD209598	Compositi	193	382	23.8	1895	6	AF276998	Rattus no
121	405	25.2	1421	2	AR341404	Sequence	194	372.5	23.2	1116	2	CQ834198	Sequence
122	404	25.2	900	5	BT020103	Homo sapi	195	370.5	23.1	824	2	BD125382	Primer fo
123	404	25.2	900	8	AY888198	Synthetic	196	370.5	23.1	824	2	BD126276	Primer fo
124	404	25.2	900	8	AY890771	Synthetic	197	370.5	23.1	824	2	CQ780673	Sequence
125	404	25.2	900	8	AY890772	Synthetic	198	370.5	23.1	824	2	CQ781567	Sequence
126	404	25.2	900	8	BT020101	Synthetic	199	366.5	22.8	1612	5	AF154005	Homo sapi
127	404	25.2	900	8	BT020102	Synthetic	200	365.5	22.8	712	2	CQ726679	Sequence
128	404	25.2	1077	5	CR533512	Homo sapi	201	352.5	22.0	891	2	A91701	Sequence 5
129	404	25.2	1089	2	CQ718721	Homo sapi	202	352.5	22.0	891	2	BD023444	Junction
130	404	25.2	1140	2	BD080010	Human F11	203	352.5	22.0	924	2	A91699	Sequence 3
131	404	25.2	1140	2	AR201016	Sequence	204	352.5	22.0	924	2	BD023442	Junction
132	404	25.2	1236	2	CQ834196	Sequence	205	344	21.4	3363	2	CQ842001	Sequence
133	404	25.2	1421	2	BD209704	Compositi	206	344	21.4	3363	5	AK125071	Homo sapi
134	404	25.2	1421	2	AR341510	Sequence	207	340	21.2	790	2	BD126359	Primer fo
135	404	25.2	1822	2	AR478942	Sequence	208	340	21.2	790	2	CQ781650	Sequence
136	404	25.2	1822	5	AF207907	Homo sapi	209	333.5	20.8	1009	2	BD080011	Human F11
137	404	25.2	1842	2	BD075465	Secretory	210	333.5	20.8	1009	2	AR201017	Sequence
138	404	25.2	1842	2	BD172335	Secreted	211	320	19.9	21767	12	AC111214	Rattus no
139	404	25.2	1842	2	BD172644	Secreted	212	313.5	19.5	726	2	CQ957870	Sequence
140	404	25.2	1842	2	BD172963	Secreted	213	313.5	19.5	726	2	CQ957932	Sequence
141	404	25.2	1842	2	BD173282	Secreted	214	313.5	19.5	726	2	AR216157	Sequence
142	404	25.2	1842	2	BD175316	Secretory	215	313.5	19.5	726	2	AR629919	Sequence
143	404	25.2	1857	2	CQ888855	Sequence	216	312	19.4	205248	12	AC151168	Bos tauru
144	404	25.2	1857	2	CQ963827	Sequence	217	296	18.4	390	2	CQ957869	Sequence
145	404	25.2	1857	2	AR410694	Sequence	218	296	18.4	390	2	CQ957931	Sequence
146	404	25.2	1857	2	AR439058	Sequence	219	296	18.4	390	2	AR216156	Sequence
147	404	25.2	1857	2	AR473078	Sequence	220	296	18.4	390	2	AR629918	Sequence
148	404	25.2	1857	2	AR527064	Sequence	221	289.5	18.0	748	2	BD124855	Primer fo
149	404	25.2	1857	2	AR566097	Sequence	222	289.5	18.0	748	2	BD126255	Primer fo

223	289.5	18.0	748	2	CQ780146	Sequence	296	210	13.1	1813	2	AR604322	Sequence
224	289.5	18.0	748	2	CQ781546	Sequence	297	210	13.1	1813	2	AR604908	Sequence
225	284.5	17.7	614	6	AF241261	Rattus no	298	210	13.1	1813	2	AR613573	Sequence
226	271.5	16.9	612	2	BD061109	Secreted	299	210	13.1	1813	2	AR635744	Sequence
227	267.5	16.7	17116	12	AP003651	AP003651 Mus muscu	300	210	13.1	1813	2	AR650473	Sequence
c 228	267.5	16.7	174250	6	AC164162	AC164162 Mus muscu	301	210	13.1	1813	2	AR657414	Sequence
c 229	253	15.8	218	2	AX524803	Sequence	302	210	13.1	1813	2	AR720366	Sequence
c 230	253	15.8	218	2	AX524803	Sequence	303	210	13.1	1813	2	AR770925	Sequence
231	239.5	14.9	3135	11	XLU43330	U43330 Xenopus lae	304	210	13.1	1813	2	AR771292	Sequence
232	238.5	14.9	1496	14	BC102517	BC102517 Bos tauru	305	210	13.1	1813	2	AX076924	Sequence
233	238	14.8	960	2	ARI70205	Sequence	306	210	13.1	1813	2	AX076924	Sequence
234	238	14.8	960	2	ARI70205	Sequence	307	210	13.1	1813	2	AX076924	Sequence
235	238	14.8	1025	5	BC074830	BC074830 Homo sapi	308	210	13.1	1813	2	AX697447	Sequence
236	238	14.8	1025	5	BC074830	BC074830 Homo sapi	309	210	13.1	1813	5	AX558382	Homo sapi
237	238	14.8	2417	5	BC107164	BC107164 Homo sapi	310	210	13.1	1816	2	AX191598	Sequence
238	238	14.8	2419	5	BC107165	BC107165 Homo sapi	311	210	13.1	1821	2	BD123533	Secretory
239	238	14.8	2565	2	ARI70210	ARI70210 Sequence	312	210	13.1	1821	2	CS051197	Sequence
240	238	14.8	2565	2	ARI70210	ARI70210 Sequence	313	210	13.1	1821	2	AX136161	Sequence
241	238	14.8	2605	5	BC069789	BC069789 Homo sapi	314	210	13.1	1821	5	AK075396	Homo sapi
242	238	14.8	2610	5	BC069705	BC069705 Homo sapi	315	210	13.1	1838	5	AF361746	Homo sapi
243	238	14.8	2610	5	BC069723	BC069723 Homo sapi	316	210	13.1	1954	2	BD270057	Secreted
244	238	14.8	2610	5	BC069745	BC069745 Homo sapi	317	210	13.1	3675	6	BC085929	Rattus no
245	238	14.8	2610	5	BC069761	BC069761 Homo sapi	318	210	13.1	264977	12	AC097564	Rattus no
246	238	14.8	2760	2	AX399902	AX399902 Sequence	319	210	13.1	283967	12	AC105589	Rattus no
247	238	14.8	2793	2	CQ727019	CQ727019 Sequence	320	209.5	13.1	959	14	AF109645	Canis fam
248	238	14.8	2793	2	CS0861595	CS0861595 Sequence	321	208.5	13.0	1184	14	AY033651	Bos tauru
249	238	14.8	2793	2	CS047200	CS047200 Sequence	322	208.5	13.0	2095	14	BC102845	Bos tauru
250	238	14.8	2793	2	CS071113	CS071113 Sequence	323	207.5	12.9	1182	2	AR214136	Sequence
251	238	14.8	2793	2	AR214142	AR214142 Sequence	324	207.5	12.9	1840	6	BC049249	Mus muscu
252	238	14.8	2793	2	AX330282	AX330282 Sequence	325	207.5	12.9	1843	6	BC049249	Mus muscu
253	238	14.8	2793	2	AX410791	AX410791 Sequence	326	207.5	12.9	1846	2	AR214135	Sequence
254	238	14.8	2793	5	HSU79725	U79725 Human A33 a	327	207	12.9	2106	11	BC067681	Danio rer
255	238	14.8	2803	2	ARI70211	ARI70211 Sequence	328	204	12.7	1287	6	AB079880	Mus muscu
256	237.5	14.8	2140	11	CR585701	CR585701 Xenopus t	329	204	12.7	1395	2	CQ789646	Sequence
257	237.5	14.8	2161	11	BC084476	BC084476 Xenopus t	330	204	12.7	1619	5	HUMEGP3	Homo sapien
258	236	14.7	1440	11	BX934867	BX934867 Gallus ga	331	204	12.7	1631	2	E03352	cDNA sequen
259	236	14.7	1451	11	BX936257	BX936257 Gallus ga	332	204	12.7	3430	6	BC057555	Mus muscu
c 260	231	14.4	427	2	AX333408	AX333408 Sequence	333	203.5	12.7	1815	11	BC092876	Danio rer
c 261	231	14.4	427	2	AX335869	AX335869 Sequence	334	203	12.6	1110	2	AR214133	Sequence
262	231	14.4	110000	12	AY819658	Continuation (3 of	335	203	12.6	1869	2	AR214132	Sequence
c 263	231	14.4	190588	6	AC083892	AC083892 Mus muscu	336	202.5	12.6	1098	8	AY888322	Synthetic
264	231	14.4	215043	6	AC087229	AC087229 Mus muscu	337	202	12.6	1242	2	CQ870620	Sequence
265	230	14.3	2566	5	AB168694	AB168694 Macaca fa	338	202	12.6	1980	2	CQ870619	Sequence
266	229	14.3	1087	11	GGV14064	Y14064 Gallus gall	339	202	12.6	2432	2	CQ731723	Sequence
267	228	14.2	1114	11	GGV14063	Y14063 Gallus gall	340	202	12.6	2434	2	AR157886	Sequence
268	226.5	14.1	721	2	AK478943	AK478943 Sequence	341	202	12.6	2434	2	CQ896201	Sequence
269	226	14.1	2239	6	BC008528	BC008528 Mus muscu	342	202	12.6	2434	2	AX536150	Sequence
270	225.5	14.0	1837	6	BC079093	BC079093 Rattus no	343	202	12.6	2434	2	AX658159	Sequence
271	222	13.8	2307	6	AF247659	AF247659 Mus muscu	344	202	12.6	2434	5	HS46KDA	Y07593 H. sapiens m
272	211.5	13.2	2166	2	BD086132	BD086132 Sequence	345	202	12.6	2447	5	BC010536	Homo sapi
273	211.5	13.2	2166	2	BD232463	BD232463 Secreted	346	202	12.6	2537	5	BC003684	Homo sapi
274	211.5	13.2	2012	5	HS0807051	BS040913 Homo sapi	347	202	12.6	3060	2	CQ970650	Sequence
275	211.5	13.2	3010	5	HS0807051	BS040913 Homo sapi	348	202	12.6	3060	2	AR252731	Sequence
276	211.5	13.2	3012	5	HS0807051	BS040913 Homo sapi	349	202	12.6	3060	2	AR693621	Sequence
277	211	13.1	1748	2	DD165304	DD165304 RECEPTORS	350	202	12.6	3060	2	AR706173	Sequence
278	211	13.1	25001	5	AF490407	AF490407 Homo sapi	351	202	12.6	3060	2	AR757546	Sequence
c 279	211	13.1	163924	12	AL162552	AL162552 Homo sapi	352	202	12.6	3060	2	AR759046	Sequence
c 280	210.5	13.1	200822	5	AL591806	AL591806 Human DNA	353	202	12.6	3060	2	AR776360	Sequence
281	210.5	13.1	1827	2	BD094115	BD094115 Shear str	354	202	12.6	3060	2	AX055476	Sequence
282	210	13.1	1173	2	AX191588	AX191588 Sequence	355	202	12.6	3060	2	AX089948	Sequence
283	210	13.1	1734	5	BC016868	BC016868 Homo sapi	356	202	12.6	3060	2	AX358962	Sequence
284	210	13.1	1813	2	BD075398	BD075398 Secretory	357	202	12.6	3060	2	AX362455	Sequence
285	210	13.1	1813	2	BD172258	BD172258 Secreted	358	202	12.6	3060	2	AX403617	Sequence
286	210	13.1	1813	2	BD172577	BD172577 Secreted	359	202	12.6	3060	2	AX454694	Sequence
287	210	13.1	1813	2	BD172896	BD172896 Secreted	360	202	12.6	3060	2	AX491172	Sequence
288	210	13.1	1813	2	BD173215	BD173215 Secreted	361	202	12.6	3276	2	AX098210	Sequence
289	210	13.1	1813	2	BD175249	BD175249 Secretory	362	202	12.6	3963	2	CQ493642	Sequence
290	210	13.1	1813	2	AR410627	AR410627 Sequence	363	201.5	12.6	959	14	AF109646	Sus scrofa
291	210	13.1	1813	2	AR438991	AR438991 Sequence	364	201.5	12.6	1593	11	CR761956	Xenopus t
292	210	13.1	1813	2	AR473011	AR473011 Sequence	365	201.5	12.6	1650	11	CR064174	Xenopus t
293	210	13.1	1813	2	AR526997	AR526997 Sequence	366	200	12.5	1831	2	AR220843	Sequence
294	210	13.1	1813	2	AR566030	AR566030 Sequence	367	200	12.5	1831	2	AX073678	Sequence
295	210	13.1	1813	2	AR592048	AR592048 Sequence	368	199.5	12.4	1033	5	AF124598	Homo sapi

369	199.5	12.4	1098	5	BT019876	BT019876 Homo sapi	442	178	11.1	981	2	BD249458	BD249458 Human pro
370	199.5	12.4	1098	8	AY888323	AY888323 Synthetic	443	178	11.1	1221	5	AK000460	AK000460 Homo sapi
371	199.5	12.4	2354	6	HSU90716	U90716 Human cell	444	178	11.1	11850	14	AY136513	AY136513 Canis fam
372	198.5	12.4	1256	6	BC048589	BC048589 Mus muscu	445	177	11.0	65649	13	AF003131	AF003131 Caenorhab
373	198	12.3	1584	2	AR144702	AR144702 Sequence	446	177	11.0	96468	12	AC006902	AC006902 Caenorhab
374	196.5	12.2	1098	2	AR583675	AR583675 Sequence	447	177	11.0	299719	12	AC006858	AC006858 Caenorhab
375	196	12.2	1338	2	BD190112	BD190112 Polypepti	448	176.5	11.0	1380	14	BC109985	BC109985 Bos tauru
376	196	12.2	1562	6	BC088943	BC088943 Rattus no	449	176	11.0	1158	5	BC012567	BC012567 Homo sapi
377	195.5	12.2	917	11	BC097774	BC097774 Xenopus l	450	175.5	10.9	834	2	BD062092	BD062092 Alternati
378	195.5	12.2	1095	2	AR144703	AR144703 Sequence	451	175.5	10.9	1871	14	BC105434	BC105434 Bos tauru
379	195	12.1	10000	5	AP000086	AP000086 Homo sapi	452	175.5	10.9	18848	14	OCY14852	Y14852 Oryctolagus
380	194.5	12.1	10000	5	AP000138	AP000138 Homo sapi	453	175	10.9	206846	12	AC165513	AC165513 Bos tauru
381	194.5	12.1	1296	2	DD170727	DD170727 Diagnosti	454	174.5	10.9	1254	6	AB183401	AB183401 Mus muscu
382	194.5	12.1	1296	2	AX781653	AX781653 Sequence	455	174.5	10.9	1254	6	AY351388	AY351388 Mus muscu
383	194.5	12.1	1296	5	AB079879	AB079879 Homo sapi	456	174.5	10.9	2116	2	CQ893573	CQ893573 Sequence
384	194.5	12.1	1585	2	DD165325	DD165325 RECEPTORS	457	174.5	10.9	2116	2	AX058616	AX058616 Sequence
385	194.5	12.1	1652	5	AY358141	AY358141 Homo sapi	458	174.5	10.9	3868	5	BC105999	BC105999 Homo sapi
386	194.5	12.1	3423	2	AX961978	AX961978 Sequence	459	174.5	10.9	177476	5	AC010680	AC010680 Homo sapi
387	194.5	12.1	3423	5	AB071618	AB071618 Homo sapi	460	174.5	10.9	294540	5	BSA277892	AJ277892 Homo sapi
388	194	12.1	1778	11	BC092033	BC092033 Xenopus l	461	174	10.8	2340	2	CQ870000	CQ870000 Sequence
389	194	12.1	1883	11	AF268197	AF268197 Danio rer	462	174	10.8	164987	12	CR848720	CR848720 Danio rer
390	194	12.1	1932	11	BC045286	BC045286 Danio rer	463	174	10.8	176009	12	CR936415	CR936415 Danio rer
391	193.5	12.1	1515	2	AR144704	AR144704 Sequence	464	174	10.8	261943	11	BX294188	BX294188 Zebrafish
392	193.5	12.1	1742	5	HUMBGP1	D90311 Homo sapien	465	173	10.8	1121	2	CQ727036	CQ727036 Sequence
393	193.5	12.1	1760	2	E03350	E03350 cDNA sequen	466	172	10.7	1194	2	BD062093	BD062093 Alternati
394	193.5	12.1	1773	5	HUMBGPAB	M72238 Human bilia	467	172	10.7	1954	6	AB114443	AB114443 Rattus no
395	193.5	12.1	2243	2	AR718566	AR718566 Sequence	468	171.5	10.7	4460	12	AC2020249	AC202049 Drosophil
396	193.5	12.1	2243	2	AX747541	AX747541 Sequence	469	171.5	10.7	5390	2	DD212622	DD212622 DNA VACCI
397	193.5	12.1	2243	5	AK092429	AK092429 Homo sapi	470	171.5	10.7	5464	6	BC020530	BC020530 Mus muscu
398	193	12.0	1855	5	AB060855	AB060855 Macaca fa	471	171.5	10.7	5470	2	AR068047	AR068047 Sequence
399	193	12.0	10921	2	CQ789658	CQ789658 Sequence	472	171.5	10.7	5470	2	AR125598	AR125598 Sequence
400	192.5	12.0	1098	6	MMCARH	Y10320 M.musculus	473	171.5	10.7	5470	2	AX969176	AX969176 Sequence
401	192.5	12.0	1206	6	MMU90715	U90715 Mus musculus	474	171.5	10.7	5470	2	AR534574	AR534574 Sequence
402	192.5	12.0	1669	6	MMCARHOM	Y11929 M.musculus	475	171.5	10.7	5470	2	AR534574	AR534574 Sequence
403	192.5	12.0	1696	6	BC016457	BC016457 Mus muscu	476	171.5	10.7	5470	6	MMFLK1M	X70842 M.musculus
404	189.5	11.8	1033	6	AF109643	AF109643 Rattus no	477	171.5	10.7	5890	6	BC087029	BC087029 Rattus no
405	189.5	11.8	1076	6	AF109644	AF109644 Rattus no	478	171.5	10.7	16557	2	AR643923	AR643923 Sequence
406	189.5	11.8	1639	6	BC088313	BC088313 Rattus no	479	171.5	10.7	66168	13	DMSG00007	AL033125 Drosophil
407	189.5	11.8	1905	5	CQ789642	CQ789642 Sequence	480	171.5	10.7	165928	13	AC023725	AC023725 Drosophil
408	189.5	11.8	1905	5	BC034411	BC034411 Homo sapi	481	171.5	10.7	172784	13	AC105352	AC105352 Drosophil
409	188.5	11.7	723	2	CQ789648	CQ789648 Sequence	482	171.5	10.7	296227	13	AB003430	AB003430 Drosophil
410	188.5	11.7	10477	2	CQ789659	CQ789659 Sequence	483	171	10.7	1880	2	AX714170	AX714170 Sequence
411	184.5	11.5	4286	2	AR583674	AR583674 Sequence	484	171	10.7	1880	5	AK056336	AK056336 Homo sapi
412	184	11.5	2818	13	DROFAS2A	M71165 D.melanogas	485	171	10.7	18207	2	CS145814	CS145814 Sequence
413	184	11.5	2901	13	BT014661	BT014661 Drosophil	486	171	10.7	18207	2	AX828384	AX828384 Sequence
414	184	11.5	3070	13	DROFAS2B	M71166 D.melanogas	487	171	10.7	18207	5	AF156100	AF156100 Homo sapi
415	184	11.5	3414	2	CQ579258	CQ579258 Sequence	488	171	10.7	18209	2	CS161060	CS161060 Sequence
416	183	11.4	1932	2	BD205661	BD205661 97 human	489	171	10.7	211127	11	CR626890	CR626890 Zebrafish
417	182	11.3	10516	2	CQ789657	CQ789657 Sequence	490	171	10.7	219226	6	CT025660	CT025660 Mouse DNA
418	182	11.3	10961	2	CQ789656	CQ789656 Sequence	491	170.5	10.6	795	2	BD062091	BD062091 Alternati
419	181.5	11.3	1198	11	BX935151	BX935151 Gallus ga	492	170.5	10.6	5391	6	MMFLK1	X59397 Mouse Flk-1
420	181	11.3	1674	5	BC047021	BC047021 Homo sapi	493	170.5	10.6	5406	2	AR005213	AR005213 Sequence
421	181	11.3	1800	11	BC082496	BC082496 Xenopus t	494	170.5	10.6	5406	2	AR071705	AR071705 Sequence
422	181	11.3	75114	5	AP000226	AP000226 Homo sapi	495	170.5	10.6	5406	2	I25171	I25171 Sequence 5
423	180	11.2	738	7	BV524917	BV524917 G591P6062	496	170.5	10.6	5406	2	I40602	I40602 Sequence 5
424	180	11.2	754	7	BV515511	BV515511 rok91b06.	497	170.5	10.6	5406	2	AR452606	AR452606 Sequence
425	180	11.2	772	7	BV554814	BV554814 S217P6063	498	170.5	10.6	5406	2	AR760575	AR760575 Sequence
426	180	11.2	914	7	BV525303	BV525303 G591P6050	499	170.5	10.6	102624	12	AC116905	AC116905 Homo sapi
427	180	11.2	1130	2	BD233731	BD233731 31 human	500	169.5	10.6	23887	5	HSTITINN2	X90569 H.sapiens m
428	180	11.2	12692	5	AC117515	AC117515 Homo sapi	501	169.5	10.6	89623	2	CQ730839	CQ730839 Sequence
429	179.5	11.2	735	2	CQ789644	CQ789644 Sequence	502	169.5	10.6	93801	2	BD186121	BD186121 Preventio
430	179	11.2	1100	2	BD249468	BD249468 Human pro	503	169.5	10.6	93805	2	CQ730837	CQ730837 Sequence
431	179	11.2	1138	5	BC007313	BC007313 Homo sapi	504	169.5	10.6	103053	2	CQ848088	CQ848088 Sequence
432	179	11.2	1161	2	CQ970670	CQ970670 Homo sapi	505	169.5	10.6	104299	2	CS119317	CS119317 Sequence
433	179	11.2	1161	2	AX056679	AX056679 Sequence	506	169	10.5	1287	6	AB183400	AB183400 Mus muscu
434	179	11.2	1161	2	AX358982	AX358982 Sequence	507	169	10.5	1548	2	BD123602	BD123602 Secretary
435	179	11.2	1161	2	AX362475	AX362475 Sequence	508	169	10.5	1548	2	CS051335	CS051335 Sequence
436	179	11.2	1161	5	AX358897	AX358897 Homo sapi	509	169	10.5	1548	2	AX136299	AX136299 Sequence
437	179	11.2	1173	2	BD222682	BD222682 Homo sapi	510	169	10.5	1548	5	AK075502	AK075502 Homo sapi
438	179	11.2	1349	11	BC077626	BC077626 Xenopus l	511	169	10.5	1796	6	BC090970	BC090970 Mus muscu
439	179	11.2	2611	13	HMU92814	U92814 Hirudo medi	512	169	10.5	1958	6	BC057125	BC057125 Mus muscu
440	179	11.2	2877	5	HSM805288	AL834256 Homo sapi	513	169	10.5	164638	11	BX324206	BX324206 Zebrafish
441	178.5	11.1	1401	2	AR282743	AR282743 Sequence	514	168.5	10.5	2220	2	AR719239	AR719239 Sequence

515	168.5	10.5	2220	2	AX748214	Sequence	AX748214	Sequence	588	163.5	10.2	2458	2	AR762126	Sequence	AR762126	Sequence
516	168.5	10.5	2220	5	AK093583	Homo sapi	AK093583	Homo sapi	589	163.5	10.2	2458	2	AR776359	Sequence	AR776359	Sequence
517	168.5	10.5	4272	2	CQ715893	Sequence	CQ715893	Sequence	590	163.5	10.2	2458	2	AR777397	Sequence	AR777397	Sequence
518	168.5	10.5	4525	5	HSM805354	Sequence	AL834139	Homo sapi	591	163.5	10.2	2458	2	AX358876	Sequence	AX358876	Sequence
519	168.5	10.5	147867	12	AC179594	Sequence	AC179594	Strongylo	592	163.5	10.2	2458	2	AX362369	Sequence	AX362369	Sequence
520	168	10.5	603	2	CQ412020	Sequence	CQ412020	Sequence	593	163.5	10.2	2458	2	AX403615	Sequence	AX403615	Sequence
521	168	10.5	930	2	E01971	Sequence	E01971	DNA encodin	594	163.5	10.2	2458	2	AX454478	Sequence	AX454478	Sequence
522	168	10.5	1035	5	BT009774	Homo sapi	BT009774	Homo sapi	595	163.5	10.2	2458	2	AX464254	Sequence	AX464254	Sequence
523	168	10.5	1035	8	AX889715	Synthetic	AX889715	Synthetic	596	163.5	10.2	2458	2	AX490956	Sequence	AX490956	Sequence
524	168	10.5	2249	2	CQ834032	Sequence	CQ834032	Sequence	597	163.5	10.2	2458	2	AX538183	Sequence	AX538183	Sequence
525	168	10.5	2249	2	CQ875304	Sequence	CQ875304	Sequence	598	163.5	10.2	2458	5	AY326422	Homo sapi	AY326422	Homo sapi
526	168	10.5	2249	2	CS063173	Sequence	CS063173	Sequence	599	163.5	10.2	2458	5	AY358340	Homo sapi	AY358340	Homo sapi
527	168	10.5	2249	2	CS080954	Sequence	CS080954	Sequence	600	163.5	10.2	2627	5	AK026068	Homo sapi	AK026068	Homo sapi
528	168	10.5	2249	5	BC005008	Homo sapi	BC005008	Homo sapi	601	163.5	10.2	4398	11	D85084	Cynops pyrr	D85084	Cynops pyrr
529	168	10.5	2533	2	CQ800161	Sequence	CQ800161	Sequence	602	163.5	10.2	5120	2	CQ802458	Sequence	CQ802458	Sequence
530	168	10.5	2533	2	CS160475	Sequence	CS160475	Sequence	603	163.5	10.2	140127	12	AC141742	Sequence	AC141742	Sequence
531	168	10.5	2533	2	AX331130	Sequence	AX331130	Sequence	604	163	10.2	2879	11	BC075300	Xenopus t	BC075300	Xenopus t
532	168	10.5	2533	2	AX335345	Sequence	AX335345	Sequence	605	163	10.2	6332	6	AK122223	Mus muscu	AK122223	Mus muscu
533	168	10.5	2533	2	AX409638	Sequence	AX409638	Sequence	606	162.5	10.1	3870	2	AX714318	Homo sapi	AX714318	Homo sapi
534	168	10.5	2533	5	HUMANCA	Sequence	M18728	Human nonsp	607	162.5	10.1	3870	5	AK056557	Homo sapi	AK056557	Homo sapi
535	168	10.5	2534	2	E01972	Sequence	E01972	DNA encodin	608	162.5	10.1	84852	11	CR792456	Sequence	CR792456	Sequence
536	168	10.5	168180	5	BS000002	Sequence	BS000002	Pan trogl	609	162	10.1	2178	11	AB008163	Xenopus l	AB008163	Xenopus l
537	167.5	10.4	578	2	BD014251	Method fo	BD014251	Method fo	610	162	10.1	2431	2	AR100641	Sequence	AR100641	Sequence
538	167.5	10.4	4016	6	RNU93307	Sequence	U93307	Rattus norv	611	162	10.1	2431	2	E34072	Carrier/DNA	E34072	Carrier/DNA
539	167.5	10.4	5892	6	RNU93306	Sequence	U93306	Rattus norv	612	162	10.1	3015	2	CQ842363	Sequence	CQ842363	Sequence
540	167	10.4	1670	2	AX713827	Sequence	AX713827	Sequence	613	162	10.1	3015	5	AK123850	Homo sapi	AK123850	Homo sapi
541	167	10.4	1670	5	AK055684	Homo sapi	AK055684	Homo sapi	614	162	10.1	12255	11	AJ584653	Gallus ga	AJ584653	Gallus ga
542	167	10.4	2127	5	BC024300	Homo sapi	BC024300	Homo sapi	615	161.5	10.1	1338	6	AB183399	Mus muscu	AB183399	Mus muscu
543	167	10.4	2447	6	AY506558	Mus muscu	AY506558	Mus muscu	616	161.5	10.1	1817	6	AF539424	Mus muscu	AF539424	Mus muscu
544	167	10.4	2463	6	AY158090	Mus muscu	AY158090	Mus muscu	617	161.5	10.1	1935	2	BD247473	Molecules	BD247473	Molecules
545	167	10.4	2746	2	AX135099	Sequence	AX135099	Sequence	618	161.5	10.1	1935	2	CS019551	Sequence	CS019551	Sequence
546	167	10.4	4719	2	AX250047	Sequence	AX250047	Sequence	619	161.5	10.1	1935	2	AR278814	Sequence	AR278814	Sequence
547	167	10.4	4719	5	AB028984	Homo sapi	AB028984	Homo sapi	620	161.5	10.1	2024	6	AB052293	Mus muscu	AB052293	Mus muscu
548	167	10.4	5502	2	AX250004	Sequence	AX250004	Sequence	621	161.5	10.1	2030	6	BC095986	Mus muscu	BC095986	Mus muscu
549	166.5	10.4	712	14	AY649414	Oryctolag	BD261770	12 human	622	161.5	10.1	4444	6	AF434663	Mus muscu	AF434663	Mus muscu
550	166.5	10.4	1329	5	CD261770	Sequence	BD261770	12 human	623	161.5	10.1	10976	2	CQ869763	Sequence	CQ869763	Sequence
551	166.5	10.4	1329	5	CR457157	Homo sapi	CR457157	Homo sapi	624	161	10.0	1189	5	HUMANCB	Human norma	M29541	Human norma
552	166.5	10.4	1448	5	BC035930	Homo sapi	BC035930	Homo sapi	625	161	10.0	1278	2	DD178443	SECRETED	DD178443	SECRETED
553	166.5	10.4	1598	2	BD247472	Molecules	BD247472	Molecules	626	161	10.0	1450	6	AB064265	Mus muscu	AB064265	Mus muscu
554	166.5	10.4	1598	2	CS019549	Sequence	CS019549	Sequence	627	161	10.0	1833	2	CQ413276	Sequence	CQ413276	Sequence
555	166.5	10.4	1598	2	AX278813	Sequence	AX278813	Sequence	628	161	10.0	1964	2	I08158	Sequence	I08158	Sequence
556	166.5	10.4	1862	2	AX399846	Sequence	AX399846	Sequence	629	161	10.0	1964	2	I08168	Sequence 12	I08168	Sequence 12
557	166.5	10.4	3512	2	CQ981582	Sequence	CQ981582	Sequence	630	161	10.0	2527	5	HUMANTNCA	Human nonsp	M18216	Human nonsp
558	166.5	10.4	3512	2	DD171238	A diagnos	DD171238	A diagnos	631	161	10.0	3412	6	AY495696	Rattus no	AY495696	Rattus no
559	166.5	10.4	3512	5	AF132811	Homo sapi	AF132811	Homo sapi	632	161	10.0	4249	6	AY495695	Rattus no	AY495695	Rattus no
560	166.5	10.4	4790	6	S53103	Sequence	S53103	NYK/FIK-1=	633	161	10.0	160223	11	CR318597	Sequence	CR318597	Sequence
561	166.5	10.4	6599	2	AR578174	Sequence	AR578174	Sequence	634	161	10.0	162400	5	AC012414	Homo sapi	AC012414	Homo sapi
562	166.5	10.4	12381	2	AR643924	Sequence	AR643924	Sequence	635	161	10.0	167635	12	CR383673	Danio rer	CR383673	Danio rer
563	166	10.3	2895	11	AY029403	Sequence	AY029403	Danio rer	636	160.5	10.0	14785	6	AY429596	Rattus no	AY429596	Rattus no
564	166	10.3	203638	12	AC180713	Sequence	AC180713	Strongylo	637	160.5	10.0	158465	5	AC068446	Homo sapi	AC068446	Homo sapi
565	165	10.3	2256	11	BC057517	Sequence	BC057517	Danio rer	638	160.5	10.0	172233	5	AC060814	Homo sapi	AC060814	Homo sapi
566	164.5	10.2	1006	2	CS072352	Sequence	CS072352	Sequence	639	160	10.0	2350	2	CQ878954	Sequence	CQ878954	Sequence
567	164	10.2	3488	6	AF016619	Mus muscu	AF016619	Mus muscu	640	160	10.0	2350	2	CQ891882	Sequence	CQ891882	Sequence
568	164	10.2	3488	6	AF001287	Mus muscu	AF001287	Mus muscu	641	160	10.0	4723	5	HSU75330	Human neu	U75330	Human neu
569	164	10.2	4821	6	AF001286	Mus muscu	AF001286	Mus muscu	642	160	10.0	173270	5	AC024886	Homo sapi	AC024886	Homo sapi
570	163.5	10.2	1135	2	BD233754	Sequence	BD233754	Sequence	643	159.5	9.9	1247	11	Y08823	Gallus gall	Y08823	Gallus gall
571	163.5	10.2	1413	2	BD140567	Polypteri	BD140567	Polypteri	644	159.5	9.9	117345	5	AP001775	Homo sapi	AP001775	Homo sapi
572	163.5	10.2	1413	2	AR429086	Sequence	AR429086	Sequence	645	159.5	9.9	187235	12	AP001785	Homo sapi	AP001785	Homo sapi
573	163.5	10.2	1413	2	AR534977	Sequence	AR534977	Sequence	646	159.5	9.9	196928	12	AP000847	Homo sapi	AP000847	Homo sapi
574	163.5	10.2	1413	2	AR691124	Sequence	AR691124	Sequence	647	159	9.9	1165	2	CS032235	Sequence	CS032235	Sequence
575	163.5	10.2	1413	2	AR705562	Sequence	AR705562	Sequence	648	159	9.9	1165	2	CS041187	Sequence	CS041187	Sequence
576	163.5	10.2	1413	2	AR708634	Sequence	AR708634	Sequence	649	159	9.9	1165	2	CS161962	Sequence	CS161962	Sequence
577	163.5	10.2	1413	2	AX375966	Sequence	AX375966	Sequence	650	159	9.9	1165	2	AX780066	Sequence	AX780066	Sequence
578	163.5	10.2	1413	5	AY358334	Homo sapi	AY358334	Homo sapi	651	159	9.9	1165	5	HSMLADRB	Sequence	HSMLADRB	Sequence
579	163.5	10.2	2298	5	BC009371	Homo sapi	BC009371	Homo sapi	652	159	9.9	1766	2	CQ731700	Sequence	CQ731700	Sequence
580	163.5	10.2	2458	2	CQ767591	Sequence	CQ767591	Sequence	653	159	9.9	2943	6	AY167411	Rattus no	AY167411	Rattus no
581	163.5	10.2	2458	2	CQ970564	Sequence	CQ970564	Sequence	654	159	9.9	3619	5	BC052946	Homo sapi	BC052946	Homo sapi
582	163.5	10.2	2458	2	AK252730	Sequence	AK252730	Sequence	655	159	9.9	105350	12	AP000661	Homo sapi	AP000661	Homo sapi
583	163.5	10.2	2458	2	AR693620	Sequence	AR693620	Sequence	656	158	9.8	1852	11	CR761594	Xenopus t	CR761594	Xenopus t
584	163.5	10.2	2458	2	AR697403	Sequence	AR697403	Sequence	657	158	9.8	2144	2	CQ714926	Sequence	CQ714926	Sequence
585	163.5	10.2	2458	2	AR706172	Sequence	AR706172	Sequence	658	158	9.8	3814	11	XELNCAMA	Xenopus lae	M76710	Xenopus lae
586	163.5	10.2	2458	2	AR757545	Sequence	AR757545	Sequence	659	158	9.8	4321	2	AX921112	Sequence	AX921112	Sequence
587	163.5	10.2	2458	2	AR759045	Sequence	AR759045	Sequence	660	158	9.8	4640	13	DMSTRK	D.melanogas	X63453	D.melanogas

c	661	158	9.8	83495	13	AC087076	AC087076 Caenorhab	734	156	9.7	5194	13	BT010247	BT010247 Droso
	662	157.5	9.8	245	14	DQ152972	DQ152972 Ovis arie	735	156	9.7	6398	5	AB177856	AB177856 Homo sapi
	663	157.5	9.8	1129	11	AF337034	AF337034 Danio rer	736	156	9.7	6412	5	BC048768	BC048768 Homo sapi
	664	157.5	9.8	1520	2	BD261709	BD261709 12 human	737	156	9.7	7673	5	AB177857	AB177857 Homo sapi
	665	157.5	9.8	3063	11	AB231586	AB231586 Danio rer	738	156	9.7	7702	2	CQ871861	CQ871861 Sequence
	666	157.5	9.8	6860	11	AF304130	AF304130 Danio rer	739	156	9.7	7702	2	AR380791	AR380791 Sequence
	667	157.5	9.8	18534	2	CQ730656	CQ730656 Sequence	740	156	9.7	7702	2	AR633321	AR633321 Sequence
	668	157	9.8	993	2	AR072053	AR072053 Sequence	741	156	9.7	7702	2	AR707042	AR707042 Sequence
	669	157	9.8	1173	2	CQ720045	CQ720045 Sequence	742	156	9.7	7702	2	AX658135	AX658135 Sequence
	670	157	9.8	1422	5	HUMCEAX	M16234 Human carci	743	156	9.7	7702	5	HSLARR	Y00815 Human mRNA
	671	157	9.8	2658	2	CQ583539	CQ583539 Sequence	744	156	9.7	7945	2	CQ496043	CQ496043 Sequence
	672	157	9.8	2888	5	BC034671	BC034671 Homo sapi	745	156	9.7	79405	6	AL928721	AL928721 Mouse DNA
	673	157	9.8	2928	2	E01630	M01630 cDNA encodi	c 746	156	9.7	199446	6	AC125069	AC125069 Mus muscu
	674	157	9.8	2928	2	E13123	E13123 Human gene	c 747	156	9.7	202887	6	AL928789	AL928789 Mouse DNA
	675	157	9.8	2929	5	HUMCEA	M15042 Human carci	748	155.5	9.7	1119	11	EX935530	EX935530 Gallus ga
	676	157	9.8	2943	11	BC089177	BC089177 Xenopus l	749	155.5	9.7	1459	2	AR494544	AR494544 Sequence
	677	157	9.8	2947	6	D89995	D89995 Rattus sp.	750	155.5	9.7	1508	2	BD261716	BD261716 12 human
	678	157	9.8	2960	11	BC108932	BC108932 Xenopus l	751	155.5	9.7	2666	5	BC098579	BC098579 Homo sapi
	679	157	9.8	2974	2	CQ833969	CQ833969 Sequence	752	155.5	9.7	3363	11	AJ781309	AJ781309 Danio rer
	680	157	9.8	2974	2	CQ981503	CQ981503 Sequence	753	155.5	9.7	3407	11	AJ781308	AJ781308 Danio rer
	681	157	9.8	2974	2	CS017569	CS017569 Sequence	754	155.5	9.7	3788	11	CHKKUG	M63437 Chicken KLG
	682	157	9.8	2974	2	CS130722	CS130722 Sequence	755	155.5	9.7	4491	2	CQ848038	CQ848038 Sequence
	683	157	9.8	2974	2	DD161432	DD161432 BPITOPF S	756	155.5	9.7	4491	2	CQ848044	CQ848044 Sequence
	684	157	9.8	2974	2	AX332574	AX332574 Sequence	757	155.5	9.7	5510	2	AX409111	AX409111 Sequence
	685	157	9.8	2974	2	AX409670	AX409670 Sequence	758	155.5	9.7	5510	5	D86983	D86983 Homo sapien
	686	157	9.8	2974	2	AX658324	AX658324 Sequence	759	155.5	9.7	6847	2	CQ896237	CQ896237 Sequence
	687	157	9.8	2974	2	AX677147	AX677147 Sequence	760	155.5	9.7	6847	2	CQ896549	CQ896549 Sequence
	688	157	9.8	2974	2	AX805532	AX805532 Sequence	761	155.5	9.7	6847	2	CS247679	CS247679 Sequence
	689	157	9.8	2974	5	HUMCEAF	M29540 Human carci	762	155.5	9.7	6847	2	CS247680	CS247680 Sequence
	690	157	9.8	3036	2	CQ800159	CQ800159 Sequence	763	155.5	9.7	6847	5	AF200348	AF200348 Homo sapi
	691	157	9.8	3036	5	HUMANTCE	M17303 Human carci	c 764	155.5	9.7	255090	12	AC073798	AC073798 Mus muscu
	692	157	9.8	3076	2	E16456	E16456 Rat mRNA fo	765	155	9.7	906	5	BC103983	BC103983 Homo sapi
	693	157	9.8	3077	6	D89996	D89996 Rattus sp.	766	155	9.7	906	5	BC103984	BC103984 Homo sapi
	694	157	9.8	3441	2	AR072052	AR072052 Sequence	767	155	9.7	994	2	AR655000	AR655000 Sequence
	695	157	9.8	4306	13	AF312580	AF312580 Droso	768	155	9.7	1801	6	BC078966	BC078966 Rattus no
	696	157	9.8	5514	13	BT015246	BT015246 Droso	769	155	9.7	2178	11	BC078966	BC078966 Rattus no
	697	157	9.8	17255	5	AC136352	AC136352 Homo sapi	770	155	9.7	2613	2	CQ841466	CQ841466 Sequence
	698	156.5	9.8	1266	2	AR634772	AR634772 Sequence	771	155	9.7	2613	5	AK124504	AK124504 Homo sapi
	699	156.5	9.8	1314	5	AF538973	AF538973 Homo sapi	772	155	9.7	2922	6	MMEGPD	X67279 M.musculus
	700	156.5	9.8	1335	2	AR634774	AR634774 Sequence	773	155	9.7	3020	5	AB005060	AB005060 Homo sapi
	701	156.5	9.8	1422	5	BC112136	BC112136 Homo sapi	774	155	9.7	3720	11	XELNCAM	M25696 X.laevvis ne
	702	156.5	9.8	1435	5	BC112138	BC112138 Homo sapi	775	155	9.7	4454	11	BC081181	BC081181 Xenopus l
	703	156.5	9.8	2713	2	AR717761	AR717761 Sequence	776	154.5	9.6	789	5	DQ234351	DQ234351 Homo sapi
	704	156.5	9.8	2713	2	AX746736	AX746736 Sequence	777	154.5	9.6	1161	2	AX645013	AX645013 Sequence
	705	156.5	9.8	2713	5	AK091023	AK091023 Homo sapi	778	154.5	9.6	1263	5	AY766113	AY766113 Homo sapi
	706	156.5	9.8	3173	2	CS108360	CS108360 Sequence	779	154.5	9.6	1302	2	CQ591387	CQ591387 Sequence
	707	156.5	9.8	3173	2	I08159	I08159 Sequence 8	780	154.5	9.6	1307	2	AX512897	AX512897 Sequence
	708	156.5	9.8	3173	2	I08162	I08162 Sequence 1	781	154.5	9.6	1339	2	I08161	I08161 Sequence 12
	709	156.5	9.8	3173	5	HSTW2CRA	X14831 Human mRNA	782	154.5	9.6	1339	2	I08164	I08164 Sequence 5
	710	156.5	9.8	3738	2	CQ715811	CQ715811 Sequence	783	154.5	9.6	1514	2	AX645011	AX645011 Sequence
	711	156.5	9.8	3864	2	CQ715175	CQ715175 Sequence	784	154.5	9.6	1981	13	AY089628	AY089628 Droso
	712	156.5	9.8	4053	13	AF103399	AF103399 Manduca s	785	154.5	9.6	2173	5	BC068457	BC068457 Homo sapi
	713	156.5	9.8	4682	2	CS185644	CS185644 Sequence	786	154.5	9.6	2176	5	AF363368	AF363368 Homo sapi
	714	156.5	9.8	5598	5	AB046788	AB046788 Homo sapi	787	154.5	9.6	3373	11	AF461120	AF461120 Danio rer
	715	156.5	9.8	5626	13	AF103390	AF103390 Manduca s	788	154.5	9.6	3971	11	CHKCONNE	D16541 Gallus gall
	716	156.5	9.8	6215	2	AX556709	AX556709 Sequence	789	154.5	9.6	6939	2	AX780120	AX780120 Sequence
	717	156.5	9.8	6814	2	AR220825	AR220825 Sequence	790	154.5	9.6	6939	2	AX780121	AX780121 Sequence
	718	156.5	9.8	21852	12	AP003671	AP003671 Mus muscu	791	154.5	9.6	13149	2	CQ728817	CQ728817 Sequence
	719	156	9.7	605	2	BD125229	BD125229 Primer fo	792	154.5	9.6	13793	5	HSMHSP	X62515 H.sapiens m
	720	156	9.7	605	2	CQ780520	CQ780520 Sequence	793	154.5	9.6	14327	2	CS070215	CS070215 Sequence
	721	156	9.7	897	2	AR655001	AR655001 Sequence	794	154.5	9.6	14327	5	HUMHSP2B	M85289 Human hepar
	722	156	9.7	1507	2	CQ610827	CQ610827 Sequence	795	154	9.6	2188	6	AB001576	AB001576 Rattus ap
	723	156	9.7	1826	11	BC082514	BC082514 Xenopus t	796	154	9.6	5923	11	AF603753	AF603753 Danio rer
	724	156	9.7	1837	2	CQ869997	CQ869997 Sequence	797	154	9.6	8883	6	AY273816	AY273816 Rattus no
	725	156	9.7	1841	13	DME312132	DME312132 Droso	798	154	9.6	251435	12	AC128510	AC128510 Rattus no
	726	156	9.7	1842	2	AR098145	AR098145 Sequence	c 799	154	9.6	221235	12	AC128510	AC128510 Rattus no
	727	156	9.7	1884	2	AR116617	AR116617 Sequence	c 800	154	9.6	264547	12	AC094432	AC094432 Rattus no
	728	156	9.7	1965	5	BC012102	BC012102 Homo sapi	801	153.5	9.6	1290	14	AY487419	AY487419 Bos tauru
	729	156	9.7	2687	13	DME312133	DME312133 Droso	802	153.5	9.6	1316	11	BC095690	BC095690 Danio rer
	730	156	9.7	4355	5	AB209170	AB209170 Homo sapi	803	153.5	9.6	1538	14	BC109595	BC109595 Bos tauru
	731	156	9.7	4579	13	DME312134	DME312134 Droso	804	153.5	9.6	1565	11	AF364048	AF364048 Gallus ga
	732	156	9.7	5099	13	DME312135	DME312135 Droso	805	153.5	9.6	2654	11	AF257353	AF257353 Gallus ga
	733	156	9.7	5105	11	AB185923	AB185923 Gallus ga	806	153.5	9.6	4171	6	BC060226	BC060226 Mus muscu

807	153.5	9.6	4305	2	CQ613728	CQ613728 Sequence	880	150.5	9.4	1399	6	AB236330	AB236330 Mus muscu
808	153.5	9.6	4346	6	BC055333	BC055333 Mus muscu	881	150.5	9.4	1921	6	RATRECTO	J04963 Rat ecto-AT
809	153.5	9.6	4715	13	AY121698	AY121698 Drosophil	882	150.5	9.4	5287	2	CQ895657	CQ895657 Sequence
810	153.5	9.6	4726	6	AF210316	AF210316 Drosophil	883	150.5	9.4	5287	2	CS036446	CS036446 Sequence
811	153	9.5	1786	6	MWCEP1	X15351 Mouse mRNA	884	150.5	9.4	5287	2	CS045398	CS045398 Sequence
812	153	9.5	2839	2	I08156	I08156 Sequence 2	885	150.5	9.4	5287	2	CS063105	CS063105 Sequence
813	153	9.5	2839	2	I08166	I08166 Sequence 8	886	150.5	9.4	5287	2	CS080886	CS080886 Sequence
814	153	9.5	3316	2	CQ841586	CQ841586 Sequence	887	150.5	9.4	5287	5	AB050468	AB050468 Homo sapi
815	153	9.5	3316	11	AK122611	AK122611 Homo sapi	888	150.5	9.4	8035	13	AF254867	AF254867 Drosophil
816	153	9.5	3738	11	AY029401	AY029401 Danio rer	889	150.5	9.4	20435	5	HSJ2535	AJ002535 Homo sapi
817	153	9.5	4102	13	DMTRCRGA	Z21641 D.melanogas	890	150.5	9.4	25782	2	CS211523	CS211523 Sequence
818	153	9.5	4102	13	DROIRRCRP	L11040 Drosophila	891	150.5	9.3	1302	14	AY345129	AY345129 Bos tauru
819	153	9.5	4645	2	CQ591393	CQ591393 Sequence	892	150.5	9.3	1334	14	AY345128	AY345128 Bos tauru
820	153	9.5	4645	2	CQ847776	CQ847776 Sequence	893	150.5	9.3	1362	2	CQ719636	CQ719636 Sequence
821	153	9.5	4755	5	AB033089	AB033089 Homo sapi	894	150.5	9.3	1364	2	AR561703	AR561703 Sequence
822	153	9.5	4775	13	BT015249	BT015249 Drosophil	895	150.5	9.3	1364	5	HSCGM6MR	X52378 Human CGM6
823	153	9.5	4868	5	BC036502	BC036502 Homo sapi	896	150.5	9.3	2287	2	AR380671	AR380671 Sequence
824	153	9.5	12699	11	D83390	D83390 Gallus gall	897	150.5	9.3	2287	5	HUMNCAM	D90064 Homo sapien
825	152.5	9.5	1273	2	AR278799	AR278799 Sequence	898	150.5	9.3	2287	5	HUMNCAX	M33326 Human nonsp
826	152.5	9.5	1281	14	AY345130	AY345130 Bos tauru	899	150.5	9.3	2297	2	CQ834034	CQ834034 Sequence
827	152.5	9.5	1396	13	AY529704	AY529704 Antheraea	900	150.5	9.3	2297	5	BC026263	BC026263 Homo sapi
828	152.5	9.5	1715	2	CQ722664	CQ722664 Sequence	901	150.5	9.3	2459	2	CQ583689	CQ583689 Sequence
829	152.5	9.5	2070	5	AY650370	AY650370 Macaca fa	902	150.5	9.3	2645	6	MUSHPVRA	M77196 Mouse hepat
830	152.5	9.5	2131	2	CQ590793	CQ590793 Sequence	903	150.5	9.3	3364	6	AF374460	AF374460 Mus muscu
831	152.5	9.5	2157	13	AY051829	AY051829 Drosophil	904	150.5	9.3	3866	6	BC109176	BC109176 Mus muscu
832	152.5	9.5	2377	6	AF195662	AF195662 Mus muscu	905	150.5	9.3	4068	14	DQ269018	DQ269018 Canis fam
833	152.5	9.5	2728	2	CQ413817	CQ413817 Sequence	906	150.5	9.3	4724	6	RATMYRPHOS	L19933 Rattus norv
834	152.5	9.5	2994	6	BC029659	BC029659 Mus muscu	907	150.5	9.3	4783	6	BC075640	BC075640 Mus muscu
835	152.5	9.5	3366	6	AY059393	AY059393 Mus muscu	908	150.5	9.3	5383	6	RATLARPTPB	L12329 Rat leukocy
836	152.5	9.5	3887	5	BC070119	BC070119 Homo sapi	909	150.5	9.3	5690	2	AR060681	AR060681 Sequence
837	152.5	9.5	4844	2	CQ728171	CQ728171 Sequence	910	150.5	9.3	5690	2	AR064169	AR064169 Sequence
838	152	9.5	2099	6	AK220367	AK220367 Mus muscu	911	150.5	9.3	6469	6	RATLARPTPA	L11587 Rat leukocy
839	152	9.5	2544	14	AY790331	AY790331 Felis cat	912	150.5	9.3	6545	6	RATLARA	L11586 Rat leukocy
840	152	9.5	2832	2	CQ580356	CQ580356 Sequence	913	150.5	9.3	7119	6	BC105753	BC105753 Rattus no
841	152	9.5	2919	14	AB195841	AB195841 Felis cat	914	150.5	9.3	46638	13	CEU33058	U33058 Caenorhabdi
842	152	9.5	3853	13	DRONRGAA	M28231 Drosophila	c 915	150.5	9.3	166987	5	AC097004	AC097004 Papio anu
843	152	9.5	4041	2	CQ573942	CQ573942 Sequence	c 916	150.5	9.3	167543	5	AC092554	AC092554 Papio anu
844	152	9.5	4433	13	AY1058284	AY1058284 Drosophil	917	149.5	9.3	1050	8	AY890598	AY890598 Synthetic
845	152	9.5	4455	13	AY128456	AY128456 Drosophil	918	149.5	9.3	1122	6	AY259213	AY259213 Mus muscu
846	152	9.5	8574	13	DMRG2	AF050085 Drosophil	919	149.5	9.3	1322	6	AY326421	AY326421 Mus muscu
847	152	9.5	15597	13	AF074901	AF074901 Caenorhab	920	149.5	9.3	1364	14	AY487416	AY487416 Bos tauru
848	152	9.5	20510	2	CQ573941	CQ573941 Sequence	921	149.5	9.3	1410	6	AF282980	AF282980 Mus muscu
849	152	9.5	71320	12	AC020124	AC020124 Drosophil	922	149.5	9.3	1605	2	CQ599856	CQ599856 Sequence
c 850	152	9.5	77635	12	DMBR40010	AL122024 Drosophil	923	149.5	9.3	1609	5	AB056375	AB056375 Macaca fa
851	152	9.5	174367	13	AC023696	AC023696 Drosophil	924	149.5	9.3	1830	6	BC026447	BC026447 Mus muscu
852	152	9.5	185405	13	AC023743	AC023743 Drosophil	925	149.5	9.3	1972	6	AY059394	AY059394 Mus muscu
853	152	9.5	299633	13	AE003444	AE003444 Drosophil	926	149.5	9.3	2157	2	AR494543	AR494543 Sequence
854	151.5	9.4	658	2	CQ719456	CQ719456 Sequence	927	149.5	9.3	3578	6	BC061740	BC061740 Rattus no
855	151.5	9.4	851	11	BX932255	BX932255 Gallus ga	928	149.5	9.3	3925	6	AF302047	AF302047 Rattus no
856	151.5	9.4	1638	6	MWBGPF	X67281 M.musculus	929	149.5	9.3	4054	13	MSU50719	US0719 Manduca sex
857	151.5	9.4	2547	13	HVU59448	U59448 Hydra vulga	930	149.5	9.3	5381	13	AF312579	AF312579 Drosophil
858	151.5	9.4	2799	5	HSNCAME	X16841 Human mRNA	931	149.5	9.3	6445	2	AX556703	AX556703 Sequence
859	151.5	9.4	2857	6	BC044882	BC044882 Mus muscu	c 932	149.5	9.3	36859	13	U80022	U80022 Caenorhabdi
860	151.5	9.4	2960	2	AX658287	AX658287 Sequence	c 933	149.5	9.3	96322	5	AL512640	AL512640 Human DNA
861	151.5	9.4	2960	5	S71824	S71824 N-CAM=145 k	934	149.5	9.3	126899	13	AY130758	AY130758 Caenorhab
862	151.5	9.4	3266	2	CQ728451	CQ728451 Sequence	935	149.5	9.3	183007	12	AC021540	AC021540 Homo sapi
863	151.5	9.4	3309	2	AX714869	AX714869 Sequence	936	149.5	9.3	206395	5	AC008759	AC008759 Homo sapi
864	151.5	9.4	3309	5	BC057509	BC057509 Homo sapi	c 937	149.5	9.3	266597	12	AL3390714	AL3390714 Homo sapi
865	151.5	9.4	4050	5	AC072444	BC047244 Homo sapi	c 938	149.5	9.3	744	7	BV577419	BV577419 Homo sapi
866	151.5	9.4	4214	5	AF004841	AF004841 Homo sapi	c 939	149.5	9.3	934	7	BV5774495	BV5774495 G591P6049
867	151.5	9.4	4696	5	AB209443	AB209443 Homo sapi	940	149.5	9.3	1607	2	AR098144	AR098144 Sequence
868	151.5	9.4	5526	5	BC098583	BC098583 Homo sapi	941	149.5	9.3	1607	2	AR116616	AR116616 Sequence
869	151.5	9.4	8513	2	AX207284	AX207284 Sequence	942	149.5	9.3	2467	2	AR098143	AR098143 Sequence
c 870	151.5	9.4	164239	5	BX072566	BX072566 Human DNA	943	149.5	9.3	2467	2	AR116615	AR116615 Sequence
871	151.5	9.4	166239	5	HS214G14	AL050303 Homo sapi	944	149.5	9.3	2706	6	MUSPTPT9A	D28531 Mouse mRNA
872	151.5	9.4	172545	5	AL162851	AL162851 Human DNA	945	149.5	9.3	3770	11	BC073488	BC073488 Xenopus l
c 873	151.5	9.4	184770	5	AP005670	AP005670 Homo sapi	946	149.5	9.3	4613	11	CHKCRYP	L32780 Gallus gall
874	151.5	9.4	340000	5	HS21C004	AL163204 Homo sapi	947	149.5	9.3	5588	6	BC052462	BC052462 Mus muscu
875	151	9.4	1311	14	AY487418	AY487418 Bos tauru	948	149.5	9.3	5612	6	BC083188	BC083188 Mus muscu
876	151	9.4	1418	5	AY487417	AY487417 Bos tauru	949	149.5	9.3	5978	6	MMPTPN03	X82288 M.musculus
877	151	9.4	4188	5	HSMB02147	AL137695 Homo sapi	950	149.5	9.3	6734	2	AX305472	AX305472 Sequence
878	151	9.4	5723	6	AF300943	AF300943 Mus muscu	951	149.5	9.3	6734	6	MUSPTPT9	D28530 Mouse mRNA
879	151	9.4	7097	2	AX921114	AX921114 Sequence	952	149.5	9.3	189519	12	CT025730	CT025730 Drosophil

953	148.5	9.3	536	2	AR494542	AR494542 Sequence	1026	146.5	9.1	4783	2	E34509	E34509 Novel rpoA.
954	148.5	9.3	1110	2	AX429018	AX429018 Sequence	1027	146.5	9.1	4783	2	E34511	E34511 Novel rtaA.
955	148.5	9.3	1355	14	AX345127	AX345127 Bos tauru	1028	146.5	9.1	4783	2	E34513	E34513 Novel uttli
956	148.5	9.3	1872	2	AX429014	AX429014 Sequence	1029	146.5	9.1	4783	2	E34515	E34515 Human LIG-1
957	148.5	9.3	2726	11	AY029402	AY029402 Danio rer	1030	146.5	9.1	4805	5	AY730707	AY730707 Homo sapi
958	148.5	9.3	4146	2	BD085987	BD085987 Method of	1031	146.5	9.1	4956	6	AF041082	AF041082 Rattus no
959	148.5	9.3	5011	5	BC106716	BC106716 Homo sapi	1032	146.5	9.1	5038	5	BC106713	BC106713 Homo sapi
960	148.5	9.3	5807	2	AR447664	AR447664 Sequence	1033	146.5	9.1	5396	11	AF388036	AF388036 Xenopus 1
C 961	148.5	9.3	39130	13	CBRG42821	AC084594 Caenorhab	1034	146.5	9.1	6222	6	MMU17793	Y17793 Mus musculu
C 962	148.5	9.3	173520	12	AC160883	AC160883 Papio anu	1035	146.5	9.1	198334	5	AF411849S1	AF411849 Homo sapi
C 963	148.5	9.3	174758	12	AC149552	AC149552 Papio anu	1036	146	9.1	1265	5	HSTM3CEA	X16356 Human mRNA
964	148	9.2	431167	2	AR079552	AR43167 Sequence 33	1037	146	9.1	1306	5	AY654628	AY654628 Homo sapi
965	148	9.2	1103	2	AR079552	AR079552 Sequence 33	1038	146	9.1	1399	6	MUSHEPVR	M96934 Mus musculu
966	148	9.2	1476	2	AR098146	AR098146 Sequence	1039	146	9.1	1473	2	AR3165	AR3165 Sequence 31
967	148	9.2	2116	2	AR116618	AR098146 Sequence	1040	146	9.1	1473	2	AR079551	AR079551 Sequence
968	148	9.2	2216	2	CQ730970	AR116618 Sequence	1041	146	9.1	1473	5	S71326	S71326 BGPC-billar
969	148	9.2	2262	6	MMNCAM1	CQ730970 Sequence	1042	146	9.1	1630	2	I08160	I08160 Sequence 10
970	148	9.2	2268	2	AR098155	X15049 Mouse commo	1043	146	9.1	1630	2	I08163	I08163 Sequence 3
971	148	9.2	2268	2	AR116627	AR098155 Sequence	1044	146	9.1	1636	5	BC014473	BC014473 Homo sapi
972	148	9.2	3117	6	AF374459	AR116627 Sequence	1045	146	9.1	1653	5	BC024164	BC024164 Homo sapi
973	148	9.2	3170	6	RNNCAM4	AF374459 Mus muscu	1046	146	9.1	2168	5	BC048416	BC048416 Homo sapi
974	148	9.2	3210	6	BC101924	X06564 Rat mRNA fo	1047	146	9.1	2197	5	HUMBGF1	J03858 Human blla
975	148	9.2	4617	11	CQ00EX2	BC101924 Rattus no	1048	146	9.1	2461	14	AB032195	AB032195 Sus scrof
976	148	9.2	4871	11	AF337035	X83287 C.coturnix	1049	146	9.1	2544	6	BC011310	BC011310 Mus muscu
977	148	9.2	224500	12	AC136530	AF337035 Danio rer	1050	146	9.1	2547	2	CQ413250	CQ413250 Sequence
C 978	148	9.2	246871	12	AC094352	AC136530 Rattus no	1051	146	9.1	2851	14	BT020673	BT020673 Bos tauru
C 979	148	9.2	257671	12	AC094352	AC094352 Rattus no	1052	146	9.1	3009	2	AX060542	AX060542 Sequence
980	147.5	9.2	1073	11	DRU63292	AC097871 Rattus no	1053	146	9.1	3461	2	I08157	I08157 Sequence 4
981	147.5	9.2	1103	2	CQ728252	U63292 Danio rerio	1054	146	9.1	3461	2	I08167	I08167 Sequence 10
982	147.5	9.2	1110	2	CQ575874	CQ728252 Sequence	1055	146	9.1	3464	2	CQ834029	CQ834029 Sequence
983	147.5	9.2	1247	11	BC078527	CQ575874 Sequence	1056	146	9.1	3464	2	CQ875303	CQ875303 Sequence
984	147.5	9.2	1563	13	AY051911	BC078527 Xenopus 1	1057	146	9.1	3464	2	AX330303	AX330303 Sequence
985	147.5	9.2	1767	11	BC041253	AY051911 Drosophil	1058	146	9.1	3464	2	AX818143	AX818143 Sequence
986	147.5	9.2	2135	13	DROAMA	BC041253 Xenopus 1	1059	146	9.1	3464	5	HSTM1CEA	X16354 Human mRNA
987	147.5	9.2	2167	2	CS148786	M23561 D.melanogas	1060	146	9.1	3574	14	BTADCYC	X16451 Bovine mRNA
988	147.5	9.2	2271	11	BC085419	CS148786 Sequence	1061	146	9.1	7297	11	AF197945	AF197945 Xenopus 1
989	147.5	9.2	2350	5	AY189281	BC085419 Danio rer	1062	146	9.1	39823	5	AC004785	AC004785 Homo sapi
990	147.5	9.2	2845	2	CQ716675	AY189281 Homo sapi	1063	146	9.1	211521	12	CR790369	CR790369 Danio rer
C 991	147.5	9.2	3426	2	CQ575873	CQ716675 Sequence	1064	145.5	9.1	830	11	EX933439	EX933439 Callus ga
992	147.5	9.2	3966	11	AY524000	CQ575873 Sequence	1065	145.5	9.1	1927	2	BD101818	BD101818 The genae
993	147.5	9.2	4119	11	AX376856	AY524000 Danio rer	1066	145.5	9.1	1927	6	AB040490	AB040490 Mus muscu
994	147.5	9.2	4717	2	AX463544	AX376856 Danio rer	1067	145.5	9.1	2092	5	HSCEAASP	X16455 Human mRNA
995	147.5	9.2	4759	2	AX463530	AX463544 Sequence	1068	145.5	9.1	2106	2	CS141685	CS141685 Sequence
996	147.5	9.2	5038	5	BC106715	AX463530 Sequence	1069	145.5	9.1	2106	2	AX133657	AX133657 Sequence
997	147.5	9.2	5041	5	BC106714	BC106715 Homo sapi	1070	145.5	9.1	2106	2	AX192349	AX192349 Sequence
998	147.5	9.2	5101	2	DD161157	BC106714 Homo sapi	1071	145.5	9.1	2106	2	AX393888	AX393888 Sequence
999	147.5	9.2	5719	2	CQ859705	DD161157 Novel Ant	1072	145.5	9.1	2259	2	BD204924	BD204924 Novel mol
C1000	147.5	9.2	6228	12	AC020270	CQ859705 Sequence	1073	145.5	9.1	2633	2	CS018095	CS018095 Sequence
1001	147.5	9.2	6263	2	AR380928	AC020270 Drosophil	1074	145.5	9.1	2633	2	CS025610	CS025610 Sequence
1002	147.5	9.2	6263	5	HUMTPD	AR380928 Sequence	1075	145.5	9.1	2633	2	AR380405	AR380405 Sequence
1003	147.5	9.2	84246	13	AC002512	LJ3829 Homo sapien	1076	145.5	9.1	2633	5	HSU63041	U63041 Human neuca
C1004	147.5	9.2	110000	13	AE001572.2	AC002512 Drosophil	1077	145.5	9.1	3384	2	AX714308	AX714308 Sequence
1005	147.5	9.2	170801	13	AC095014	Continuation (3 of	1078	145.5	9.1	3384	5	AK056544	AK056544 Homo sapi
1006	147.5	9.2	298020	13	AE003674	AC095014 Drosophil	1079	145.5	9.1	4291	2	BD204923	BD204923 Novel mol
1007	147	9.2	1552	6	BC064106	AE003674 Drosophil	1080	145.5	9.1	4955	5	BC112336	BC112336 Homo sapi
1008	147	9.2	1952	2	CS168825	BC064106 Mus muscu	1081	145.5	9.1	4956	5	BD085389	BD085389 Method of
1009	147	9.2	1952	2	AX834946	CS168825 Sequence	1082	145.5	9.1	4956	5	AF040990	AF040990 Homo sapi
1010	147	9.2	1952	5	AK097667	AX834946 Sequence	1083	145.5	9.1	5130	2	CS108003	CS108003 Sequence
1011	147	9.2	2110	13	DROLACH	AK097667 Homo sapi	1084	145.5	9.1	5130	2	CS108174	CS108174 Sequence
1012	147	9.2	2243	14	AY860629	L13255 Fruitfly la	1085	145.5	9.1	5130	6	AF230073	AF230073 Homo sapi
1013	147	9.2	2626	14	AY860627	AY860629 Canis fam	1086	145.5	9.1	5326	6	AF630256	AF630256 Rattus no
1014	147	9.2	2656	14	AY860628	AY860627 Canis fam	1087	145.5	9.1	61953	5	HSUDTTL	HSUDTTL Human DNA s
1015	147	9.2	3261	13	AF456360	AY860628 Canis fam	1088	145.5	9.1	61953	5	BX248408	BX248408 Human DNA
1016	147	9.2	3444	6	BC016891	AF456360 Caenorhab	1089	145.5	9.1	115498	12	BX664701	BX664701 Homo sapi
1017	146.5	9.1	1710	2	CQ588165	BC016891 Mus muscu	1090	145.5	9.1	189276	5	AP006261	AP006261 Homo sapi
1018	146.5	9.1	1846	2	CS105833	CQ588165 Sequence	1091	145.5	9.1	200548	12	AC040962	AC040962 Homo sapi
1019	146.5	9.1	1846	2	CS133156	CS105833 Sequence	1092	145.5	9.1	3446	5	HSN804897	HSN804897 Sequence
1020	146.5	9.1	2573	5	AY358130	CS133156 Sequence	1093	145	9.0	3461	2	CQ591386	CQ591386 Sequence
1021	146.5	9.1	2573	5	AY043465	AY358130 Homo sapi	1094	145	9.0	3914	6	AF090866	AF090866 Mus muscu
1022	146.5	9.1	2580	5	AX459633	AY043465 Homo sapi	1095	145	9.0	4073	2	AX269342	AX269342 Sequence
1023	146.5	9.1	4129	2	CQ849703	AX459633 Homo sapi	1096	145	9.0	4188	2	BD085986	BD085986 Method of
1024	146.5	9.1	4129	5	AK126745	CQ849703 Sequence	1097	145	9.0	4355	2	CQ603804	CQ603804 Sequence
1025	146.5	9.1	4762	5	AF381545	AK126745 Homo sapi	1098	145	9.0				

1099	145	9.0	4473	11	AY833404	AY833404	Danio rer	1172	144	9.0	2583	6	MMNCAMR	Y00051	Mouse mRNA
1100	145	9.0	4491	11	AY524001	AY524001	Danio rer	1173	144	9.0	4078	2	AR270569	AR270569	Sequence
1101	145	9.0	5095	11	BC072368	BC072368	Xenopus l	1174	144	9.0	4094	2	CQ714181	CQ714181	Sequence
1102	145	9.0	5103	2	AX399250	AX399250	Sequence	1175	144	9.0	4773	5	HSU41725	U41725	Human prote
1103	145	9.0	6440	13	AF040989	AF040989	Drosophila	1176	144	9.0	6000	2	AR031690	AR031690	Sequence
1104	145	9.0	8546	2	CS145836	CS145836	Sequence	1177	144	9.0	6000	2	I61404	I61404	Sequence
1105	145	9.0	8546	2	AX288406	AX288406	Sequence	1178	144	9.0	6000	5	HSU40317	U40317	Human prote
1106	145	9.0	8546	5	HS030690	HS030690	Homo sapi	1179	144	9.0	6435	11	AF461119	AF461119	Xenopus l
1107	145	9.0	107820	2	AX567314	AX567314	Sequence	1180	144	9.0	8066	5	AB209851	AB209851	Homo sapi
1108	145	9.0	107820	2	AX282509	AX282509	Sequence	1181	144	9.0	11008	13	AF078161	AF078161	Manduca s
1109	145	9.0	120775	12	AC181351	AC181351	Strongylo	1182	144	9.0	176257	5	CNS01RHJ	AF078161	Human chr
1110	145	9.0	154331	12	AC136622	AC136622	Homo sapi	1183	144	9.0	191071	5	AP004248	AP004248	Homo sapi
1111	145	9.0	172970	12	AC178253	AC178253	Strongylo	1184	144	9.0	199447	11	BX510918	BX510918	Zebrafish
1112	145	9.0	172984	2	AX706963	AX706963	Sequence	1185	144	9.0	325791	2	AR606191	AR606191	Sequence
1113	145	9.0	172984	2	AX707893	AX707893	Sequence	1186	144	9.0	325791	2	AX234657	AX234657	Sequence
1114	145	9.0	172984	5	HU91318	US1318	Human chrom	1187	143.5	8.9	928	2	CQ728059	CQ728059	Sequence
1115	145	9.0	173613	13	AC007475	AC007475	Drosophila	1188	143.5	8.9	1242	5	AY046418	AY046418	Homo sapi
1116	145	9.0	173911	5	AC130465	AC130465	Homo sapi	1189	143.5	8.9	1299	2	CQ728323	CQ728323	Sequence
1117	145	9.0	177963	12	AC137502	AC137502	Homo sapi	1190	143.5	8.9	1317	2	BD016752	BD016752	Protein n
1118	145	9.0	186591	2	AX706984	AX706984	Sequence	1191	143.5	8.9	1317	2	BD097475	BD097475	Protein n
1119	145	9.0	186591	2	AX707914	AX707914	Sequence	1192	143.5	8.9	1371	6	AY065557	AY065557	Mus muscu
1120	145	9.0	192763	13	AC007474	AC007474	Drosophila	1193	143.5	8.9	1465	6	MMBGPE	X67280	M. musculus
1121	145	9.0	194380	12	AC137505	AC137505	Homo sapi	1194	143.5	8.9	1533	2	BD016751	BD016751	Protein n
1122	145	9.0	194634	12	AC020286	AC020286	Drosophila	1195	143.5	8.9	1533	2	BD097474	BD097474	Protein n
1123	145	9.0	208417	5	AC025778	AC025778	Homo sapi	1196	143.5	8.9	1542	2	BD193028	BD193028	207 human
1124	145	9.0	208648	2	AX706965	AX706965	Sequence	1197	143.5	8.9	1542	2	CQ822024	CQ822024	Sequence
1125	145	9.0	208648	2	AX706970	AX706970	Sequence	1198	143.5	8.9	1542	2	AR693919	AR693919	Sequence
1126	145	9.0	208648	2	AX707895	AX707895	Sequence	1199	143.5	8.9	1614	2	BD177640	BD177640	Mus muscu
1127	145	9.0	208648	2	AX707900	AX707900	Sequence	1200	143.5	8.9	1614	2	E37854	E37854	MBGPI poly
1128	145	9.0	211896	5	AC136624	AC136624	Homo sapi	1201	143.5	8.9	1614	2	AX003003	AX003003	Sequence
1129	145	9.0	292919	13	AE003823	AE003823	Drosophila	1202	143.5	8.9	1625	6	AF195834	AF195834	Mus muscu
1130	144.5	9.0	517	2	AX397213	AX397213	Sequence	1203	143.5	8.9	1650	2	BD016750	BD016750	Protein n
1131	144.5	9.0	892	7	BV576768	BV576768	G591P6094	1204	143.5	8.9	1650	2	BD097473	BD097473	Protein n
1132	144.5	9.0	950	13	AY052156	AY052156	Drosophila	1205	143.5	8.9	1688	6	AF195835	AF195835	Mus muscu
1133	144.5	9.0	950	13	AY052157	AY052157	Drosophila	1206	143.5	8.9	1688	5	BC033819	BC033819	Homo sapi
1134	144.5	9.0	950	13	AY052158	AY052158	Drosophila	1207	143.5	8.9	1685	2	BD075436	BD075436	Secreted
1135	144.5	9.0	950	13	AY052159	AY052159	Drosophila	1208	143.5	8.9	1685	2	BD172296	BD172296	Secreted
1136	144.5	9.0	950	13	AY052160	AY052160	Drosophila	1209	143.5	8.9	1685	2	BD172615	BD172615	Secreted
1137	144.5	9.0	950	13	AY052161	AY052161	Drosophila	1210	143.5	8.9	1685	2	BD172934	BD172934	Secreted
1138	144.5	9.0	950	13	AY052162	AY052162	Drosophila	1211	143.5	8.9	1685	2	BD173253	BD173253	Secreted
1139	144.5	9.0	950	13	AY052163	AY052163	Drosophila	1212	143.5	8.9	1685	2	BD175287	BD175287	Secretory
1140	144.5	9.0	1110	2	AX428991	AX428991	Sequence	1213	143.5	8.9	1685	2	CS105892	CS105892	Sequence
1141	144.5	9.0	1110	2	AX429015	AX429015	Sequence	1214	143.5	8.9	1685	2	AR410665	AR410665	Sequence
1142	144.5	9.0	1110	2	AX429016	AX429016	Sequence	1215	143.5	8.9	1685	2	AR439029	AR439029	Sequence
1143	144.5	9.0	1110	2	AX429017	AX429017	Sequence	1216	143.5	8.9	1685	2	AR473049	AR473049	Sequence
1144	144.5	9.0	1146	11	AM076719	AM076719	Gallus ga	1217	143.5	8.9	1685	2	AR527035	AR527035	Sequence
1145	144.5	9.0	1284	6	BC050133	BC050133	Mus muscu	1218	143.5	8.9	1685	2	AR566068	AR566068	Sequence
1146	144.5	9.0	1321	6	AF101164	AF101164	Mus muscu	1219	143.5	8.9	1685	2	AR592086	AR592086	Sequence
1147	144.5	9.0	1872	2	AX428990	AX428990	Sequence	1220	143.5	8.9	1685	2	AR604360	AR604360	Sequence
1148	144.5	9.0	1872	2	AX429011	AX429011	Sequence	1221	143.5	8.9	1685	2	AR604946	AR604946	Sequence
1149	144.5	9.0	1872	2	AX429012	AX429012	Sequence	1222	143.5	8.9	1685	2	AR613611	AR613611	Sequence
1150	144.5	9.0	1872	2	AX429013	AX429013	Sequence	1223	143.5	8.9	1685	2	AR635782	AR635782	Sequence
1151	144.5	9.0	2190	2	CQ604731	CQ604731	Sequence	1224	143.5	8.9	1685	2	AR650511	AR650511	Sequence
1152	144.5	9.0	3650	6	AF182037	AF182037	Rattus no	1225	143.5	8.9	1685	2	AR657452	AR657452	Sequence
1153	144.5	9.0	3798	6	AF388037	AF388037	Mus muscu	1226	143.5	8.9	1685	2	AR720404	AR720404	Sequence
1154	144.5	9.0	3822	13	AF041053	AF041053	Ctenorhab	1227	143.5	8.9	1685	2	AR770963	AR770963	Sequence
1155	144.5	9.0	3894	2	BD085988	BD085988	Method of	1228	143.5	8.9	1685	2	AR771330	AR771330	Sequence
1156	144.5	9.0	4376	6	BC078631	BC078631	Mus muscu	1229	143.5	8.9	1685	2	AX454458	AX454458	Sequence
1157	144.5	9.0	4430	6	BC062892	BC062892	Mus muscu	1230	143.5	8.9	1685	2	AX464214	AX464214	Sequence
1158	144.5	9.0	4813	5	AK125056	AK125056	Homo sapi	1231	143.5	8.9	1685	2	AX490936	AX490936	Sequence
1159	144.5	9.0	5933	2	CQ869760	CQ869760	Sequence	1232	143.5	8.9	1685	2	AX697492	AX697492	Sequence
1160	144.5	9.0	9295	2	CQ573225	CQ573225	Sequence	1233	143.5	8.9	1685	5	AY358332	AY358332	Homo sapi
1161	144.5	9.0	12667	6	MUSPERPA	M77174	Mouse perle	1234	143.5	8.9	1718	2	BD247477	BD247477	Molecules
1162	144.5	9.0	16799	12	AC020355	AC020355	Drosophila	1235	143.5	8.9	1718	2	CS019557	CS019557	Sequence
1163	144.5	9.0	68727	13	AC004516	AC004516	Drosophila	1236	143.5	8.9	1718	2	BD278800	BD278800	Sequence
1164	144.5	9.0	71023	12	AC004426	AC004426	Drosophila	1237	143.5	8.9	1820	2	BD247476	BD247476	Molecules
1165	144.5	9.0	95983	5	AC004874	AC004874	Homo sapi	1238	143.5	8.9	1820	2	CS019555	CS019555	Sequence
1166	144.5	9.0	167886	12	AC162772	AC162772	Gasterost	1239	143.5	8.9	1820	2	AR278798	AR278798	Sequence
1167	144.5	9.0	185563	5	AC104452	AC104452	Homo sapi	1240	143.5	8.9	1892	11	AB117614	AB117614	Xenopus l
1168	144.5	9.0	186925	12	AC087503	AC087503	Homo sapi	1241	143.5	8.9	2166	6	AF195833	AF195833	Mus muscu
1169	144.5	9.0	193262	13	AC007579	AC007579	Drosophila	1242	143.5	8.9	2178	2	BD016753	BD016753	Protein n
1170	144.5	9.0	196528	5	AC145858	AC145858	Pan trogl	1243	143.5	8.9	2178	2	BD097476	BD097476	Protein n
1171	144.5	9.0	260367	13	AE003808	AE003808	Drosophila	1244	143.5	8.9	2437	5	BC046109	BC046109	Homo sapi

1245	143.5	8.9	2496	2	BD191411	Secreted	1318	143	8.9	3321	2	CS148787	CS148787 Sequence
1246	143.5	8.9	2540	5	AF062733	Homo sapi	1319	143	8.9	4002	5	BC075829	BC075829 Homo sapi
1247	143.5	8.9	3376	5	BC101068	Homo sapi	1320	143	8.9	4277	2	AR702658	AR702658 Sequence
1248	143.5	8.9	3357	5	AF363367	Homo sapi	1321	143	8.9	4277	2	AR709028	AR709028 Sequence
1249	143.5	8.9	4345	11	AJ829921	Xenopus 1	1322	143	8.9	4277	2	AR714569	AR714569 Sequence
1250	143.5	8.9	4241	2	CQ869962	Sequence	1323	143	8.9	4277	2	AR720738	AR720738 Sequence
1251	143.5	8.9	4381	2	AY509035	Homo sapi	1324	143	8.9	4277	2	AR722381	AR722381 Sequence
1252	143.5	8.9	4569	5	AY509035	Homo sapi	1325	143	8.9	4277	2	AR723131	AR723131 Sequence
1253	143.5	8.9	4800	6	BC086654	Mus muscu	1326	143	8.9	4277	2	AR723485	AR723485 Sequence
1254	143.5	8.9	5193	2	AC698038	Sequence	1327	143	8.9	4277	2	AR723485	AR723485 Sequence
1255	143.5	8.9	7416	2	CQ613727	Sequence	1328	143	8.9	4277	2	AR757610	AR757610 Sequence
1256	143.5	8.9	10232	6	AF525411	Rattus no	1329	143	8.9	4277	2	AR776421	AR776421 Sequence
1257	143.5	8.9	18510	12	AC017804	Drosophil	1330	143	8.9	4277	2	AX376372	AX376372 Sequence
1258	143.5	8.9	41971	13	AC003765	Drosophil	1331	143	8.9	4277	2	AX454572	AX454572 Sequence
1259	143.5	8.9	110000	12	AC010714_2	Continuation (3 of	1332	143	8.9	4277	2	AX491050	AX491050 Sequence
1260	143.5	8.9	168238	13	AC009844	Drosophil	1333	143	8.9	4277	2	AX596989	AX596989 Sequence
1261	143.5	8.9	186286	13	AC090900	Drosophil	1334	143	8.9	4277	5	AY358328	AY358328 Homo sapi
1262	143.5	8.9	189967	12	AC079553	Mus muscu	1335	143	8.9	8577	2	CQ612483	CQ612483 Sequence
1263	143	8.9	255772	13	AE003812	Sequence	1336	143	8.9	182726	12	AC150809	AC150809 Callithri
1264	143	8.9	542	2	CQ405751	Sequence	1337	142.5	8.9	804	2	CS113136	CS113136 Sequence
1265	143	8.9	607	13	AF254364	Drosophil	1338	142.5	8.9	804	5	AF006622	AF006622 Homo sapi
1266	143	8.9	695	13	AF254369	Drosophil	1339	142.5	8.9	811	2	CS113159	CS113159 Sequence
1267	143	8.9	738	7	BV578045	GS91P6118	1340	142.5	8.9	811	5	HUMCGM2A	L31792 Homo sapien
1268	143	8.9	834	2	AX429004	Sequence	1341	142.5	8.9	904	7	BV570092	BV570092 GS91P6060
1269	143	8.9	901	7	BV572812	GS91P6668	1342	142.5	8.9	1011	2	E09891	E09891 Insertion s
1270	143	8.9	1058	5	AF226639	Papio ham	1343	142.5	8.9	1011	6	MUSMPTPC	D13904 Mus musculu
1271	143	8.9	1188	2	AX191609	Sequence	1344	142.5	8.9	2271	6	AF302046	AF302046 Mus muscu
1272	143	8.9	1363	2	CS074769	Sequence	1345	142.5	8.9	2291	2	CQ720042	CQ720042 Sequence
1273	143	8.9	1627	2	AX805542	Sequence	1346	142.5	8.9	2292	2	AX926599	AX926599 Sequence
1274	143	8.9	1861	6	AF061260	Mus muscu	1347	142.5	8.9	2292	2	AX926648	AX926648 Sequence
1275	143	8.9	1864	11	BC095877	Danio rer	1348	142.5	8.9	2292	2	CQ834033	CQ834033 Sequence
1276	143	8.9	1933	2	CS105871	Sequence	1349	142.5	8.9	2292	2	CQ896451	CQ896451 Sequence
1277	143	8.9	1933	2	CS133166	Sequence	1350	142.5	8.9	2292	2	CS162187	CS162187 Sequence
1278	143	8.9	1961	2	AX191619	Sequence	1351	142.5	8.9	2292	2	AX330315	AX330315 Sequence
1279	143	8.9	1937	5	AX131201	Homo sapi	1352	142.5	8.9	2292	5	HSCGM2ANT	X98311 H.sapiens m
1280	143	8.9	2031	2	A39900	Sequence 2	1353	142.5	8.9	3295	13	AF196553	AF196553 Drosophil
1281	143	8.9	2031	2	167748	Sequence 2	1354	142.5	8.9	3387	11	AB231587	AB231587 Danio rer
1282	143	8.9	2034	2	CQ947075	Sequence	1355	142.5	8.9	3521	13	DME289882	AJ289982 Drosophil
1283	143	8.9	2037	2	CS148782	Sequence	1356	142.5	8.9	4290	11	AY848694	AY848694 Danio rer
1284	143	8.9	2059	2	AX805534	Sequence	1357	142.5	8.9	4290	5	BC014205	BC014205 Homo sapi
1285	143	8.9	2057	2	A31169	Sequence 35	1358	142.5	8.9	4573	6	AF004840	AF004840 Rattus no
1286	143	8.9	2097	2	AR079553	Sequence	1359	142.5	8.9	4770	6	DQ360114	DQ360114 Mus muscu
1287	143	8.9	2109	2	CQ859330	Sequence	1360	142.5	8.9	5314	11	BC074401	BC074401 Xenopus 1
1288	143	8.9	2109	2	CQ947061	Sequence	1361	142.5	8.9	6363	2	AB380334	AB380334 Sequence
1289	143	8.9	2109	2	CQ947063	Sequence	1362	142.5	8.9	6363	5	HSU35234	HSU35234 Human prote
1290	143	8.9	2109	2	AX133977	Sequence	1363	142.5	8.9	6659	6	AK131182	AK131182 Mus muscu
1291	143	8.9	2109	2	AX468838	Sequence	1364	142.5	8.9	121821	5	AC023380	AC023380 Homo sapi
1292	143	8.9	2140	2	AX805538	Sequence	1365	142.5	8.9	174265	12	AL772355	AL772355 Homo sapi
1293	143	8.9	2155	2	AX805540	Sequence	1366	142.5	8.9	178254	5	AL731541	AL731541 Human DNA
1294	143	8.9	2167	2	AX805536	Sequence	1367	142	8.8	534	2	AR273582	AR273582 Sequence
1295	143	8.9	2220	2	AR044683	Sequence	1368	142	8.8	534	2	AR277163	AR277163 Sequence
1296	143	8.9	2267	13	BT011127	Drosophil	1369	142	8.8	534	2	AR407438	AR407438 Sequence
1297	143	8.9	2349	2	CQ852808	Sequence	1370	142	8.8	534	2	AR441288	AR441288 Sequence
1298	143	8.9	2349	2	CQ898819	Sequence	1371	142	8.8	534	2	AR544099	AR544099 Sequence
1299	143	8.9	2349	2	AR288121	Sequence	1372	142	8.8	534	2	AR639257	AR639257 Sequence
1300	143	8.9	2349	2	AR567108	Sequence	1373	142	8.8	534	2	AR659530	AR659530 Sequence
1301	143	8.9	2350	7	BV177759	sgm96580	1374	142	8.8	534	2	AX368615	AX368615 Sequence
1302	143	8.9	2355	2	CS148769	Sequence	1375	142	8.8	1038	11	BC083011	BC083011 Xenopus 1
1303	143	8.9	2355	2	CS148771	Sequence	1376	142	8.8	1102	2	AX083526	AX083526 Sequence
1304	143	8.9	2358	2	CS148772	Sequence	1377	142	8.8	1352	5	AY358084	AY358084 Homo sapi
1305	143	8.9	2359	5	AR0223101	Homo sapi	1378	142	8.8	1422	5	AY212514	AY212514 Homo sapi
1306	143	8.9	2434	2	AR052807	Sequence	1379	142	8.8	1564	6	RNCCAM2A	RNCCAM2A
1307	143	8.9	2434	2	AR288120	Sequence	1380	142	8.8	1824	6	BD261714	BD261714 12 human
1308	143	8.9	2434	2	AR567107	Sequence	1381	142	8.8	2008	2	CR760664	CR760664
1309	143	8.9	2664	2	CS148785	Sequence	1382	142	8.8	2118	2	CQ859385	CQ859385 Sequence
1310	143	8.9	2766	2	CS148767	Sequence	1383	142	8.8	2118	2	CQ859389	CQ859389 Sequence
1311	143	8.9	2857	2	CS148809	Sequence	1384	142	8.8	2118	2	CS047791	CS047791 Sequence
1312	143	8.9	2859	2	CS148781	Sequence	1385	142	8.8	2118	2	CS148776	CS148776 Sequence
1313	143	8.9	3022	13	AF419620	Drosophil	1386	142	8.8	2177	11	CR760664	CR760664
1314	143	8.9	3426	2	CS148784	Sequence	1387	142	8.8	2358	2	CS148774	CS148774 Sequence
1315	143	8.9	3534	5	AY027658	Homo sapi	1388	142	8.8	2359	2	CS148812	CS148812 Sequence
1316	143	8.9	3585	2	CS148788	Sequence	1389	142	8.8	2817	5	AF416903	AF416903 Homo sapi
1317	143	8.9	3902	13	AY060635	Drosophil	1390	142	8.8				

1391	142	8.8	2859	2	CS148810	Sequence	1464	140.5	8.8	110000	12	AC003656_4	Continuation (5 of		
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1409	141.5	8.8	1527	6	AF472510	Mus muscu	1482	140	8.7	3112	5	HSM803530	AL832223 Homo sapi		
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1413	141.5	8.8	1952	6	AB028174	Mus muscu	1486	140	8.7	3386	5	BC101066	BC101066 Homo sapi		
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c1420	141.5	8.8	166643	5	AL392104	Human DNA	1493	140	8.7	4608	2	AR153583	AR153583 Sequence		
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RESULT 1	BD075420	1295 bp	DNA	linear	PAT 27-AUG-2002
BD075420	Secretory and transmembrane polypeptide and nucleic acid encoding				
LOCUS	the same.				
DEFINITION	BD075420.1				
ACCESSION	BD075420.1				
VERSION	GI:22621023				
KEYWORDS	JP 2001516580-A/53.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.				
TITLE	Secretory and transmembrane polypeptide and nucleic acid encoding the same				
JOURNAL	Patent: JP 2001516580-A 53 02-OCT-2001; GENENTECH INC				
COMMENT	OS Homo sapiens (human) PN JP 2001516580-A/53 PD 02-OCT-2001 PF 16-SEP-1998 JP 2000511867 PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059263 PR 17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/062125 PR 18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062285 PR 17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062286 PR 21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR				

ALIGNMENTS

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VERSION	BD075420	JP 2001516580-A/53.				
KEYWORDS	JP 2001516580-A/53.	Homo sapiens (human)				
SOURCE	Homo sapiens	Homo sapiens				
ORGANISM	Homo sapiens	Homo sapiens				
REFERENCE	1	(bases 1 to 1295)				
AUTHORS	Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.					
TITLE	Secretory and transmembrane polypeptide and nucleic acid encoding the same					
JOURNAL	Patent: JP 2001516580-A 53	02-OCT-2001.				
COMMENT	GENENTECH INC					
	OS	Homo sapiens (human)				
	PN	JP 2001516580-A/53				
	PD	02-OCT-2001				
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24-NOV-1997 US 60/066511,24-NOV-1997 US 60/066453 PR
25-NOV-1997 US 60/066840
PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI
JEAN CHEN,
PI JEAN YUAN
PC C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,
PC C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02/(C12P21/08, PC
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DB 149 CTGGGCTATCATAGGCTATGGTTTCTGCCCAAAAGACCAACAGTAGTCACAGCA 208
QY 41 ValGluTyrGlnGluAlaIleLeuAlaCysLeuThrProLysLysThrValSerSerArg 60
DB 209 GTAGAGTACCAGAGGCTATTTAGCTGCAAAACCCCAAGAAAGACTGTTCTCTCAA 268
QY 61 LeuGluTyrLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
DB 269 TTAGAGTGGGAAGAACTGGGTGGAGTGCTCTCTTGTCTACTATCAACAGACTCTTCAA 328
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QY 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlyGlnAsn 120
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LOCUS Secreted and transmembrane polypeptides and nucleic acids encoding
DEFINITION the same.
ACCESSION BD172280
VERSION BD172280.1 GI:28413580
KEYWORDS JP 2002223786-A/53.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1295)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
JOURNAL the same
COMMENT Patent: JP 2002223786-A 53 13-AUG-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 2002223786-A/53
PD 13-AUG-2002
PF 18-DEC-2001 JP 2001385135
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
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LOCUS Secreted and transmembrane polypeptides and nucleic acids encoding
DEFINITION the same.
ACCESSION BD172599
VERSION BD172599.1 GI:28413901
KEYWORDS JP 2002238586-A/53.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Sutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1295)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238586-A 53 27-AUG-2002;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002238586-A/53
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385205
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
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24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02/C12P21/08, (C12N1/19, C12R1/645), (C12N1/21, C12R1/19), PC
(C12N5/10, C12R1/91), (C12P21/02, C12R1/91), (C12P21/02, C12R1/645), PC
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Score: 1605.00 Matches: 312
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0
US-10-785-221-9 (1-312) x BD172599 (1-1295)

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QY 301 LysAlaAlaAlaGlyGlySerArgGlyGlnGluPhe 312
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LOCUS Secreted and transmembrane polypeptides and nucleic acids encoding
DEFINITION the same.
ACCESSION BD172918
VERSION BD172918.1 GI:28414224
KEYWORDS JP 2002238587-A/53.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
REFERENCE 1 (bases 1 to 1295)
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238587-A 53 27-AUG-2002;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002238587-A/53
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385248
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
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29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR

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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
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PC
C12P21/02, C12P21/08, (C12P21/02, C12R1:91), (C12P21/02, C12R1:19), PC
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Pred. No.: 2,46e-165 Length: 1295
Score: 1605.00 Matches: 312
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Best Local Similarity: 100.0% Mismatches: 0
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US-10-785-221-9 (1-312) x BD172918 (1-1295)

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DB 149 CTGGGCTATCATAGGCTATGGTTTCTGCCCAAGACCAAGCAAGTAGTCACAGCA 208
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DB 209 GTAGAGTACCAAGAGGCTATTTAGCTCGCAAAACCCCAAGAGAGCTGTTCTCCAGCA 268
QY 61 LeuGluTrpLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
DB 269 TTAGAGTGGGAAGAACTGGGTCGGAGTGTCTCTTGTCTACTATCAACAGACTCTTCAA 328
QY 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
DB 329 GGTGATTTTAAAAATCAGAGCTGAGATGATAGATTCAATATCCGAGTCAAAATGTGACA 388
QY 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlyGlnAsn 120
DB 389 AGAAGTATCGGGGGAANTATCTGTGTGAAGTAGTAGTCCCATCTCGAAGCAAGCCAAAC 448
QY 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
DB 449 CTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGCTCCAGCAGTATCCATCATGTGAA 508
QY 141 ValProSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
DB 509 GTACCCCTCTCTCTGAGTGGAACTGTGTGAGAGCTAGATGTCAAGACCAAGAGGG 568
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RESULT 5
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LOCUS Secreted and transmembrane polypeptides and nucleic acids encoding
DEFINITION the same.
ACCESSION BD173237
VERSION BD173237.1 GI:28414546
KEYWORDS JP 2002238588-A/53.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1295)
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
JOURNAL the same
Patent: JP 2002238588-A 53 27-AUG-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 2002238588-A/53
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385315
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR
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ACCESSION AR473033
VERSION   AR473033.1 GI:42708408
KEYWORDS
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REFERENCE
1 (bases 1 to 1295)
AUTHORS Desnoyers, L., Goddard, A., Godowski, P. J., Gurney, A. L., Mather, J. P.,
Williams, P. M., and Wood, W. I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6686451-A 63 03-FEB-2004;
Genentech, Inc.; South San Francisco, CA
FEATURES
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US-10-785-221-9 (1-312) x AR473033 (1-1295)

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Qy      41  ValGluTyrGlnGluAlaLeuAlaCysLysThrProLysLysThrValSerSerArg 60
Db      209  GTAGAGTACCAAGAGGCTATTTAGCTGCAAAACCCCAAGAAAGACTGTTCTCTCCAGA 268
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Db      269  TTAGAGTGGGAAGAAACATGGGTGGAGTGTCTCTTGTCTACTATCAACAGACTCTTCAA 328
Qy      81  GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
Db      329  GGTGATTTTAAATTCAGCTGAGATGATAGATTTCAATATCCGGATCAAAATGTGACA 388
Qy      101  ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlnAsn 120
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Qy      121  LeuGluGluAspThrValThrLeuGluValLeuAlaProAlaValProSerCysGlu 140
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RESULT 13
LOCUS   AR527019
DEFINITION Sequence 63 from patent US 6723535.
ACCESSION AR527019
VERSION   AR527019.1 GI:53913936
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1295)
AUTHORS Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D. L., Ferrara, N.,
Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M. E.,
Goddard, A., Godowski, P. J., Grimaldi, J. C., Gurney, A. L., Hillan, K. J.,
Klajavin, I. J., Mather, J. P., Pan, J., Paoni, N. F., Roy, M. A.,
Stewart, T. A., Tumas, D., Williams, P. M., and Wood, W. I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6723535-A 63 20-APR-2004;
Genentech, Inc.; South San Francisco, CA
FEATURES
Source Location/Qualifiers
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/organism="unknown"
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ORIGIN
Alignment Scores:
Pred. No.: 2,46e-165 Length: 1295
Score: 1605.00 Matches: 312
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
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US-10-785-221-9 (1-312) x AR527019 (1-1295)

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Db      389  AGAAGTATGTCGGGGAATATCGTTGTGAAGTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 448
Qy      121  LeuGluGluAspThrValThrLeuGluValLeuAlaProAlaValProSerCysGlu 140
Db      449  CTGGAAGAGGAGATACAGTCACCTCGGAAGATATAGTGGCTCCAGCAGTTCATCATGTGAA 508
Qy      141  ValProSerSerAlaLeuSerGlyThrValValGluLeuLeuLeuLeuLeuLeuLeuLeuLeu 160

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[illegible]

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GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - nucleic search, using frame plus p2n model
 Run on: May 17, 2006, 16:45:48 ; Search time 714 Seconds
 (without alignments)
 4570.045 Million cell updates/sec

Title: US-10-785-221-9
 Perfect score: 1605
 Sequence: 1 MARRSRHRLLLRLVVA.....TPVIPALWKAAGSGRQEF 312
 Scoring table: BLOSUM62

	Xgapop 10.0 , Xgapext 0.5	Ygapop 10.0 , Ygapext 0.5	Fgapop 6.0 , Fgapext 7.0	Delop 6.0 , Delext 7.0
Searched:	5244920 seqs, 3486124231 residues			
Total number of hits satisfying chosen parameters:	10489840			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0%			
	Maximum Match 100%			

Listing first 1500 summaries

Command line parameters:
 -MODEL=frame+p2n.model -DEV=xlh
 -Q=/abse/ABSSEB_epool/US10785221/runat_16052006_083921_19621/app_query.fasta_1
 -DB-N Geneseq -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=1 -NATRX=BLOSUM62 -TRANS=human40.cdi -LIST=1500
 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=1500 -MODE=LOCAL
 -USER=US10785221 @CGN 1 1 727 @runat_16052006_083921_19621 -NCPU=6 -ICPU=3
 -NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

Databases :
 N Geneseq 8:
 1: Geneseqn19808:*
 2: Geneseqn19908:*
 3: Geneseqn20008:*
 4: Geneseqn2001as:*
 5: Geneseqn2001bs:*
 6: Geneseqn2002as:*
 7: Geneseqn2002bs:*
 8: Geneseqn2003as:*
 9: Geneseqn2003bs:*
 10: Geneseqn2003cs:*
 11: Geneseqn2003ds:*
 12: Geneseqn2004as:*
 13: Geneseqn2004bs:*
 14: Geneseqn2005s:*
 15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB ID	Description
-----	-------	--------------	-------	-------------

RESULT 1	ID	AA37664	standard; cDNA; 1295 BP.	
	DE	Human PRO245	cDNA.	
	PN	WO9914241-A2.		
	PD	25-MAR-1999.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 2	ID	AA52225	standard; DNA; 1295 BP.	
	DE	Protein PRO245	cDNA clone DNA35638-1141.	
	PN	WO9914328-A2.		
	PD	25-MAR-1999.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 3	ID	AA52225	standard; cDNA; 1295 BP.	
	DE	Human PRO245	protein encoding for PRO245 polypeptide.	
	PN	WO200140466-A2.		
	PD	07-JUN-2001.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 4	ID	AA52225	standard; cDNA; 1295 BP.	
	DE	Human PRO245	protein encoding cDNA, UNQ219.	
	PN	WO200015797-A2.		
	PD	23-MAR-2000.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 5	ID	AA77562	standard; cDNA; 1295 BP.	
	DE	Human PRO245	cDNA sequence SEQ ID NO:66.	
	PN	WO200032221-A2.		
	PD	08-JUN-2000.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 6	ID	ADC78383	standard; cDNA; 1295 BP.	
	DE	Human PRO245	cDNA.	
	PN	WO200015796-A2.		
	PD	23-MAR-2000.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 7	ID	AAF72383	standard; cDNA; 1295 BP.	
	DE	Human PRO245	cDNA.	
	PN	WO200104311-A1.		
	PD	18-JAN-2001.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 8	ID	AA500157	standard; cDNA; 1295 BP.	
	DE	Human cDNA clone	DNA35638-1141 encoding PRO245 (UNQ219).	
	PN	WO200119991-A1.		
	PD	22-MAR-2001.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 9	ID	AA521411	standard; cDNA; 1295 BP.	
	DE	Human cDNA sequence	encoding for PRO245 polypeptide.	
	PN	WO200140466-A2.		
	PD	07-JUN-2001.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 10	ID	AAC97437	standard; cDNA; 1295 BP.	
	DE	Human angiogenesis-associated protein	PRO245 cDNA, SEQ ID NO:90.	
	PN	WO200053753-A2.		
	PD	14-SEP-2000.		
	PA	(GETH) GENENTECH INC.		
	Percent Similarity:	100.0%	Conservative:	0
	Best Local Similarity:	100.0%	Mismatches:	0
	Query Match:	100.0%	Indels:	0
RESULT 11	ID	AAC91463	standard; cDNA; 1295 BP.	
	DE	Human PRO245	cDNA.	
	PN	WO200073452-A2.		
	PD	07-DEC-2000.		

PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 12
ID ACA60052 standard; cDNA; 1295 BP.
DE Human cDNA for secreted/transmembrane protein PRO245.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 13
ID ACD07452 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 14
ID ACA03770 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 15
ID ABX71500 standard; cDNA; 1295 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO245.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 16
ID ACH06832 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane polypeptide PRO245 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 17
ID ABX89308 standard; cDNA; 1295 BP.
DE DNA encoding novel secreted and transmembrane protein PRO245.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 18
ID ACD41962 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #168.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 19
ID ABX96069 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 20
ID ACA05390 standard; cDNA; 1295 BP.
DE cDNA encoding human secreted protein PRO245.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 21
ID ACD20057 standard; cDNA; 1295 BP.
DE Human secreted / transmembrane polypeptide PRO245 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 22
ID ABX93348 standard; cDNA; 1295 BP.
DE cDNA encoding human A-33 related antigen PRO245.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 23
ID ACA04191 standard; cDNA; 1295 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 335.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 24
ID ACA54860 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 25
ID ACD19695 standard; cDNA; 1295 BP.
DE Human secreted / transmembrane polypeptide PRO245 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 26
ID ADA45854 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 27
ID ADA76285 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 28
ID ADB29268 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 29
ID ADA18935 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 30
ID ADA61558 standard; cDNA; 1295 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 31
ID ADB19343 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 32
ID ADB27884 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 33
ID ADA86363 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 34
ID ADB15927 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 35
ID ADA47713 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0
RESULT 36
ID ADA18124 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 37
ID ACD66842 standard; cDNA; 1295 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO245.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 38
ID ADA67508 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 39
ID ADB30515 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 40
ID ADA85811 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 41
ID ADA97023 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 42
ID ADA79327 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 43
ID ADA87466 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0


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RESULT 44
ID ADB16668 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 45
ID ACD83003 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 46
ID ADA16099 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 47
ID ADA91760 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 48
ID ADB14823 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 49
ID ADB18784 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 50
ID ADA93999 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 51
ID ADB19895 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 52
ID ADB16668 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 53
ID ACD98591 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 54
ID ADA74461 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 55
ID ADA42244 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 56
ID ADB24694 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 57
ID ADA82218 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 58
ID ADA75181 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 59
ID ADA85259 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 60
ID ADA84707 standard; cDNA; 1295 BP.
```


DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 61
ID ACD23181 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 62
ID ADB29963 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 63
ID ADA80491 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 64
ID ADA75733 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 65
ID ADA46958 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 66
ID ADB25254 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 67
ID ADA93430 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 68
ID ADB26780 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.

PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 69
ID ADB31067 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 70
ID ADA60995 standard; cDNA; 1295 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 71
ID ADB24142 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 72
ID ADA96471 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 73
ID ADA81043 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 74
ID ADA95919 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 75
ID ADB26228 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 76
ID ADB21713 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082765-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 77
ID ADA77492 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 78
ID ADB18232 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003077110-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 79
ID ADA86915 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 80
ID ADA16523 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 81
ID ADA12952 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 82
ID ADA41820 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 83
ID ADA88018 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 84
ID ADA46406 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 85
ID ADA17167 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 86
ID ADA42670 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 87
ID ADB28436 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 88
ID ADB28988 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 89
ID ADA76940 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003059309-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 90
ID ADA88570 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 91
ID ADA97575 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 92
ID ADB27332 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003022339-A1.
PD 30-JAN-2003.
Percent Similarity: 100.0%
Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 93
ID ADB22265 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 94
ID ACD23543 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 95
ID ADA66956 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 96
ID ADB22817 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 97
ID ADB23590 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 98
ID ADA92312 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 99
ID ADB15375 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 100
ID ADB38627 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

RESULT 101
ID ADB38075 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 102
ID ADB66547 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 103
ID ADB89627 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 104
ID ADB90359 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 105
ID ADB77589 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 106
ID ADB39460 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 107
ID ADB74725 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 108
ID ADB47083 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 109


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ID ADB86690 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 110
ID ADB77295 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 111
ID ADB34452 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 112
ID ADB35556 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 113
ID ADB33900 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 114
ID ADB35004 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 115
ID ADB36108 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide SEQ ID NO 335.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 116
ID ADB46503 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 117
ID ADC28371 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein PRO245 cDNA, #13.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 118
ID ADC39571 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 119
ID ADC40085 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 120
ID ADC18913 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 121
ID ADC34209 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 122
ID ADC29264 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 123
ID ADC28795 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 124
ID ADC40680 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 125
ID ADC19337 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
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PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 126
ID ADC33785 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cdna, #13.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 127
ID ADC12855 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cdna, #13.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 128
ID ADC50376 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cdna.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 129
ID ADC71923 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cdna.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 130
ID ADC59902 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cdna.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 131
ID ADC52909 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cdna Seq ID335.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 132
ID ADC57263 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cdna Seq ID335.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 133
ID ADC60454 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cdna.
PN US2003087367-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 134
ID ADC50929 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cdna.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 135
ID ADC65456 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 136
ID ADC54554 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cdna Seq ID335.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 137
ID ADC53515 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cdna Seq ID335.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 138
ID ADC59038 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cdna Seq ID335.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 139
ID ADC55916 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cdna Seq ID335.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 140
ID ADC58486 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cdna Seq ID335.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 0
RESULT 141
ID ADC12307 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cdna, #13.
PN US2003082541-A1.
PD 01-MAY-2003.
```


Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 158		
ID ADD53029 standard; cDNA; 1295 BP.		
DE cDNA encoding human PRO polypeptide #168.		
PN US2003194792-A1.		
PD 16-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 159		
ID ADD53581 standard; cDNA; 1295 BP.		
DE Novel human secreted and transmembrane protein PRO245 cDNA.		
PN US2003203437-A1.		
PD 30-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 160		
ID ADD51737 standard; cDNA; 1295 BP.		
DE cDNA encoding human PRO polypeptide #168.		
PN US2003194779-A1.		
PD 16-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 161		
ID ADD02536 standard; cDNA; 1295 BP.		
DE Human PRO polynucleotide #168.		
PN US2003203431-A1.		
PD 30-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 162		
ID ADD01970 standard; cDNA; 1295 BP.		
DE Human PRO polynucleotide #168.		
PN US2003203430-A1.		
PD 30-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 163		
ID ADD54152 standard; cDNA; 1295 BP.		
DE Novel human secreted and transmembrane protein PRO245 cDNA.		
PN US2003203432-A1.		
PD 30-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 164		
ID ADD92469 standard; cDNA; 1295 BP.		
DE Human PRO polynucleotide #168.		
PN US2003199030-A1.		
PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 165		
ID ADD91365 standard; cDNA; 1295 BP.		
DE Human PRO polynucleotide #168.		
PN US2003199055-A1.		
PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 166		
ID ADE03979 standard; cDNA; 1295 BP.		
DE Human PRO polynucleotide #168.		
PN US2003199057-A1.		
PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 167		
ID ADE32276 standard; cDNA; 1295 BP.		
DE Novel human secreted and transmembrane protein PRO245 cDNA.		
PN US2003194765-A1.		
PD 16-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 168		
ID ADE22208 standard; cDNA; 1295 BP.		
DE cDNA encoding human PRO polypeptide #168.		
PN US2003199056-A1.		
PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 169		
ID ADD79432 standard; cDNA; 1295 BP.		
DE cDNA encoding human PRO polypeptide #168.		
PN US2003203428-A1.		
PD 30-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 170		
ID ADE41968 standard; cDNA; 1295 BP.		
DE Human PRO polynucleotide #168.		
PN US2003194772-A1.		
PD 16-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 171		
ID ADE17785 standard; cDNA; 1295 BP.		
DE Human PRO polynucleotide #168.		
PN US2003199023-A1.		
PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 172		
ID ADD91917 standard; cDNA; 1295 BP.		
DE Human PRO polynucleotide #168.		
PN US2003199053-A1.		
PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 173		
ID ADE33380 standard; cDNA; 1295 BP.		
DE Novel human secreted and transmembrane protein PRO245 cDNA.		
PN US2003194767-A1.		
PD 16-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
RESULT 174		
ID ADD91365 standard; cDNA; 1295 BP.		
DE Human PRO polynucleotide #168.		
PN US2003199055-A1.		
PD 23-OCT-2003.		
PA (GETH) GENENTECH INC.		
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	

RESULT 174
ID ADE33932 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 175
ID ADD79984 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 176
ID ADD93021 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 177
ID ADE19441 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 178
ID ADE34696 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 179
ID ADE18889 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 180
ID ADE43085 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 181
ID ADD95874 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 182

ID ADE22760 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 183
ID ADD78878 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 184
ID ADE32828 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 185
ID ADE42520 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 186
ID ADD80536 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 187
ID ADD89564 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 188
ID ADE40848 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 189
ID ADE04647 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 190
ID ADE92776 standard; cDNA; 1295 BP.


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DE Human PRO polynucleotide #168.
PN US2003194777-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 191
ID ADG211485 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 192
ID ADG23126 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 193
ID ADF97461 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 194
ID ADG80525 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 195
ID ADG79973 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 196
ID ADH62535 standard; cDNA; 1295 BP.
DE Human DNA35638 cDNA encoding PRO245 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 197
ID ADH59179 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Conservative: 0
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Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 198
ID ADH55265 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 199
ID ADH55817 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 200
ID ADI37958 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 201
ID ADI64036 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 202
ID ADI64985 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 203
ID ADI63484 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 204
ID ADH81898 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 205
ID ADH81346 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Conservative: 0
```



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Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 206
ID ACA58948 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #11.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 207
ID ACD24020 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 208
ID ACA58345 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #11.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 209
ID ACA67161 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 210
ID ADJ26226 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 211
ID ADM82515 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 212
ID ADN15914 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 213
ID ADN16543 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 214
ID ADN15362 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 215
ID ADN14810 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 216
ID ADC81072 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 217
ID ADE79141 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 218
ID ADD76520 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 219
ID ADD87884 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 220
ID ADD86288 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 221
ID ADE79565 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
RESULT 222
ID ADE79565 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 100.0%      Indels: 0
```



```
RESULT 222
ID ADE75736 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 223
ID ADE73241 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 224
ID ADE23312 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 225
ID ADE23864 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 226
ID ADE24507 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 227
ID ADD87332 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 228
ID ADE89198 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 229
ID ADE73776 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 230
ID ADE98449 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 231
ID ADE88646 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 232
ID ADE99330 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 233
ID ADE94666 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 234
ID ADE91077 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 235
ID ADE95218 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 236
ID ADE93328 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 237
ID ADF34909 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 238
ID ADE98449 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 239
ID ADE98449 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 240
ID ADE98449 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
```


DE Human secreted/transmembrane protein cDNA, #13.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 239
ID ADE92224 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 240
ID ADE90525 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 241
ID ADE91672 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 242
ID ADE98876 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 243
ID ADG0346 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 244
ID ADF73740 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 245
ID ADG02251 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 246
ID ADG22037 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 247
ID ADG20107 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 248
ID ADF98013 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 249
ID ADG24230 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 250
ID ADF98584 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 251
ID ADG03415 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 252
ID ADF99136 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 253
ID ADG16721 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0

Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 254	
ID ADG05180 standard; cDNA; 1295 BP.	
DE Human PRO polynucleotide #168.	
PN US2003207375-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 255	
ID ADG19447 standard; cDNA; 1295 BP.	
DE cDNA encoding human PRO polypeptide #168.	
PN US2003207425-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 256	
ID ADF73316 standard; cDNA; 1295 BP.	
DE Human secreted/transmembrane protein cDNA, #13.	
PN US2003166051-A1.	
PD 04-SEP-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 257	
ID ADG13284 standard; cDNA; 1295 BP.	
DE cDNA encoding human PRO polypeptide #168.	
PN US2003207357-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 258	
ID ADG08341 standard; cDNA; 1295 BP.	
DE Novel human secreted and transmembrane protein PRO245 cDNA.	
PN US2003207424-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 259	
ID ADG15511 standard; cDNA; 1295 BP.	
DE cDNA encoding human PRO polypeptide #168.	
PN US2003219885-A1.	
PD 27-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 260	
ID ADF96909 standard; cDNA; 1295 BP.	
DE Human PRO polynucleotide #168.	
PN US2003207371-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 261	
ID ADG06094 standard; cDNA; 1295 BP.	
DE Human PRO polynucleotide #168.	
PN US2003207374-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 262	
ID ADG23678 standard; cDNA; 1295 BP.	
DE Novel human secreted and transmembrane protein PRO245 cDNA.	
PN US2003207389-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 263	
ID ADG03967 standard; cDNA; 1295 BP.	
DE Human PRO polynucleotide #168.	
PN US2003207423-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 264	
ID ADG24868 standard; cDNA; 1295 BP.	
DE Novel human secreted and transmembrane protein PRO245 cDNA.	
PN US2003207427-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 265	
ID ADG07165 standard; cDNA; 1295 BP.	
DE Novel human secreted and transmembrane protein PRO245 cDNA.	
PN US2003207350-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 266	
ID ADG07717 standard; cDNA; 1295 BP.	
DE Novel human secreted and transmembrane protein PRO245 cDNA.	
PN US2003207356-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 267	
ID ADG55212 standard; cDNA; 1295 BP.	
DE Novel human secreted and transmembrane protein PRO245 cDNA.	
PN US2003194778-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 268	
ID ADG60876 standard; cDNA; 1295 BP.	
DE Novel human secreted and transmembrane protein PRO245 cDNA.	
PN US2003207390-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 269	
ID ADG61980 standard; cDNA; 1295 BP.	
DE Novel human secreted and transmembrane protein PRO245 cDNA.	
PN US2003207428-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0
RESULT 270	
ID ADG61980 standard; cDNA; 1295 BP.	
DE Novel human secreted and transmembrane protein PRO245 cDNA.	
PN US2003207428-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 100.0%	Indels: 0


```
RESULT 270
ID ADG92159 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein cDNA, #13.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 271
ID ADG82181 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 272
ID ADG57420 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 273
ID ADG56868 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 274
ID ADG55764 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 275
ID ADG58524 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 276
ID ADG70890 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 277
ID ADG92586 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 278
ID ADG92159 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 279
ID ADG53556 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 280
ID ADG71442 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 281
ID ADG81629 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 282
ID ADH30591 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 283
ID ADH1958 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 284
ID ADG52380 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 285
ID ADG54108 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 286
ID ADG81077 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
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PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 287
ID ADG56316 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 288
ID ADH12582 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 289
ID ADG61428 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 290
ID ADH28515 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2003222331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 291
ID ADG54660 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 292
ID ADG59700 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 293
ID ADH20375 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 294
ID ADH07230 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004006211-A1.

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PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 295
ID ADH59775 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 296
ID ADH06803 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 297
ID ADH11124 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 298
ID ADH18545 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 299
ID ADH5265 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 300
ID ADH37528 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
RESULT 301
ID ADG09867 standard; cDNA; 1295 BP.

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DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 302
ID ADH97332 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 303
ID ADI15338 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 304
ID ADG09215 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 305
ID ADI65692 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 306
ID ADI14670 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 307
ID ADH60435 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 308
ID ADI18265 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 309
ID ADJ99492 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 310
ID ADL08685 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 311
ID ADM25030 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 312
ID ADJ63546 standard; cDNA; 1295 BP.
DE Novel human secreted and transmembrane protein PRO245 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 313
ID ADM29776 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 314
ID ADJ77441 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 315
ID ADJ65563 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
RESULT 316
ID ADM27699 standard; cDNA; 1295 BP.
DE cDNA encoding human PRO polypeptide #168.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
```


Query Match: 100.0% Indels: 0
RESULT 328
ID ADT03255 standard; cDNA; 1295 BP.
DE Human PRO polynucleotide #168.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 329
ID ADT03535 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 330
ID ADT03306 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane PRO245 cDNA.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 331
ID AEA3773 standard; cDNA; 1295 BP.
DE Human secreted/transmembrane protein cDNA, #13.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 332
ID AEB14052 standard; cDNA; 1295 BP.
DE Cancer cell diagnosis method-related human cDNA sequence - SEQ ID 335.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERSINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERE/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TURNAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 333
ID AED23807 standard; cDNA; 1295 BP.
DE Human secreted protein PRO 245 encoding gene, SEQ ID 63.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 334
ID AED86250 standard; cDNA; 1295 BP.

DE Human PRO cDNA, seq id 335.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 335
ID ABE88976 standard; cDNA; 1295 BP.
DE Tyrosine kinase homologous PRO245 encoding gene, SEQ ID 63.
PN US974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 336
ID AAX81770 standard; cDNA; 1295 BP.
DE cDNA DNA35638 encoding A33 related antigen PRO245.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 99.7%
Best Local Similarity: 99.7%
Query Match: 99.7%
Conservative: 0
Mismatch: 1
Indels: 0
RESULT 337
ID ADP56686 standard; cDNA; 972 BP.
DE Human junction adhesion molecule 2 splice variant (huJAM2sv) cDNA.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 99.0%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 338
ID ADV43971 standard; cDNA; 897 BP.
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1599.
PN WO2004108899-A2.
PD 16-DEC-2004.
PA (USGH) US DEPT HEALTH & HUMAN SERVICES.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 91.9%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 339
ID AAV82780 standard; cDNA; 1076 BP.
DE Clone ct684.4 isolated from human adult brain cDNA library.
PN WO9842739-A2.
PD 01-OCT-1998.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 91.9%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 340
ID ABO92017 standard; cDNA; 1076 BP.
DE Human polynucleotide SEQ ID NO 14.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 91.9%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 341
ID AAS00512 standard; cDNA; 1131 BP.
DE Human junctional adhesion protein (JAM2) cDNA.
PN WO200114404-A1.
PD 01-MAR-2001.

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 91.9% Indels: 0
 RESULT 342
 ID AC72652 standard; cDNA; 1397 BP.
 DE Human vascular endothelial function-associated molecule cDNA.
 PN WO2003025138-A2.
 PD 27-MAR-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 91.9% Indels: 0
 RESULT 343
 ID ACN40835 standard; cDNA; 1721 BP.
 DE Tumour-associated antigenic target (TAT) cDNA DNA326887, SEQ ID NO:5879.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 91.9% Indels: 0
 RESULT 344
 ID AAL51599 standard; DNA; 897 BP.
 DE Human junctional adhesion molecule 2 (hujAM2) coding sequence.
 PN WO2003008541-A2.
 PD 30-JAN-2003.
 PA (ELIL) LILLY & CO ELI.
 Percent Similarity: 99.7% Conservative: 0
 Best Local Similarity: 99.7% Mismatches: 1
 Query Match: 91.7% Indels: 0
 RESULT 345
 ID AAV34310 standard; DNA; 1022 BP.
 DE Human secreted protein gene 25 clone HTEEB42.
 PN WO9840483-A2.
 PD 17-SEP-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 99.3% Conservative: 0
 Best Local Similarity: 99.3% Mismatches: 2
 Query Match: 91.3% Indels: 0
 RESULT 346
 ID AAD44660 standard; cDNA; 1022 BP.
 DE Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
 PN US2002077287-A1.
 PD 20-JUN-2002.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 Percent Similarity: 99.3% Conservative: 0
 Best Local Similarity: 99.3% Mismatches: 2
 Query Match: 91.3% Indels: 0
 RESULT 347
 ID AAD44878 standard; cDNA; 1022 BP.
 DE Human secreted protein-encoding gene 25 cDNA clone HTEEB42, SEQ ID NO:35.
 PN US2002076756-A1.
 PD 20-JUN-2002.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.

PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 Percent Similarity: 99.3% Conservative: 0
 Best Local Similarity: 99.3% Mismatches: 2
 Indels: 0
 Query Match: 91.3%
 RESULT 348
 ID AC50637 standard; cDNA; 1022 BP.
 DE Human secreted protein coding sequence, SEQ ID 304.
 PN WO200295010-A2.
 PD 28-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 99.3% Conservative: 0
 Best Local Similarity: 99.3% Mismatches: 2
 Indels: 0
 Query Match: 91.3%
 RESULT 349
 ID ABZ71351 standard; cDNA; 1022 BP.
 DE Secreted protein-encoding gene 162 cDNA clone HTEEB42, SEQ ID NO:172.
 PN WO200276488-A1.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 99.3% Conservative: 0
 Best Local Similarity: 99.3% Mismatches: 2
 Indels: 0
 Query Match: 91.3%
 RESULT 350
 ID ABX6990 standard; cDNA; 1022 BP.
 DE Human secreted protein gene 25, cDNA.
 PN US2002172994-A1.
 PD 21-NOV-2002.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 Percent Similarity: 99.3% Conservative: 0
 Best Local Similarity: 99.3% Mismatches: 2
 Indels: 0
 Query Match: 91.3%
 RESULT 351
 ID ADB91286 standard; cDNA; 1022 BP.
 DE Human secreted protein cDNA #SEQ ID 232.
 PN WO2003004622-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 99.3% Conservative: 0
 Best Local Similarity: 99.3% Mismatches: 2
 Indels: 0
 Query Match: 91.3%
 RESULT 352
 ID ADC73716 standard; DNA; 1022 BP.
 DE Human secreted protein-related DNA - SEQ ID 349.
 PN WO2003038063-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 99.3% Conservative: 0
 Best Local Similarity: 99.3% Mismatches: 2
 Indels: 0
 Query Match: 91.3%
 RESULT 353
 ID ADG89762 standard; cDNA; 1022 BP.
 DE Human cDNA from secreted protein gene 25.
 PN US2003225009-A1.


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PD 04-DEC-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.
Percent Similarity: 99.3%
Best Local Similarity: 99.3%
Query Match: 91.3%
Indels: 0
Conservative: 0
Mismatch: 2
Indel: 0
RESULT 354
ID AED10199 standard; cDNA; 1022 BP.
DE Human secreted protein encoding cDNA clone, SEQ ID 35.
PN US2005208621-A1.
PD 22-SEP-2005.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.3%
Best Local Similarity: 99.3%
Query Match: 91.3%
Indels: 0
Conservative: 0
Mismatch: 2
Indel: 0
RESULT 355
ID AAH98352 standard; cDNA; 1416 BP.
DE Human EST-derived coding sequence SEQ ID NO: 209.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 98.3%
Best Local Similarity: 98.0%
Query Match: 90.9%
Indels: 5
Conservative: 1
Mismatch: 0
Indel: 0
RESULT 356
ID AAL60897 standard; cDNA; 1389 BP.
DE Human novel splice variant of VEJAM (NOJAM) cDNA.
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GEST-) GENSET SA.
Percent Similarity: 99.3%
Best Local Similarity: 99.3%
Query Match: 89.8%
Indels: 2
Conservative: 0
Mismatch: 1
Indel: 0
RESULT 357
ID AAS86528 standard; cDNA; 1430 BP.
DE DNA encoding novel human diagnostic protein #22332.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 90.0%
Best Local Similarity: 89.0%
Query Match: 77.3%
Indels: 13
Conservative: 3
Mismatch: 17
Indel: 13
RESULT 358
ID AAA95305 standard; cDNA; 1626 BP.
DE Murine CRAM-2 coding sequence.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMPD-) RMP DICTAGENE SA.
Percent Similarity: 85.8%
Best Local Similarity: 76.8%
Query Match: 71.3%
Indels: 2
Conservative: 26
Mismatch: 39
Indel: 2
RESULT 359
ID AAI61103 standard; cDNA; 930 BP.
DE Human polynucleotide SEQ ID NO 5092.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 67.9%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 360
ID AAF74414 standard; DNA; 905 BP.
DE Angiogenesis protein AAAL nucleotide sequence (Fig 7).
PN WO200111086-A2.
PD 15-FEB-2001.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 65.6%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 361
ID ADQ53429 standard; DNA; 647 BP.
DE Novel canine microarray-related DNA sequence SeqID4731.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 95.0%
Best Local Similarity: 89.9%
Query Match: 57.5%
Indels: 0
Conservative: 10
Mismatch: 10
Indel: 0
RESULT 362
ID AAI59317 standard; cDNA; 561 BP.
DE Human polynucleotide SEQ ID NO 1520.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 47.5%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 363
ID AAX81783 standard; DNA; 413 BP.
DE Consensus sequence DNA30954 encoding an A33 related antigen.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH-) GENENTECH INC.
Percent Similarity: 98.5%
Best Local Similarity: 98.5%
Query Match: 42.3%
Indels: 1
Conservative: 0
Mismatch: 1
Indel: 1
RESULT 364
ID AAX37665 standard; cDNA; 413 BP.
DE Human PRO protein derived EST consensus sequence DNA30954.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Percent Similarity: 98.5%
Best Local Similarity: 98.5%
Query Match: 42.3%
Indels: 1
Conservative: 0
Mismatch: 1
Indel: 1
RESULT 365
ID ABX93489 standard; cDNA; 413 BP.
DE Consensus sequence expressed sequence tag, EST, DNA30954.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH-) GENENTECH INC.
Percent Similarity: 98.5%
Best Local Similarity: 98.5%
Query Match: 42.3%
Indels: 1
Conservative: 0
Mismatch: 1
Indel: 1
RESULT 366
ID ADH62554 standard; DNA; 413 BP.
DE Human DNA30954 consensus DNA.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK-) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Percent Similarity: 98.5%
Best Local Similarity: 98.5%
Query Match: 42.3%
Indels: 1
Conservative: 0
Mismatch: 1
Indel: 1
RESULT 367
ID ADN35306 standard; DNA; 413 BP.
DE Human PRO245 consensus DNA fragment DNA30954.
```



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PN WO2004031105-A2.
PA (GETH ) GENENTECH INC.
Percent Similarity: 98.5%
Best Local Similarity: 98.5%
Query Match: 42.3%
RESULT 368
ID ACH37074 standard; cDNA; 450 BP.
DE Human endothelial cell cDNA #5207.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 41.7%
RESULT 369
ID AAS86525 standard; cDNA; 493 BP.
DE DNA encoding novel human diagnostic protein #22329.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSQ INC.
Percent Similarity: 92.8%
Best Local Similarity: 92.8%
Query Match: 39.8%
RESULT 370
ID AAX37668 standard; cDNA; 301 BP.
DE Human PRO protein derived EST DNA sequence T89217.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 99.0%
Best Local Similarity: 99.0%
Query Match: 32.4%
RESULT 371
ID AAV89708 standard; cDNA; 343 BP.
DE EST clone CT864.
PN WO9845436-A2.
PD 15-OCT-1998.
PA (GEMY ) GENETICS INST INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 31.8%
RESULT 372
ID AAA97189 standard; cDNA; 1940 BP.
DE Murine CRAM-1 coding sequence #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Percent Similarity: 56.8%
Best Local Similarity: 36.3%
Query Match: 29.8%
RESULT 373
ID AA95304 standard; cDNA; 1943 BP.
DE Murine CRAM-1 coding sequence #1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Percent Similarity: 56.8%
Best Local Similarity: 36.3%
Query Match: 29.8%
RESULT 374
ID ADP69026 standard; cDNA; 939 BP.
DE Human NOV2b encoding cDNA SEQ ID NO:21.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 56.5%
Best Local Similarity: 37.4%
Query Match: 29.1%
PN WO2004031105-A2.
PA (GETH ) GENENTECH INC.
Conservative: 0
Mismatch: 1
Indels: 1
Percent Similarity: 98.5%
Best Local Similarity: 98.5%
Query Match: 42.3%
RESULT 368
ID ACH37074 standard; cDNA; 450 BP.
DE Human endothelial cell cDNA #5207.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Conservative: 0
Mismatch: 0
Indels: 0
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 41.7%
RESULT 369
ID AAS86525 standard; cDNA; 493 BP.
DE DNA encoding novel human diagnostic protein #22329.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSQ INC.
Conservative: 0
Mismatch: 1
Indels: 10
Percent Similarity: 92.8%
Best Local Similarity: 92.8%
Query Match: 39.8%
RESULT 370
ID AAX37668 standard; cDNA; 301 BP.
DE Human PRO protein derived EST DNA sequence T89217.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Conservative: 0
Mismatch: 0
Indels: 1
Percent Similarity: 99.0%
Best Local Similarity: 99.0%
Query Match: 32.4%
RESULT 371
ID AAV89708 standard; cDNA; 343 BP.
DE EST clone CT864.
PN WO9845436-A2.
PD 15-OCT-1998.
PA (GEMY ) GENETICS INST INC.
Conservative: 0
Mismatch: 0
Indels: 0
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 31.8%
RESULT 372
ID AAA97189 standard; cDNA; 1940 BP.
DE Murine CRAM-1 coding sequence #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Conservative: 62
Mismatch: 109
Indels: 22
Percent Similarity: 56.8%
Best Local Similarity: 36.3%
Query Match: 29.8%
RESULT 373
ID AA95304 standard; cDNA; 1943 BP.
DE Murine CRAM-1 coding sequence #1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Conservative: 62
Mismatch: 109
Indels: 22
Percent Similarity: 56.8%
Best Local Similarity: 36.3%
Query Match: 29.8%
RESULT 374
ID ADP69026 standard; cDNA; 939 BP.
DE Human NOV2b encoding cDNA SEQ ID NO:21.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Conservative: 53
Mismatch: 102
Indels: 19
Percent Similarity: 56.5%
Best Local Similarity: 37.4%
Query Match: 29.1%

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RESULT 375
ID ADP69024 standard; cDNA; 952 BP.
DE Human NOV2a encoding cDNA SEQ ID NO:19.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Conservative: 53
Mismatch: 102
Indels: 19
Percent Similarity: 56.5%
Best Local Similarity: 37.4%
Query Match: 29.0%
RESULT 376
ID ADP69034 standard; cDNA; 952 BP.
DE Human NOV2f encoding cDNA SEQ ID NO:29.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Conservative: 52
Mismatch: 103
Indels: 21
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 377
ID ABZ5894 standard; cDNA; 933 BP.
DE Human junctional adhesion molecule 3 (JAM3) encoding cDNA.
PN WO200306673-A2.
PD 23-JAN-2003.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Conservative: 52
Mismatch: 103
Indels: 21
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 378
ID ADH60143 standard; DNA; 933 BP.
DE Human JAM 3 DNA.
PN US2003232034-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Conservative: 52
Mismatch: 103
Indels: 21
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 379
ID AEB35302 standard; DNA; 933 BP.
DE Human Gefitinib sensitivity-related gene, IKIP.
PN WO2005070020-A2.
PD 04-AUG-2005.
PA (COLS ) UNIV COLORADO.
Conservative: 52
Mismatch: 103
Indels: 21
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 380
ID ADP69032 standard; cDNA; 952 BP.
DE Human NOV2e encoding cDNA SEQ ID NO:27.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Conservative: 52
Mismatch: 103
Indels: 21
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 381
ID AA95306 standard; DNA; 1296 BP.
DE Human CRAM-1 coding sequence.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Conservative: 52
Mismatch: 103
Indels: 21
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 382
ID AAK94243 standard; cDNA; 1724 BP.
DE Human full-length cDNA, SEQ ID NO: 2844.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Conservative: 52
Mismatch: 103
Indels: 21
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 383

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ID ADL30811 standard; cDNA; 1724 BP.
DE Full length human cDNA clone SeqID 2844.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 384
ID AAK94867 standard; cDNA; 3515 BP.
DE Human full-length cDNA, SEQ ID NO: 4050.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 385
ID ADL32017 standard; cDNA; 3515 BP.
DE Full length human cDNA clone SeqID 4050.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 386
ID AAAS1265 standard; cDNA; 3554 BP.
DE Human DNA encoding PRO1868, an A33 antigen homologue.
PN WO200036102-A2.
PD 22-JUN-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 387
ID AAC58622 standard; cDNA; 3554 BP.
DE Human PRO1868 protein UNQ859 encoding cDNA SEQ ID NO:192.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 388
ID AAF72433 standard; cDNA; 3554 BP.
DE Human PRO1868 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 389
ID AAS21512 standard; cDNA; 3554 BP.
DE Human cDNA sequence encoding for PRO1868 polypeptide.
PN WO200104066-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 390
ID ABS68392 standard; cDNA; 3554 BP.
DE Human cDNA encoding secreted protein PRO1868.
PN US2002098506-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 391
ID ABS67460 standard; cDNA; 3554 BP.

DE cDNA encoding novel human secreted protein #7.
PN US2002098505-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 392
ID ABL88202 standard; cDNA; 3554 BP.
DE Human PRO1868 cDNA sequence SEQ ID NO:261.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 393
ID ABS53477 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO1868 polypeptide.
PN US2002098507-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 394
ID ABL95691 standard; cDNA; 3554 BP.
DE Human angiogenesis related cDNA PRO1868 SEQ ID NO: 261.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 395
ID ACA60361 standard; cDNA; 3554 BP.
DE Human cDNA for secreted/transmembrane protein PRO1868.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 396
ID ACA03871 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match:
RESULT 397
ID ABX71810 standard; cDNA; 3554 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1868.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.


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Query Match: 28.8% Indels: 21
RESULT 414
ID ADA61760 standard; cDNA; 3554 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 415
ID ADB19545 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 416
ID ADB28086 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 417
ID ADA86565 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 418
ID ADB16129 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 419
ID ADA47915 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 420
ID ADA18483 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 421
ID ACD67151 standard; cDNA; 3554 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1868.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 422
ID ADA67710 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 423
ID ADB30717 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 424
ID ADA86013 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 425
ID ADA97225 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 426
ID ADA79529 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 427
ID ADA87668 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 428
ID ADB16870 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 429
ID ACD83312 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #61.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
```



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ID ADA16458 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein PRO1868 cDNA, #65.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 431
ID ADA91962 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 432
ID ADB15025 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 433
ID ADB18986 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 434
ID ADA94201 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 435
ID ADB20097 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 436
ID ADB13409 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 437
ID ACD98692 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 438
ID ADA74663 standard; cDNA; 3554 BP.
DE ADB30165 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
DE Human PRO polynucleotide #269.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 439
ID ADA42603 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 440
ID ADB24896 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide SEQ ID NO 537.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 441
ID ADA82420 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 442
ID ADA75383 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 443
ID ADA85461 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 444
ID ADA84909 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 445
ID ACD23490 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #61.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 446
ID ADB30165 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
```


PN US2003073214-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 447
ID ADA80693 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 448
ID ADA75935 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 449
ID ADA47160 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 450
ID ADB25456 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide SEQ ID NO 537.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 451
ID ADA93632 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 452
ID ADB26982 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 453
ID ADB31269 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 454
ID ACD26813 standard; DNA; 3554 BP.
DE cDNA encoding human PRO1868 protein.
PN US2003054447-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 455
ID ADA61197 standard; cDNA; 3554 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 456
ID ADB24344 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide SEQ ID NO 537.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 457
ID ADA96673 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 458
ID ADA81245 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 459
ID ADA96121 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 460
ID ADB26430 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 461
ID ADB21915 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
RESULT 462
ID ADA77694 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003068797-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 463
ID ADB18434 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 464
ID ADA87117 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 465
ID ADA16882 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 466
ID ADA13311 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 467
ID ADA42179 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 468
ID ADA88220 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 469
ID ADA46608 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 470
ID ADA17526 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 471
ID ADA43029 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 472
ID ADB28638 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 473
ID ADB29190 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 474
ID ACD07774 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003027256-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 475
ID ADA77142 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 476
ID ADA88772 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 477
ID ADA97777 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 478
ID ADB27534 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 479
ID ADA17526 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match: 28.8% Indels: 21
RESULT 479
ID ADB22467 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 480
ID ACD23852 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #61.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 481
ID ADA67158 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 482
ID ADB23019 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 483
ID ADB23792 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide SEQ ID NO 537.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 484
ID ADA92514 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 485
ID ADB15577 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 486
ID ADB38829 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 487

ID ADB38277 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 488
ID ADB66749 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 489
ID ADB89829 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 490
ID ADB90561 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 491
ID ADB77947 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 492
ID ADB39662 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 493
ID ADB75083 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 494
ID ADB47285 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 495
ID ADB86892 standard; cDNA; 3554 BP.

DE Human PRO polynucleotide #269.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 496
ID ADB77497 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 497
ID ADB34654 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide SEQ ID NO 537.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 498
ID ADB35758 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide SEQ ID NO 537.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 499
ID ADB34102 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide SEQ ID NO 537.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 500
ID ADB35206 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide SEQ ID NO 537.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 501
ID ADB36310 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide SEQ ID NO 537.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 502
ID ADB46705 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 503
ID ADC28730 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.

PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 504
ID ADC39930 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 505
ID ADC40444 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 506
ID ADC19268 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 507
ID ADC34568 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 508
ID ADC29623 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 509
ID ADC29154 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 510
ID ADC41039 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 511
ID ADC19696 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003054441-A1.


```
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 512
ID ADC34144 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA, #65.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 513
ID ADC13214 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA, #65.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 514
ID AAD58950 standard; cDNA; 3554 BP.
DE Human PRO1868 cDNA.
PN US2003077657-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 515
ID ADC50578 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 516
ID ADC71215 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 517
ID ADC60104 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 518
ID ADC53111 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID537.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 519
ID ADC57465 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID537.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 520
ID ADC60656 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 521
ID ADC51131 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 522
ID ADC65658 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 523
ID ADC54756 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID537.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 524
ID ADC53717 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID537.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 525
ID ADC59240 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID537.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 526
ID ADC56118 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID537.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 527
ID ADC58688 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID537.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
```



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Query Match: 28.8% Indels: 21
RESULT 544
ID ADD03803 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 545
ID ADD41352 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 546
ID ADD52491 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 547
ID ADD53231 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 548
ID ADD53783 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 549
ID ADD37303 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #131.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 550
ID ADD51939 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 551
ID ADD02738 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 552
ID ADD02172 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 553
ID ADD54354 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 554
ID ADD2671 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 555
ID ADD91567 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 556
ID ADE04181 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 557
ID ADE32478 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 558
ID ADE22410 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 559
ID ADD79634 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
RESULT 560
ID ADD79634 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatch: 103
Indels: 21
Query Match: 28.8%
```


ID ADE42170 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003194772-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 561

ID ADE17987 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199023-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 562

ID ADD92119 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199053-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 563

ID ADE33582 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003194767-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 564

ID ADE34134 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003194791-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 565

ID ADD80186 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003207417-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 566

ID ADD93223 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003194768-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 567

ID ADE19643 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199025-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 568

ID ADE35055 standard; cDNA; 3554 BP.

DE Human secreted/transmembrane protein cDNA, #65.
PN US2003077583-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 569

ID ADE19091 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199026-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 570

ID ADE43287 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199033-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 571

ID ADD96076 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199059-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 572

ID ADE22962 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003199064-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 573

ID ADD79080 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003203429-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 574

ID ADE33030 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003194766-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 575

ID ADE42722 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199032-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 576

ID ADD80738 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.


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PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 577
ID ADD89766 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 578
ID ADE41050 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 579
ID ADE04849 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 580
ID ADE92978 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 581
ID ADG21687 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 582
ID ADG23328 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 583
ID ADF97663 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 584
ID ADG80727 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 585
ID ADG80175 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 586
ID ADH59538 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 587
ID ADH55467 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 588
ID ADH56019 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 589
ID ADI38317 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 590
ID ADI64238 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 591
ID ADI65187 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 592
ID ADI63686 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
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RESULT 625
ID ADE99689 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 626
ID ADE94868 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 627
ID ADE91279 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 628
ID ADE95420 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 629
ID ADE93530 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 630
ID ADF35111 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 631
ID ADE98808 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 632
ID ADE92426 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 633
ID ADE99689 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 634
ID ADE91874 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 635
ID ADE99235 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 636
ID ADG40705 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 637
ID ADF74099 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 638
ID ADG02453 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 639
ID ADG22239 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatch: 103
Indels: 21
RESULT 640
ID ADG20309 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003207376-A1.
PD 06-NOV-2003.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 641
ID ADF98215 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 642
ID ADG24432 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 643
ID ADP98786 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 644
ID ADG03617 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 645
ID ADP99338 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 646
ID ADG16923 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 647
ID ADG05382 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 648
ID ADG19649 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 649
ID ADF77675 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 650
ID ADG13486 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 651
ID ADG08543 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 652
ID ADG15713 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 653
ID ADF97111 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 654
ID ADG06296 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 655
ID ADG23880 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 656
ID ADG04169 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
```



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Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 657
ID ADG25070 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 658
ID ADG07367 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 659
ID ADG07919 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 660
ID ADG55414 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 661
ID ADG61078 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 662
ID ADG62182 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 663
ID ADG92518 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 664
ID ADG82383 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 665
ID ADG57622 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 666
ID ADG57070 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 667
ID ADG55966 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 668
ID ADG58726 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 669
ID ADG71092 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 670
ID ADG92945 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 671
ID ADG58174 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
RESULT 672
ID ADG53758 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%      Conservative: 52
Best Local Similarity: 37.1%      Mismatches: 103
Query Match: 28.8%      Indels: 21
```


RESULT 673
ID ADG71644 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207421-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 674
ID ADG81831 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 675
ID ADH30793 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 676
ID ADH12160 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 677
ID ADG52582 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 678
ID ADG54310 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 679
ID ADG81279 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 680
ID ADG56518 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 681
ID ADH12784 standard; cDNA; 3554 BP.

DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 682
ID ADG61630 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 683
ID ADH28717 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 684
ID ADG54862 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 685
ID ADG59902 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 686
ID ADH20734 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 687
ID ADH43694 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #131.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Query Match: 28.8%
Conservative: 52
Mismatches: 103
Indels: 21
RESULT 688
ID ADH07589 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHUR J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 689	
ID ADH60134 standard; cDNA; 3554 BP.	
DE Human secreted/transmembrane protein cDNA, #65.	
PN US2003215904-A1.	
PD 20-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 690	
ID ADH07162 standard; cDNA; 3554 BP.	
DE Human secreted/transmembrane protein cDNA, #65.	
PN US2004005665-A1.	
PD 08-JAN-2004.	
PA (DESN/) DESNOYERS L.	
PA (GODD/) GODDARD A.	
PA (GODO/) GODOWSKI P J.	
PA (GURN/) GURNEY A L.	
PA (MATH/) MATHER J P.	
PA (WILL/) WILLIAMS P M.	
PA (WOOD/) WOOD W I.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 691	
ID ADH18326 standard; cDNA; 3554 BP.	
DE cDNA encoding human PRO polypeptide #269.	
PN US2003207361-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 692	
ID ADH18904 standard; cDNA; 3554 BP.	
DE Human secreted/transmembrane protein cDNA, #65.	
PN US2003152999-A1.	
PD 14-AUG-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 693	
ID ADI37883 standard; cDNA; 3554 BP.	
DE Human secreted/transmembrane protein cDNA, #65.	
PN US2003096340-A1.	
PD 22-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 694	
ID ADG10069 standard; cDNA; 3554 BP.	
DE Novel human secreted and transmembrane protein PRO1868 cDNA.	
PN US2004009548-A1.	
PD 15-JAN-2004.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 695	
ID ADH97683 standard; cDNA; 3554 BP.	
DE Human secreted/transmembrane protein cDNA, #65.	
PN US2003190610-A1.	
PD 09-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 696	
ID ADH97683 standard; cDNA; 3554 BP.	
DE Human secreted/transmembrane protein cDNA, #65.	
PN US2003190610-A1.	
PD 09-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 697	
ID ADG09417 standard; cDNA; 3554 BP.	
DE Novel human secreted and transmembrane protein PRO1868 cDNA.	
PN US2004009547-A1.	
PD 15-JAN-2004.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 698	
ID ADH10340 standard; cDNA; 3554 BP.	
DE Human PRO1868 cDNA from DNA77624-2515 clone.	
PN US2003228664-A1.	
PD 11-DEC-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 699	
ID ADH14872 standard; cDNA; 3554 BP.	
DE Novel human secreted and transmembrane protein PRO1868 cDNA.	
PN US2003207383-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 700	
ID ADH60794 standard; cDNA; 3554 BP.	
DE Human secreted/transmembrane protein cDNA, #65.	
PN US2004023331-A1.	
PD 05-FEB-2004.	
PA (DESN/) DESNOYERS L.	
PA (GODD/) GODDARD A.	
PA (GODO/) GODOWSKI P J.	
PA (GURN/) GURNEY A L.	
PA (MATH/) MATHER J P.	
PA (WILL/) WILLIAMS P M.	
PA (WOOD/) WOOD W I.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 701	
ID ADH18467 standard; cDNA; 3554 BP.	
DE Novel human secreted and transmembrane protein PRO1868 cDNA.	
PN US2003207349-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 702	
ID ADJ99851 standard; cDNA; 3554 BP.	
DE Human secreted/transmembrane protein cDNA, #65.	
PN US2003187238-A1.	
PD 02-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 55.7%	Conservative: 52
Best Local Similarity: 37.1%	Mismatches: 103
Query Match: 28.8%	Indels: 21
RESULT 703	
ID ADL09044 standard; cDNA; 3554 BP.	
DE Human secreted/transmembrane protein cDNA, #65.	
PN US2003186358-A1.	
PD 02-OCT-2003.	


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PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 704
ID ADM25385 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 705
ID ADJ63748 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 706
ID ADM30135 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 707
ID ADJ77643 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 708
ID ADK83039 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #131.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 709
ID ADJ65765 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 710
ID ADM27901 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 711
ID ADM42625 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 712
ID ADO66457 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #63.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 713
ID ADM28487 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 714
ID ADRI1309 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 715
ID ADRI8218 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 716
ID ADI95969 standard; cDNA; 3554 BP.
DE cDNA encoding human PRO polypeptide #269.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Mismatches: 52
Indels: 103
Query Match: 21
RESULT 717
ID ADI96521 standard; cDNA; 3554 BP.

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DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 718
ID ADI66051 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 719
ID ADS74857 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane cDNA #65.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 720
ID ADS32473 standard; cDNA; 3554 BP.
DE Novel human secreted and transmembrane protein PRO1868 cDNA.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 721
ID ADT03457 standard; cDNA; 3554 BP.
DE Human PRO polynucleotide #269.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 722
ID ADT03894 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52

Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 723
ID ADZ03508 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane PRO1868 cDNA.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 724
ID AEA38132 standard; cDNA; 3554 BP.
DE Human secreted/transmembrane protein cDNA, #65.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 725
ID AEB14254 standard; cDNA; 3554 BP.
DE Cancer cell diagnosis method-related human cDNA sequence - SEQ ID 537.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERSINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 726
ID AED24166 standard; cDNA; 3554 BP.
DE Human secreted protein PRO 1868 encoding gene, SEQ ID 422.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 727
ID AED86452 standard; cDNA; 3554 BP.
DE Human PRO cDNA, seq id 537.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 728
ID AEB69335 standard; cDNA; 3554 BP.
DE Dayhoff homologous PRO1868 encoding gene, SEQ ID 422.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 729
ID AEB69335 standard; cDNA; 3554 BP.
DE Dayhoff homologous PRO1868 encoding gene, SEQ ID 422.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21

ID ABD73468 standard; cDNA; 3663 BP.
DE Human placental protein encoding cDNA SEQ ID NO:296.
PN U92005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 730
ID AAC69574 standard; DNA; 4385 BP.
DE Human secreted protein gene 13 clone HAPSA79.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 731
ID AAF72836 standard; DNA; 4385 BP.
DE Secreted protein gene #38.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 732
ID ADC73991 standard; DNA; 4385 BP.
DE Human secreted protein-related DNA - SEQ ID 624.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 733
ID ADD37816 standard; cDNA; 4385 BP.
DE Human secreted protein encoding sequence #298.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 734
ID ADA56717 standard; DNA; 4385 BP.
DE Gene encoding human secreted protein #592.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 735
ID AAC69524 standard; DNA; 4386 BP.
DE Human secreted protein gene 13 clone HAPSA79.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 736
ID AAC69575 standard; DNA; 4386 BP.
DE Human secreted protein gene 13 clone HAPSA79.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 737
ID AAF72811 standard; DNA; 4386 BP.

DE Secreted protein gene #13.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 738
ID AAF72837 standard; DNA; 4386 BP.
DE Secreted protein gene #39.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 739
ID ADC73992 standard; DNA; 4386 BP.
DE Human secreted protein-related DNA - SEQ ID 625.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 740
ID ADC73768 standard; DNA; 4386 BP.
DE Human secreted protein-related DNA - SEQ ID 401.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 741
ID ADD37817 standard; cDNA; 4386 BP.
DE Human secreted protein encoding sequence #299.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 742
ID ADD37720 standard; cDNA; 4386 BP.
DE Human secreted protein encoding sequence #202.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 743
ID ADA56413 standard; DNA; 4386 BP.
DE Gene encoding human secreted protein #592.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 744
ID ADA56718 standard; DNA; 4386 BP.
DE Gene encoding human secreted protein #592.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC. 55.7% Conservative: 52
Best Local Similarity: 37.1% Mismatches: 103
Query Match: 28.8% Indels: 21
RESULT 745
ID ADR41307 standard; cDNA; 4391 BP.
DE Human CD-like molecule HISA60 cDNA, SEQ ID NO:106.


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PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 55.7%
Best Local Similarity: 37.1%
Conservative: 52
Mismatches: 103
Indels: 21
Query Match: 28.8%
RESULT 746
ID ABQ54979 standard; cDNA; 3612 BP.
DE Human ovarian antigen HISP60 cDNA, SEQ ID NO:859.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 57.9%
Best Local Similarity: 37.9%
Conservative: 52
Mismatches: 99
Indels: 11
Query Match: 28.7%
RESULT 747
ID AAC74237 standard; cDNA; 3560 BP.
DE Human secreted protein gene 15 SEQ ID NO:25.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 57.5%
Best Local Similarity: 37.9%
Conservative: 51
Mismatches: 100
Indels: 11
Query Match: 28.6%
RESULT 748
ID ACH04172 standard; cDNA; 3717 BP.
DE Human cDNA differentially expressed in lung cancer #377.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Percent Similarity: 61.1%
Best Local Similarity: 39.7%
Conservative: 49
Mismatches: 85
Indels: 4
Query Match: 28.5%
RESULT 749
ID AAA27386 standard; cDNA; 1956 BP.
DE Human IGFAM-6 immunoglobulin coding sequence.
PN WO200029583-A2.
PD 25-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
Percent Similarity: 55.4%
Best Local Similarity: 37.1%
Conservative: 51
Mismatches: 104
Indels: 21
Query Match: 28.4%
RESULT 750
ID AAX37669 standard; cDNA; 253 BP.
DE Human PRO protein derived EST DNA sequence 1861250.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 28.3%
RESULT 751
ID ADP28230 standard; DNA; 270 BP.
DE Human secreted protein encoding sequence SEQ ID #228.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Conservative: 0
Mismatches: 0
Indels: 0
Query Match: 27.4%
RESULT 752
ID ABL39691 standard; cDNA; 980 BP.
DE Human NS cDNA sequence SEQ ID NO:1.
PN WO200206315-A2.
PD 24-JAN-2002.
PA (COMP-) COMPUGEN LTD.
Percent Similarity: 56.1%
Best Local Similarity: 36.3%
Conservative: 55
Mismatches: 107
Indels: 15
Query Match: 27.3%
RESULT 753
ID AAL51600 standard; DNA; 933 BP.
DE Human junctional adhesion molecule 3 (hujAM3) coding sequence.
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 55.5%
Best Local Similarity: 37.7%
Conservative: 50
Mismatches: 103
Indels: 23
Query Match: 26.8%
RESULT 754
ID AAS28784 standard; cDNA; 1812 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 30.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.0%
Best Local Similarity: 34.7%
Conservative: 47
Mismatches: 105
Indels: 37
Query Match: 25.5%
RESULT 755
ID ABA06454 standard; cDNA; 1812 BP.
DE Human cDNA SEQ ID NO: 120.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.0%
Best Local Similarity: 34.7%
Conservative: 47
Mismatches: 105
Indels: 37
Query Match: 25.5%
RESULT 756
ID ABV83791 standard; cDNA; 1812 BP.
DE Human polynucleotide SEQ ID NO 120.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 51.0%
Best Local Similarity: 34.7%
Conservative: 47
Mismatches: 105
Indels: 37
Query Match: 25.5%
RESULT 757
ID ADB31509 standard; cDNA; 1812 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 30.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.0%
Best Local Similarity: 34.7%
Conservative: 47
Mismatches: 105
Indels: 37
Query Match: 25.5%
RESULT 758
ID ADR41346 standard; cDNA; 1897 BP.
DE Human CD-like molecule HKAC103 cDNA, SEQ ID NO:145.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.0%
Best Local Similarity: 34.7%
Conservative: 47
Mismatches: 105
Indels: 37
Query Match: 25.5%
RESULT 759
ID ABA06428 standard; cDNA; 1894 BP.
DE Human cDNA SEQ ID NO: 94.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 52.5%
Best Local Similarity: 37.3%
Conservative: 43
Mismatches: 122
Indels: 14
Query Match: 25.4%
RESULT 760
ID ABV83765 standard; cDNA; 1894 BP.
DE Human polynucleotide SEQ ID NO 94.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 52.5%
Best Local Similarity: 37.3%
Conservative: 43
Mismatches: 122
Indels: 14
Query Match: 25.4%
RESULT 761

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ID ADJ67405 standard; DNA; 4249 BP.
DE Human ovarian specific gene SEQ ID NO:119.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 49.6%
Best Local Similarity: 34.4%
Conservative: 43
Mismatches: 104
Indels: 38
Query Match: 25.3%
RESULT 762
ID AA261675 standard; cDNA; 1421 BP.
DE cDNA encoding human A33 receptor homologue, SEQ ID NO:70.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 763
ID AAC99608 standard; cDNA; 1421 BP.
DE Skin cell cDNA, SEQ ID NO: 70.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 764
ID ABL34760 standard; cDNA; 1421 BP.
DE Human cDNA isolated from skin cells SEQ ID NO: 70.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 765
ID AAL51598 standard; DNA; 900 BP.
DE Human junctional adhesion molecule 1 (hJAM1) coding sequence.
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 766
ID AAX21837 standard; cDNA; 1140 BP.
DE F11 antigen coding sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 767
ID ADQ95889 standard; cDNA; 1236 BP.
DE T cell activation associated cDNA #34.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASahi Kasei PHARMA CORP.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 768
ID AA261781 standard; cDNA; 1421 BP.
DE cDNA encoding human A33 receptor homologue, SEQ ID NO:254.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 769
ID AAC99714 standard; cDNA; 1421 BP.

DE Skin cell cDNA, SEQ ID NO: 254.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 770
ID ABL34866 standard; cDNA; 1421 BP.
DE Human cDNA isolated from skin cells SEQ ID NO: 254.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 771
ID ABL90699 standard; cDNA; 1772 BP.
DE Human polynucleotide SEQ ID NO 1261.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 772
ID ADK40842 standard; cDNA; 1822 BP.
DE DNA encoding human platelet F11 receptor #1.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UNYV) UNIV NEW YORK STATE RES FOUND.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 773
ID ADR27640 standard; cDNA; 1822 BP.
DE Full length human F11 receptor cDNA Seq 6.
PN WO2004063327-A2.
PD 29-JUL-2004.
PA (KORN/) KORNECKI E.
PA (BAB/) BABINSKA A.
PA (EHL/) EHLICH Y H.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 774
ID ADU66682 standard; DNA; 1822 BP.
DE Human platelet F11 receptor, F11R-A DNA.
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 775
ID ABX93343 standard; cDNA; 1831 BP.
DE cDNA DNA40628 encoding human A-33 related antigen PRO301.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%
RESULT 776
ID AAX37714 standard; DNA; 1842 BP.
DE Human cDNA clone DNA40628 encoding PRO301.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Conservative: 46
Mismatches: 126
Indels: 16
Query Match: 25.2%


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RESULT 777
ID AAX52235 standard; DNA; 1842 BP.
DE Protein PRO301 cDNA clone DNA40628-1216.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 778
ID ADH62538 standard; cDNA; 1842 BP.
DE Human DNA40628 cDNA encoding PRO301 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (PONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 779
ID ADN35294 standard; DNA; 1842 BP.
DE Human PRO301 gene DNA40628.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 780
ID ADR11005 standard; cDNA; 1856 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 781
ID AAZ52204 standard; cDNA; 1857 BP.
DE Human PRO301 protein encoding cDNA, UNQ264.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 782
ID AAA77581 standard; cDNA; 1857 BP.
DE Human PRO301 cDNA sequence SEQ ID NO:89.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 783
ID AAA49723 standard; cDNA; 1857 BP.
DE Human PRO301 cDNA clone DNA40628-1216.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 784
ID ADC78438 standard; cDNA; 1857 BP.
DE Human PRO301 cDNA.
PN WO200015796-A2.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 785
ID AAF72393 standard; cDNA; 1857 BP.
DE Human PRO301 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 786
ID AAC87026 standard; cDNA; 1857 BP.
DE Nucleotide sequence of human polypeptide PRO301.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 787
ID AAS00159 standard; cDNA; 1857 BP.
DE Human cDNA clone DNA40628-1216 encoding PRO301 (UNQ264).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 788
ID AAS21426 standard; cDNA; 1857 BP.
DE Human cDNA sequence encoding for PRO301 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 789
ID AAC97460 standard; cDNA; 1857 BP.
DE Human angiogenesis-associated protein PRO301 cDNA, SEQ ID NO:118.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 790
ID ABL88098 standard; cDNA; 1857 BP.
DE Human PRO301 cDNA sequence SEQ ID NO:53.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 791
ID ABL95587 standard; cDNA; 1857 BP.
DE Human angiogenesis related cDNA PRO301 SEQ ID NO: 53.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
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PA (WARS/) MARSTERS S A.
 PA (PANU/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 792
 ID ACA60097 standard; cDNA; 1857 BP.
 DE Human cDNA for secreted/transmembrane protein PRO301.
 PN US200303530-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 793
 ID ACD07497 standard; cDNA; 1857 BP.
 DE Novel human secreted and transmembrane protein PRO301 cDNA.
 PN US2002197671-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 794
 ID ACA03785 standard; cDNA; 1857 BP.
 DE cDNA encoding human PRO polypeptide #183.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 795
 ID ABX71545 standard; cDNA; 1857 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO301.
 PN US2002132240-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 796
 ID ACA04985 standard; cDNA; 1857 BP.
 DE Novel human secreted and transmembrane protein PRO301 cDNA.
 PN US2003032063-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 797
 ID ACH06877 standard; cDNA; 1857 BP.
 DE Human secreted/transmembrane polypeptide PRO301 cDNA.
 PN US2003044839-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 798
 ID ABX89323 standard; cDNA; 1857 BP.
 DE DNA encoding novel secreted and transmembrane protein PRO301.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 799
 ID ACD41977 standard; cDNA; 1857 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #183.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 800
 ID ABX96114 standard; cDNA; 1857 BP.
 DE Human secreted/transmembrane protein cDNA, #23.
 PN US2002160374-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 801
 ID ACA05015 standard; cDNA; 1857 BP.
 DE Novel human secreted and transmembrane protein PRO301 cDNA.
 PN US2002177165-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 802
 ID ACA05435 standard; cDNA; 1857 BP.
 DE cDNA encoding human secreted protein PRO301.
 PN US2003023054-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 803
 ID ACA04505 standard; cDNA; 1857 BP.
 DE Novel human secreted and transmembrane protein PRO301 DNA.
 PN US2003032062-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 804
 ID ACD20102 standard; cDNA; 1857 BP.
 DE Human secreted / transmembrane polypeptide PRO301 cDNA.
 PN US2003036060-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 805
 ID ACA04206 standard; cDNA; 1857 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 365.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 806
 ID ACA54905 standard; cDNA; 1857 BP.
 DE Novel human secreted and transmembrane protein PRO301 cDNA.
 PN US2003017463-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

RESULT 807
 ID ACD07497 standard; cDNA; 1857 BP.
 DE Novel human secreted and transmembrane protein PRO301 cDNA.
 PN US2002197671-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Indels: 16
 Conservative: 46
 Mismatches: 126
 Indels: 16

ID ACA65646 standard; cDNA; 1857 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO301.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 808
ID ACD19740 standard; cDNA; 1857 BP.
DE Human secreted / transmembrane polypeptide PRO301 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 809
ID ADA45884 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 810
ID ADA76315 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 811
ID ADB29323 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 812
ID ADA1965 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 813
ID ADA61588 standard; cDNA; 1857 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 814
ID ADB19373 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 815
ID ADB27914 standard; cDNA; 1857 BP.

DE cDNA encoding human PRO polypeptide #183.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 816
ID ADA86393 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 817
ID ADB15957 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 818
ID ADA47743 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 819
ID ADA18179 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 820
ID ACD66887 standard; cDNA; 1857 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO301.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 821
ID ADA67538 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 822
ID ADB30545 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 823
ID ADA85841 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.

PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 824
ID ADA97053 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 825
ID ADA79357 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 826
ID ADA87496 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 827
ID ADB16698 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 828
ID ACD83048 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #21.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 829
ID ADA16154 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 830
ID ADA91790 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 831
ID ADB14853 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003087351-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 832
ID ADA47262 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane polypeptide PRO301 cDNA.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 833
ID ADB18814 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 834
ID ADA94029 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 835
ID ADB19925 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 836
ID ADB13237 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 837
ID ACD98606 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 838
ID ADA74491 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 839
ID ADA42299 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003054401-A1.
PD 20-MAR-2003.

Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 856
ID ADA96501 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 857
ID ADA81073 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 858
ID ADA95949 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 859
ID ADB26258 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 860
ID ADB21743 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 861
ID ADA77522 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 862
ID ADB18262 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 863
ID ADA86945 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126

Query Match: 25.2% Indels: 16
RESULT 864
ID ADA16578 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003039869-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 865
ID ADA13007 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 866
ID ADA1875 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 867
ID ADA88048 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 868
ID ADA6436 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 869
ID ADA17222 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 870
ID ADA42725 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 871
ID ADB28466 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 872
ID ADB18262 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126
Indels: 16
Query Match:
RESULT 873
ID ADA86945 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Mismatches: 126


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RESULT 872
ID ADB29018 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003082706-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 873
ID ADA76970 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003059909-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 874
ID ADA86600 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003073213-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 875
ID ADA97605 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082686-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 876
ID ADB27362 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003022239-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 877
ID ADB22295 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087344-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 878
ID ACD30262 standard; cDNA; 1857 BP.
DE Human cDNA encoding Pro302.
PN US2003044902-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 879
ID ACD23588 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #21.
PN US2003064923-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 880
ID ADA65986 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082698-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 881
ID ADB22847 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003077711-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 882
ID ADB23620 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide SEQ ID NO 365.
PN US2003077712-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 883
ID ADA92342 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082712-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 884
ID ADB15405 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003087352-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 885
ID ADB38657 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082766-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 886
ID ADB38105 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087347-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 887
ID ADB66577 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082689-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 888
ID ADB89657 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082698-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 889
ID ADB90389 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 890
ID ADB77644 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 891
ID ADB39490 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 892
ID ADB74780 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 893
ID ADB47113 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 894
ID ADB86720 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 895
ID ADB77325 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 896
ID ADB34482 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide SEQ ID NO 365.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 897
ID ADB35586 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide SEQ ID NO 365.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 898
ID ADB33930 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide SEQ ID NO 365.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 899
ID ADB35034 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide SEQ ID NO 365.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 900
ID ADB36138 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide SEQ ID NO 365.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 901
ID ADB46533 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003082592-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 902
ID ADC28426 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 903
ID ADC39626 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 904
ID ADC40140 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
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Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 905	
ID ADC18968 standard; cDNA; 1857 BP.	
DE Human secreted/transmembrane protein cDNA, #25.	
PN US2003036061-A1.	
PD 20-FEB-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 906	
ID ADC34264 standard; cDNA; 1857 BP.	
DE Human secreted/transmembrane protein cDNA, #25.	
PN US2003036094-A1.	
PD 20-FEB-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 907	
ID ADC29319 standard; cDNA; 1857 BP.	
DE Human secreted/transmembrane protein cDNA, #25.	
PN US2003049676-A1.	
PD 13-MAR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 908	
ID ADC28850 standard; cDNA; 1857 BP.	
DE Human secreted/transmembrane protein cDNA, #25.	
PN US2003049677-A1.	
PD 13-MAR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 909	
ID ADC40735 standard; cDNA; 1857 BP.	
DE Human secreted/transmembrane protein cDNA, #25.	
PN US2003054400-A1.	
PD 20-MAR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 910	
ID ADC19392 standard; cDNA; 1857 BP.	
DE Human secreted/transmembrane protein cDNA, #25.	
PN US2003054441-A1.	
PD 20-MAR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 911	
ID ADC38840 standard; cDNA; 1857 BP.	
DE Human secreted/transmembrane protein cDNA, #25.	
PN US2003073077-A1.	
PD 17-APR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 912	
ID ADC12910 standard; cDNA; 1857 BP.	
DE Human secreted/transmembrane protein cDNA, #25.	
PN US2003073079-A1.	
PD 17-APR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 913	
ID ADC50406 standard; cDNA; 1857 BP.	
DE Novel human secreted and transmembrane protein PRO301 cDNA.	
PN US2003092106-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 914	
ID ADC71953 standard; cDNA; 1857 BP.	
DE Novel human secreted and transmembrane protein PRO301 cDNA.	
PN US2003092107-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 915	
ID ADC59932 standard; cDNA; 1857 BP.	
DE Novel human secreted and transmembrane protein PRO301 cDNA.	
PN US2003092105-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 916	
ID ADC52939 standard; cDNA; 1857 BP.	
DE Novel human secreted and transmembrane protein cDNA Seq ID365.	
PN US2003087365-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 917	
ID ADC57293 standard; cDNA; 1857 BP.	
DE Novel human secreted and transmembrane protein cDNA Seq ID365.	
PN US2003087366-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 918	
ID ADC60484 standard; cDNA; 1857 BP.	
DE Novel human secreted and transmembrane protein PRO301 cDNA.	
PN US2003087367-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 919	
ID ADC50959 standard; cDNA; 1857 BP.	
DE Novel human secreted and transmembrane protein PRO301 cDNA.	
PN US2003087361-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 920	
ID ADC65486 standard; cDNA; 1857 BP.	
DE Human PRO Polynucleotide #183.	
PN US2003087362-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16
RESULT 921	
ID ADC12910 standard; cDNA; 1857 BP.	
DE Human secreted/transmembrane protein cDNA, #25.	
PN US2003073079-A1.	
PD 17-APR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 51.0%	Conservative: 46
Best Local Similarity: 35.2%	Mismatches: 126
Query Match: 25.2%	Indels: 16

Query Match: 25.2% Indels: 16
RESULT 921
ID ADC54584 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID365.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 922
ID ADC53545 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID365.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 923
ID ADC59068 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID365.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 924
ID ADC55946 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID365.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 925
ID ADC58516 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID365.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 926
ID ADC12362 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 927
ID ADD03190 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 928
ID ADC90182 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16

RESULT 929
ID ADC59601 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 930
ID ADC48490 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 931
ID ADD10019 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 932
ID ADD04594 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 933
ID ADC80550 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 934
ID ADD11057 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 935
ID ADD10342 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #27.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 936
ID ADC47938 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 937
ID ADC53545 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID365.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16

ID ADD04917 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 938
ID ADC79998 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 939
ID ADD11302 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #27.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 940
ID ADD09467 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 941
ID ADD03923 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 942
ID ADD03499 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 943
ID ADD41180 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 944
ID ADD52319 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 945
ID ADD53059 standard; cDNA; 1857 BP.

DE cDNA encoding human PRO polypeptide #183.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 946
ID ADD53611 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 947
ID ADD37095 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #27.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 948
ID ADD51767 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 949
ID ADD02566 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 950
ID ADD02000 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 951
ID ADD54182 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 952
ID ADD92499 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 953
ID ADD91395 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.


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PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 954
ID ADE04009 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 955
ID ADE32306 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 956
ID ADE22238 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 957
ID ADD79462 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 958
ID ADE41998 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 959
ID ADE17815 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 960
ID ADD91947 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 961
ID ADE33410 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003194767-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 962
ID ADE33962 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 963
ID ADD80014 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 964
ID ADD93051 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 965
ID ADE19471 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 966
ID ADE34751 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 967
ID ADE18919 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 968
ID ADE43115 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 969
ID ADD95904 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199059-A1.
PD 23-OCT-2003.
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PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 970
ID ADE22790 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 971
ID AD078908 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 972
ID ADE32858 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 973
ID ADE42550 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 974
ID ADD80566 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 975
ID ADD89594 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 976
ID ADE40978 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 977
ID ADE504677 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 978
ID ADE92806 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 979
ID ADG21515 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 980
ID ADG31156 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 981
ID ADP97491 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 982
ID ADG80555 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 983
ID ADG80003 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 984
ID ADG63771 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane polypeptide PRO301 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
RESULT 985
ID ADH59234 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0%
Conservative: 46
Mismatches: 126
Indels: 16

Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 986
ID ADH5295 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 987
ID ADH55847 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 988
ID ADH58013 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 989
ID ADI64066 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 990
ID ADI65015 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 991
ID ADI63514 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 992
ID ADH81928 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 993
ID ADH81376 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16

Query Match: 25.2% Indels: 16
RESULT 994
ID ACAS8993 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #21.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 995
ID ACD24035 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 996
ID ACAS8390 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #21.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 997
ID ACD42376 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 998
ID ACAS7176 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 999
ID ADJ26281 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1000
ID ADM82545 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1001
ID ADN15944 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16


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RESULT 1002
ID ADN16573 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1003
ID ADN15392 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1004
ID ADN14840 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1005
ID ADN14840 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1006
ID ADE79196 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1007
ID ADD76550 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1008
ID ADD87914 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1009
ID ADD86318 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1010
ID ADE89228 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1011
ID ADE75766 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1012
ID ADE73296 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1013
ID ADE41303 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #27.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1014
ID ADE23342 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1015
ID ADE23894 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1016
ID ADE24537 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1017
ID ADD87362 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16

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DE Human PRO polynucleotide #183.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1019
ID ADE41185 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane polypeptide PRO301 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1020
ID ADE41185 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane polypeptide PRO301 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1021
ID ADE18367 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1022
ID ADE88676 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1023
ID ADE99385 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1024
ID ADE94696 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1025
ID ADE91107 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1026
ID ADE95248 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003225253-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1027
ID ADE93358 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1028
ID ADE93358 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1029
ID ADE98504 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1030
ID ADE92254 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1031
ID ADE90555 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1032
ID ADE91702 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1033
ID ADE98931 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1034
ID ADG40401 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003225253-A1.
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PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1035
ID ADF73795 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cdna, #25.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1036
ID ADG02281 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1037
ID ADG22067 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cdna.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1038
ID ADG20137 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1039
ID ADF98043 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1040
ID ADG24260 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cdna.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1041
ID ADF98614 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16

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Query Match: 25.2%
Indels: 16
RESULT 1042
ID ADG03445 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1043
ID ADF99166 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1044
ID ADG16751 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1045
ID ADG05210 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1046
ID ADG19477 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1047
ID ADF73371 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cdna, #25.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1048
ID ADG13314 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1049
ID ADG08371 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cdna.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16

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RESULT 1050
ID ADG15541 standard; cDNA; 1857 BP.
DE cDNA encoding human PRO polypeptide #183.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1051
ID ADF96939 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1052
ID ADG06124 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1053
ID ADG23708 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1054
ID ADG03997 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1055
ID ADG24898 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1056
ID ADG07195 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1057
ID ADG07747 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1058
ID ADG58554 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1059
ID ADG55242 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1060
ID ADG62010 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1061
ID ADG92214 standard; cDNA; 1857 BP.
DE Human secreted/transmembrane protein cDNA, #25.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1062
ID ADG82211 standard; cDNA; 1857 BP.
DE Human PRO polynucleotide #183.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1063
ID ADG57450 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1064
ID ADG56898 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1065
ID ADG55794 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
RESULT 1066
ID ADG58554 standard; cDNA; 1857 BP.
DE Novel human secreted and transmembrane protein PRO301 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatches: 126
Indels: 16
```


PA (GETH) GENENTECH INC.	PA (MATH/) MATHER J P.
Percent Similarity: 51.0%	PA (WILL/) WILLIAMS P M.
Best Local Similarity: 35.2%	PA (WOOD/) WOOD W I.
Query Match: 25.2%	Percent Similarity: 51.0%
Conservative: 46	Best Local Similarity: 35.2%
Mismatches: 126	Query Match: 25.2%
Indels: 16	Conservative: 46
RESULT 1083	Mismatches: 126
ID ADG54690 standard; cDNA; 1857 BP.	Indels: 16
DE Novel human secreted and transmembrane protein PRO301 cDNA.	RESULT 1090
PN US2003207367-A1.	ID ADI81154 standard; cDNA; 1857 BP.
PD 06-NOV-2003.	DE cDNA encoding human PRO polypeptide #183.
PA (GETH) GENENTECH INC.	PN US2003207361-A1.
Percent Similarity: 51.0%	PD 06-NOV-2003.
Best Local Similarity: 35.2%	PA (GETH) GENENTECH INC.
Query Match: 25.2%	Percent Similarity: 51.0%
Conservative: 46	Best Local Similarity: 35.2%
Mismatches: 126	Query Match: 25.2%
Indels: 16	Conservative: 46
RESULT 1084	Mismatches: 126
ID ADG59730 standard; cDNA; 1857 BP.	Indels: 16
DE Novel human secreted and transmembrane protein PRO301 cDNA.	RESULT 1091
PN US2003207369-A1.	ID ADI18600 standard; cDNA; 1857 BP.
PD 06-NOV-2003.	DE Human secreted/transmembrane protein cDNA, #25.
PA (GETH) GENENTECH INC.	PN US2003152959-A1.
Percent Similarity: 51.0%	PD 14-AUG-2003.
Best Local Similarity: 35.2%	PA (GETH) GENENTECH INC.
Query Match: 25.2%	Percent Similarity: 51.0%
Conservative: 46	Best Local Similarity: 35.2%
Mismatches: 126	Query Match: 25.2%
Indels: 16	Conservative: 46
RESULT 1085	Mismatches: 126
ID ADH20430 standard; cDNA; 1857 BP.	Indels: 16
DE Human secreted/transmembrane protein cDNA, #25.	RESULT 1092
PN US2004005553-A1.	ID ADI85320 standard; cDNA; 1857 BP.
PD 08-JAN-2004.	DE Human secreted/transmembrane protein cDNA, #25.
PA (GETH) GENENTECH INC.	PN US2003148419-A1.
Percent Similarity: 51.0%	PD 07-AUG-2003.
Best Local Similarity: 35.2%	PA (GETH) GENENTECH INC.
Query Match: 25.2%	Percent Similarity: 51.0%
Conservative: 46	Best Local Similarity: 35.2%
Mismatches: 126	Query Match: 25.2%
Indels: 16	Conservative: 46
RESULT 1086	Mismatches: 126
ID ADH43486 standard; cDNA; 1857 BP.	Indels: 16
DE Human PRO polynucleotide #27.	RESULT 1093
PN US2003224984-A1.	ID ADI37583 standard; cDNA; 1857 BP.
PD 04-DEC-2003.	DE Human secreted/transmembrane protein cDNA, #25.
PA (GETH) GENENTECH INC.	PN US2003096340-A1.
Percent Similarity: 51.0%	PD 22-MAY-2003.
Best Local Similarity: 35.2%	PA (GETH) GENENTECH INC.
Query Match: 25.2%	Percent Similarity: 51.0%
Conservative: 46	Best Local Similarity: 35.2%
Mismatches: 126	Query Match: 25.2%
Indels: 16	Conservative: 46
RESULT 1087	Mismatches: 126
ID ADH07285 standard; cDNA; 1857 BP.	Indels: 16
DE Human secreted/transmembrane protein cDNA, #25.	RESULT 1094
PN US2004006211-A1.	ID ADG09897 standard; cDNA; 1857 BP.
PD 08-JAN-2004.	DE Novel human secreted and transmembrane protein PRO301 cDNA.
PA (DESN/) DESNOYERS L.	PN US2004009548-A1.
PA (GODD/) GODDARD A.	PD 15-JAN-2004.
PA (GODO/) GODOWSKI P J.	PA (GETH) GENENTECH INC.
PA (GURN/) GURNEY A L.	Percent Similarity: 51.0%
PA (MATH/) MATHER J P.	Best Local Similarity: 35.2%
PA (WILL/) WILLIAMS P M.	Query Match: 25.2%
PA (WOOD/) WOOD W I.	Conservative: 46
Percent Similarity: 51.0%	Mismatches: 126
Best Local Similarity: 35.2%	Indels: 16
Query Match: 25.2%	RESULT 1095
Conservative: 46	ID ADH97379 standard; cDNA; 1857 BP.
Mismatches: 126	DE Human secreted/transmembrane protein cDNA, #25.
Indels: 16	PN US2003190610-A1.
RESULT 1088	PD 09-OCT-2003.
ID ADH59830 standard; cDNA; 1857 BP.	PA (GETH) GENENTECH INC.
DE Human secreted/transmembrane protein cDNA, #25.	Percent Similarity: 51.0%
PN US2003215904-A1.	Best Local Similarity: 35.2%
PD 20-NOV-2003.	Query Match: 25.2%
PA (GETH) GENENTECH INC.	Conservative: 46
Percent Similarity: 51.0%	Mismatches: 126
Best Local Similarity: 35.2%	Indels: 16
Query Match: 25.2%	RESULT 1096
Conservative: 46	ID ADI15368 standard; cDNA; 1857 BP.
Mismatches: 126	DE Novel human secreted and transmembrane protein PRO301 cDNA.
Indels: 16	PN US2003207382-A1.
RESULT 1089	PD 06-NOV-2003.
ID ADH06858 standard; cDNA; 1857 BP.	PA (GETH) GENENTECH INC.
DE Human secreted/transmembrane protein cDNA, #25.	Percent Similarity: 51.0%
PN US2004005665-A1.	Best Local Similarity: 35.2%
PD 08-JAN-2004.	Query Match: 25.2%
PA (DESN/) DESNOYERS L.	Conservative: 46
PA (GODD/) GODDARD A.	Mismatches: 126
PA (GODO/) GODOWSKI P J.	Indels: 16
PA (GURN/) GURNEY A L.	RESULT 1097
	ID ADG09245 standard; cDNA; 1857 BP.
	DE Novel human secreted and transmembrane protein PRO301 cDNA.
	PN US2004009547-A1.

RESULT 1113
 ID ADM28315 standard; cDNA; 1857 BP.
 DE cDNA encoding human PRO polypeptide #183.
 PN US2004077064-A1.
 PD 22-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1114
 ID ADRI17914 standard; cDNA; 1857 BP.
 DE Human secreted/transmembrane protein cDNA, #25.
 PN US2004147017-A1.
 PD 29-JUL-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1115
 ID ADI95797 standard; cDNA; 1857 BP.
 DE cDNA encoding human PRO polypeptide #183.
 PN US2003077659-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1116
 ID ADI96349 standard; cDNA; 1857 BP.
 DE Human secreted and transmembrane protein PRO301 cDNA.
 PN US2003207354-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1117
 ID ADT94259 standard; cDNA; 1857 BP.
 DE Human PRO301 cDNA sequence.
 PN AU2003259607-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1118
 ID ADS74553 standard; cDNA; 1857 BP.
 DE Human secreted/transmembrane cDNA #25.
 PN US2004185531-A1.
 PD 23-SEP-2004.

PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1119
 ID ADS32301 standard; cDNA; 1857 BP.
 DE Novel human secreted and transmembrane protein PRO301 cDNA.
 PN US2004203125-A1.
 PD 14-OCT-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1120
 ID ADT03285 standard; cDNA; 1857 BP.
 DE Human PRO polynucleotide #183.
 PN US2004214269-A1.
 PD 28-OCT-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1121
 ID ADT03590 standard; cDNA; 1857 BP.
 DE Human secreted/transmembrane protein cDNA, #25.
 PN US2003152922-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1122
 ID ADZ03336 standard; cDNA; 1857 BP.
 DE Human secreted/transmembrane PRO301 cDNA.
 PN US2005074837-A1.
 PD 07-APR-2005.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1123
 ID AEA37828 standard; cDNA; 1857 BP.
 DE Human secreted/transmembrane protein cDNA, #25.
 PN US200512725-A1.
 PD 26-MAY-2005.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 51.0%
 Best Local Similarity: 35.2%
 Query Match: 25.2%
 Conservative: 46
 Mismatches: 126
 Indels: 16
 RESULT 1124
 ID ADS74553 standard; cDNA; 1857 BP.
 DE Human secreted/transmembrane cDNA #25.
 PN US2004185531-A1.
 PD 23-SEP-2004.


```
ID ABE14082 standard; cDNA; 1857 BP.
DE Cancer cell diagnosis method-related human cDNA sequence - SEQ ID 365.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1125
ID AED23862 standard; cDNA; 1857 BP.
DE Human secreted protein PRO 301 encoding gene, SEQ ID 118.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1126
ID AED86280 standard; cDNA; 1857 BP.
DE Human PRO cDNA, seq id 365.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1127
ID ABE69031 standard; cDNA; 1857 BP.
DE Cancer associated antigen homologous PRO301 encoding gene, SEQ ID 118.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH ) GENENTECH INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1128
ID AAS22709 standard; cDNA; 1902 BP.
DE Human cDNA encoding a novel human protein #275.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1129
ID AAS22710 standard; cDNA; 1902 BP.
DE Human cDNA encoding a novel human protein #276.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1130
ID ADE08095 standard; DNA; 1902 BP.
DE Novel DNA-related contig nucleotide sequence #139.
PN WO2003054152-A2.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1131
ID ADU40509 standard; cDNA; 1902 BP.
DE Novel human polynucleotide seq id 294.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1132
ID ABE23842 standard; DNA; 1902 BP.
DE Novel human protein coding sequence (contig) - SEQ ID 511.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1133
ID AEE23843 standard; DNA; 1902 BP.
DE Novel human protein coding sequence (contig) - SEQ ID 512.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1134
ID AAD08305 standard; cDNA; 1915 BP.
DE Human secreted protein-encoding gene 23 cDNA clone HACAA29, SEQ ID NO:33.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1135
ID AAD08335 standard; cDNA; 1918 BP.
DE Human secreted protein-encoding gene 23 cDNA clone HACAA29, SEQ ID NO:63.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1136
ID ADE07127 standard; DNA; 1943 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #193.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
RESULT 1137
ID ADU40284 standard; cDNA; 1943 BP.
DE Novel human polynucleotide seq id 69.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 51.0%
Best Local Similarity: 35.2%
Query Match: 25.2%
Conservative: 46
Mismatch: 126
Indels: 16
```


Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1138
ID ADR46572 standard; DNA; 2009 BP.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4, encoding gene.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1139
ID ADL26799 standard; cDNA; 2100 BP.
DE Human JAM1 encoding cDNA SEQ ID NO:53.
PN WO2004022778-A1.
PD 18-MAR-2004.
PA (GARV-) GARVAN INST MEDICAL RES.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1140
ID AAK94509 standard; cDNA; 2141 BP.
DE Human full-length cDNA, SEQ ID NO: 3364.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1141
ID ADL31331 standard; cDNA; 2141 BP.
DE Full length human cDNA clone SeqID 3364.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1142
ID ADQ68025 standard; cDNA; 2141 BP.
DE Recombinant vector preparation human clone cDNA, PLACE1005544.
PN JP2004215665-A.
PD 05-AUG-2004.
PA (ZOIJ-) ZOIJIN KK.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1143
ID ADN05139 standard; cDNA; 2187 BP.
DE Antipeptidic cDNA sequence #785.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1144
ID AAS22473 standard; cDNA; 2259 BP.
DE Human cDNA encoding a novel human protein #39.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1145
ID AEE23370 standard; DNA; 2259 BP.
DE Novel human protein coding sequence - SEQ ID 39.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Percent Similarity: 51.0% Conservative: 46

Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1146
ID ABV28103 standard; cDNA; 3389 BP.
DE Human prostate expression marker cDNA 28094.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1147
ID ABV22266 standard; cDNA; 3389 BP.
DE Human prostate expression marker cDNA 22257.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1148
ID ADR46570 standard; DNA; 3660 BP.
DE Human JAM-1, F11 receptor (F11R) transcript variant 1, encoding gene.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1149
ID ADM7859 standard; DNA; 3738 BP.
DE Human junctional adhesion molecule-1 (JAM-1) cDNA.
PN US2005025776-A1.
PD 03-FEB-2005.
PA (WEBE/) WEBER C.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1150
ID ADR46578 standard; DNA; 3794 BP.
DE Human JAM-1, F11 receptor (F11R) transcript variant 5, encoding gene.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1151
ID ADU05993 standard; DNA; 3794 BP.
DE Novel bronchial cancer-associated human gene SeqID215.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1152
ID ADU05868 standard; DNA; 3794 BP.
DE Novel bronchial cancer-associated human gene SeqID90.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1153
ID ADR46576 standard; DNA; 3861 BP.
DE Human F11 receptor (F11R) transcript variant 4, encoding gene, SEQ ID 7.
PN JP2004242513-A.

PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSBI HOJIN KAGAKU GIJUTSU SH.
Percent Similarity: 51.0% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 126
Query Match: 25.2% Indels: 16
RESULT 1154
ID AAX37716 standard; DNA; 2066 BP.
DE Human cDNA clone DNA35936 consensus sequence.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 54.4% Conservative: 41
Best Local Similarity: 38.0% Mismatches: 104
Query Match: 25.0% Indels: 11
RESULT 1155
ID ADJ67404 standard; DNA; 4633 BP.
DE Human ovarian specific gene SEQ ID NO:118.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 51.8% Conservative: 44
Best Local Similarity: 35.7% Mismatches: 119
Query Match: 24.6% Indels: 12
RESULT 1156
ID AAV28137 standard; cDNA to mRNA; 1374 BP.
DE Mouse junctional adhesion molecule gene.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Percent Similarity: 52.8% Conservative: 52
Best Local Similarity: 34.8% Mismatches: 125
Query Match: 24.5% Indels: 12
RESULT 1157
ID AUR46580 standard; DNA; 2453 BP.
DE Mouse junctional adhesion molecule-1 encoding gene, SEQ ID 11.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSBI HOJIN KAGAKU GIJUTSU SH.
Percent Similarity: 52.8% Conservative: 52
Best Local Similarity: 34.8% Mismatches: 125
Query Match: 24.5% Indels: 12
RESULT 1158
ID AAX37666 standard; cDNA; 228 BP.
DE Human PRO protein derived EST DNA sequence 2715631.
PN WO9914241-A2.
PD 23-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 24.1% Indels: 0
RESULT 1159
ID ADB53509 standard; DNA; 1895 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4051.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 50.7% Conservative: 51
Best Local Similarity: 33.1% Mismatches: 125
Query Match: 23.8% Indels: 18
RESULT 1160
ID AAX37667 standard; cDNA; 241 BP.
DE Human PRO protein derived EST DNA sequence 1622388.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 96.1% Conservative: 0
Best Local Similarity: 96.1% Mismatches: 3
Query Match: 23.7% Indels: 0
RESULT 1161
ID ADQ95891 standard; cDNA; 1116 BP.
DE T cell activation associated cDNA #35.
PN WO2004058805-A2.
PD 15-JUL-2004.

PA (ASAH-) ASahi KASEI PHARMA CORP.
Percent Similarity: 54.5% Conservative: 38
Best Local Similarity: 37.3% Mismatches: 93
Query Match: 23.2% Indels: 7
RESULT 1162
ID ADR46574 standard; DNA; 3527 BP.
DE Human JAM-1, Fil receptor (F1IR) transcript variant 3, encoding gene.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSBI HOJIN KAGAKU GIJUTSU SH.
Percent Similarity: 54.5% Conservative: 38
Best Local Similarity: 37.3% Mismatches: 93
Query Match: 23.2% Indels: 7
RESULT 1163
ID AAK92353 standard; cDNA; 824 BP.
DE Human cDNA 5'-end sequence, SEQ ID NO: 813.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 53.7% Conservative: 47
Best Local Similarity: 35.3% Mismatches: 96
Query Match: 23.1% Indels: 22
RESULT 1164
ID AAK93247 standard; cDNA; 824 BP.
DE Human cDNA clone representative sequence, SEQ ID NO: 1707.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 53.7% Conservative: 47
Best Local Similarity: 35.3% Mismatches: 96
Query Match: 23.1% Indels: 22
RESULT 1165
ID ADL28780 standard; cDNA; 824 BP.
DE 5' end of a human cDNA molecule SeqID 813.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 53.7% Conservative: 47
Best Local Similarity: 35.3% Mismatches: 96
Query Match: 23.1% Indels: 22
RESULT 1166
ID ADL29674 standard; cDNA; 824 BP.
DE 5' end of a representative human cDNA cluster SeqID 1707.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 53.7% Conservative: 47
Best Local Similarity: 35.3% Mismatches: 96
Query Match: 23.1% Indels: 22
RESULT 1167
ID AAS22474 standard; cDNA; 777 BP.
DE Human cDNA encoding a novel human protein #40.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 54.1% Conservative: 38
Best Local Similarity: 36.8% Mismatches: 94
Query Match: 22.8% Indels: 7
RESULT 1168
ID AEE23371 standard; DNA; 777 BP.
DE Novel human protein coding sequence - SEQ ID 40.
PN US2005266423-A1.
PD 01-DEC-2005.
PA (NUVE-) NUVELO INC.
Percent Similarity: 54.1% Conservative: 38
Best Local Similarity: 36.8% Mismatches: 94
Query Match: 22.8% Indels: 7
RESULT 1169
ID ADF12430 standard; cDNA; 714 BP.
DE Human adhesion molecule JAM-2 coding sequence.
PN WO2003087128-A2.
PD 23-OCT-2003.
PA (RMFD-) RMP DICTAGENE SA.

PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 53.5%
Best Local Similarity: 34.7%
Query Match: 22.8%
Conservative: 46
Mismatches: 93
Indels: 21
RESULT 1170
ID ADG39448 standard; cDNA; 714 BP.
DE Human JAM-2 encoding cDNA SEQ ID NO:17.
PN WO2003104400-A2.
PD 18-DEC-2003.
PA (RMFD-) RMF DICTAGENE SA.
PA (UYPE-) UNIV PENNSYLVANIA.
Percent Similarity: 53.5%
Best Local Similarity: 34.7%
Query Match: 22.8%
Conservative: 46
Mismatches: 93
Indels: 21
RESULT 1171
ID ADP56688 standard; cDNA; 798 BP.
DE Human junction adhesion molecule 3 splice variant 2 (huJAM3sv2) cDNA.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 53.5%
Best Local Similarity: 34.7%
Query Match: 22.8%
Conservative: 46
Mismatches: 93
Indels: 21
RESULT 1172
ID ADU06871 standard; cDNA; 1787 BP.
DE Cell adhesion and extracellular matrix protein cDNA clone 7518734CB1.
PN WO2004094623-A2.
PD 04-NOV-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 53.5%
Best Local Similarity: 34.7%
Query Match: 22.8%
Conservative: 46
Mismatches: 93
Indels: 21
RESULT 1173
ID ADP69028 standard; cDNA; 637 BP.
DE Human NOV2c encoding cDNA SEQ ID NO:23.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 59.5%
Best Local Similarity: 36.4%
Query Match: 22.4%
Conservative: 45
Mismatches: 75
Indels: 4
RESULT 1174
ID AAS86526 standard; cDNA; 208 BP.
DE DNA encoding novel human diagnostic protein #22330.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 22.2%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 1175
ID ADP69030 standard; cDNA; 618 BP.
DE Human NOV2d encoding cDNA SEQ ID NO:25.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 59.1%
Best Local Similarity: 36.8%
Query Match: 22.2%
Conservative: 43
Mismatches: 75
Indels: 4
RESULT 1176
ID ADP69097 standard; cDNA; 618 BP.
DE Human NOV2a mature extracellular domain encoding cDNA SEQ ID NO:67.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 59.1%
Best Local Similarity: 36.8%
Query Match: 22.2%
Conservative: 43
Mismatches: 75
Indels: 4
RESULT 1177
ID AAV28136 standard; cDNA to mRNA; 924 BP.
DE Human junctional adhesion molecule gene.
PN WO9824897-A1.
PD 11-JUN-1998.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Percent Similarity: 49.0%
Best Local Similarity: 33.4%
Query Match: 22.0%
Conservative: 47
Mismatches: 126
Indels: 28
RESULT 1178
ID ADQ63487 standard; cDNA; 3363 BP.
DE Novel human cDNA sequence #648.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 44.1%
Best Local Similarity: 30.1%
Query Match: 21.4%
Conservative: 39
Mismatches: 86
Indels: 70
RESULT 1179
ID AEC02080 standard; mRNA; 3363 BP.
DE Nucleotide sequence of junction adhesion molecule 3.
PN WO2005075636-A1.
PD 18-AUG-2005.
PA (UYOU) UNIV QUEENSLAND.
PA (MONU) UNIV MONASH.
Percent Similarity: 44.1%
Best Local Similarity: 30.1%
Query Match: 21.4%
Conservative: 39
Mismatches: 86
Indels: 70
RESULT 1180
ID AAK93330 standard; cDNA; 790 BP.
DE Human cDNA clone representative sequence, SEQ ID NO: 1790.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 50.6%
Best Local Similarity: 36.4%
Query Match: 21.2%
Conservative: 35
Mismatches: 106
Indels: 16
RESULT 1181
ID ADL29757 standard; cDNA; 790 BP.
DE 5' end of a representative human cDNA cluster SeqID 1790.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 50.6%
Best Local Similarity: 36.4%
Query Match: 21.2%
Conservative: 35
Mismatches: 106
Indels: 16
RESULT 1182
ID AAS86588 standard; cDNA; 1088 BP.
DE DNA encoding novel human diagnostic protein #22392.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 51.7%
Best Local Similarity: 33.0%
Query Match: 21.0%
Conservative: 50
Mismatches: 94
Indels: 36
RESULT 1183
ID AAX21838 standard; cDNA; 1009 BP.
DE F11 antigen coding sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Percent Similarity: 51.3%
Best Local Similarity: 38.4%
Query Match: 20.8%
Conservative: 29
Mismatches: 97
Indels: 12
RESULT 1184
ID ACH29690 standard; cDNA; 433 BP.
DE Human testis cDNA #76.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 98.5%
Best Local Similarity: 98.5%
Query Match: 20.2%
Conservative: 0
Mismatches: 1
Indels: 0
RESULT 1185

ID ADP56687 standard; cDNA; 690 BP.
DE Human junction adhesion molecule 3 splice variant 1 (huJAM3sv1) cDNA.
PN W02004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 52.1% Conservative: 44
Best Local Similarity: 33.6% Mismatches: 86
Query Match: 19.5% Indels: 28
RESULT 1186
ID AAX81767 standard; DNA; 726 BP.
DE Nucleotide sequence used to isolate DNA40628.
PN W09927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 25
Best Local Similarity: 41.5% Mismatches: 73
Query Match: 19.5% Indels: 6
RESULT 1187
ID ABX93346 standard; cDNA; 726 BP.
DE Consensus sequence expressed sequence tag, EST, consen01.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 25
Best Local Similarity: 41.5% Mismatches: 73
Query Match: 19.5% Indels: 6
RESULT 1188
ID ADH62531 standard; DNA; 726 BP.
DE Human consen01 DNA used to isolate DNA40628 encoding PRO301 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Percent Similarity: 55.7% Conservative: 25
Best Local Similarity: 41.5% Mismatches: 73
Query Match: 19.5% Indels: 6
RESULT 1189
ID ADN35287 standard; DNA; 726 BP.
DE Human PRO301 DNA fragment consen01.
PN W02004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 55.7% Conservative: 25
Best Local Similarity: 41.5% Mismatches: 73
Query Match: 19.5% Indels: 6
RESULT 1190
ID AAS68832 standard; cDNA; 1539 BP.
DE DNA encoding novel human diagnostic protein #4636.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 47.3% Conservative: 54
Best Local Similarity: 29.3% Mismatches: 116
Query Match: 19.1% Indels: 43
RESULT 1191
ID AAS76296 standard; cDNA; 2509 BP.
DE DNA encoding novel human diagnostic protein #12100.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 47.3% Conservative: 54
Best Local Similarity: 29.3% Mismatches: 116
Query Match: 19.1% Indels: 43
RESULT 1192
ID AAX81766 standard; DNA; 390 BP.
DE Nucleotide sequence of DNA35936 encoding a A33 related antigen.
PN W09927098-A2.
PD 03-JUN-1999.

PA (GETH) GENENTECH INC.
Percent Similarity: 61.6% Conservative: 15
Best Local Similarity: 49.6% Mismatches: 46
Query Match: 18.4% Indels: 2
RESULT 1193
ID AAX37715 standard; DNA; 390 BP.
DE Human cDNA clone DNA35936.
PN W09914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 61.6% Conservative: 15
Best Local Similarity: 49.6% Mismatches: 46
Query Match: 18.4% Indels: 2
RESULT 1194
ID ABX93345 standard; cDNA; 390 BP.
DE Consensus assembly expressed sequence tag, EST, DNA35936.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 61.6% Conservative: 15
Best Local Similarity: 49.6% Mismatches: 46
Query Match: 18.4% Indels: 2
RESULT 1195
ID ADH62530 standard; DNA; 390 BP.
DE Human DNA35936 used to isolate DNA40628 encoding PRO301 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Percent Similarity: 61.6% Conservative: 15
Best Local Similarity: 49.6% Mismatches: 46
Query Match: 18.4% Indels: 2
RESULT 1196
ID ADN35286 standard; DNA; 390 BP.
DE Human PRO301 DNA fragment DNA35936.
PN W02004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 61.6% Conservative: 15
Best Local Similarity: 49.6% Mismatches: 46
Query Match: 18.4% Indels: 2
RESULT 1197
ID AAK91826 standard; cDNA; 748 BP.
DE Human cDNA 5'-end sequence, SEQ ID NO: 286.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 51.7% Conservative: 44
Best Local Similarity: 33.3% Mismatches: 93
Query Match: 18.0% Indels: 24
RESULT 1198
ID AAK93226 standard; cDNA; 748 BP.
DE Human cDNA clone representative sequence, SEQ ID NO: 1686.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 51.7% Conservative: 44
Best Local Similarity: 33.3% Mismatches: 93
Query Match: 18.0% Indels: 24
RESULT 1199
ID ADL28253 standard; cDNA; 748 BP.
DE 5' end of a human cDNA molecule SeqID 286.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 51.7% Conservative: 44
Best Local Similarity: 33.3% Mismatches: 93
Query Match: 18.0% Indels: 24

RESULT 1200
ID ADL29653 standard; cDNA; 748 BP.
DE 5' end of a representative human cDNA cluster SeqID 1686.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 51.7%
Best Local Similarity: 33.3%
Query Match: 18.0%
Conservative: 44
Mismatches: 93
Indels: 24
RESULT 1201
ID ACH03847 standard; cDNA; 604 BP.
DE Human cDNA differentially expressed in lung cancer #52.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE-) LASEK A W.
Percent Similarity: 75.3%
Best Local Similarity: 71.9%
Query Match: 17.9%
Conservative: 3
Mismatches: 16
Indels: 7
RESULT 1202
ID AAV88991 standard; cDNA; 612 BP.
DE EST clone l0638.
PN WO9845437-A2.
PD 15-OCT-1998.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 49.5%
Best Local Similarity: 35.1%
Query Match: 16.9%
Conservative: 29
Mismatches: 91
Indels: 11
RESULT 1203
ID AAS86527 standard; cDNA; 581 BP.
DE DNA encoding novel human diagnostic protein #22331.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 58.9%
Best Local Similarity: 54.8%
Query Match: 16.8%
Conservative: 5
Mismatches: 14
Indels: 37
RESULT 1204
ID ACA10115 standard; cDNA; 750 BP.
DE Human NOVX polynucleotide #5.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 53.0%
Best Local Similarity: 37.3%
Query Match: 16.7%
Conservative: 26
Mismatches: 58
Indels: 21
RESULT 1205
ID ADO8262 standard; cDNA; 750 BP.
DE Human NOVX polynucleotide #5.
PN US2004018594-A1.
PD 23-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOGF F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAE/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALV/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.

PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERR/) ZERHUSEN B D.
Percent Similarity: 53.0%
Best Local Similarity: 37.3%
Query Match: 16.7%
Conservative: 26
Mismatches: 58
Indels: 21
RESULT 1206
ID AAK54268 standard; cDNA; 218 BP.
DE Murine transport and binding associated protein encoding cDNA SEQ ID 833.
PN DE20103510-U1.
PD 07-JUN-2001.
PA (LION-) LION BIOSCIENCE AG.
Percent Similarity: 85.1%
Best Local Similarity: 81.1%
Query Match: 15.8%
Conservative: 3
Mismatches: 7
Indels: 4
RESULT 1207
ID ADA10946 standard; cDNA; 1556 BP.
DE Human cDNA differentially expressed in colon cancer #43.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Percent Similarity: 45.6%
Best Local Similarity: 29.0%
Query Match: 14.8%
Conservative: 42
Mismatches: 95
Indels: 42
RESULT 1208
ID ADE28280 standard; DNA; 1625 BP.
DE Human MDDT DNA - SEQ ID 130.
PN WO2003046152-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 45.6%
Best Local Similarity: 29.0%
Query Match: 14.8%
Conservative: 42
Mismatches: 95
Indels: 42
RESULT 1209
ID AAT62369 standard; cDNA; 2565 BP.
DE Human A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Percent Similarity: 45.6%
Best Local Similarity: 29.0%
Query Match: 14.8%
Conservative: 42
Mismatches: 95
Indels: 42
RESULT 1210
ID ABQ93360 standard; cDNA; 2760 BP.
DE Human cDNA SEQ ID NO 73.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.6%
Best Local Similarity: 29.0%
Query Match: 14.8%
Conservative: 42
Mismatches: 95
Indels: 42
RESULT 1211
ID AAF44988 standard; cDNA; 2793 BP.
DE Human A33 coding sequence SEQ ID NO: 68.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 45.6%
Best Local Similarity: 29.0%
Query Match: 14.8%
Conservative: 42
Mismatches: 95
Indels: 42
RESULT 1212
ID AAH57436 standard; cDNA; 2793 BP.
DE Human intestine cell specific cDNA sequence SEQ ID NO:276.
PN WO200132927-A2.
PD 10-MAY-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 45.6%
Best Local Similarity: 29.0%
Query Match: 14.8%
Conservative: 42
Mismatches: 95
Indels: 42

Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1213			
ID ABL62454 standard; DNA; 2793 BP.			
DE Colon adenocarcinoma related gene sequence SEQ ID NO:791.			
PN WO200194629-A2.			
PD 13-DEC-2001.			
PA (AVAL-) AVALON PHARM.			
Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1214			
ID ABL84445 standard; cDNA; 2793 BP.			
DE Human cDNA differentially expressed in granulocytic cells #1016.			
PN WO200228999-A2.			
PD 11-APR-2002.			
PA (GENE-) GENE LOGIC INC.			
Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1215			
ID ABL96940 standard; DNA; 2793 BP.			
DE Gene #3438 used to diagnose liver cancer.			
PN WO200229103-A2.			
PD 11-APR-2002.			
PA (GENE-) GENE LOGIC INC.			
Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1216			
ID ABL39629 standard; cDNA; 2793 BP.			
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:CI.			
PN WO2003042661-A2.			
PD 22-MAY-2003.			
PA (BOSB-) EOS BIOTECHNOLOGY INC.			
Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1217			
ID ABL54586 standard; cDNA; 2793 BP.			
DE Human PRO cDNA sequence SEQ ID NO:562.			
PN WO2004039956-A2.			
PD 13-MAY-2004.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1218			
ID ABL52877 standard; DNA; 2793 BP.			
DE Drug therapy altered expressed gene #228.			
PN WO2004072265-A2.			
PD 26-AUG-2004.			
PA (AMHP) WYETH.			
PA (BURC/) BURCZYNSKI M.			
PA (TWIN/) TWINE N. J.			
PA (DORN/) DORNER A. J.			
PA (TREP/) TREPICCHIO W. L.			
Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1219			
ID ABL44420 standard; DNA; 2793 BP.			
DE Human colorectal cancer associated gene sequence SEQ ID NO:40.			
PN US2005048526-A1.			
PD 03-MAR-2005.			
PA (WANG/) WANG Y.			
Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1220			
ID ABL39331 standard; DNA; 2793 BP.			
DE Human colorectal cancer-related gene sequence - SEQ ID NO:40.			
PN US2005048494-A1.			
PD 03-MAR-2005.			
PA (WANG/) WANG Y.			
Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1221			
ID ABL62384 standard; cDNA; 2803 BP.			
DE Human A33 antigen (from clone 18).			
PN WO9708189-A1.			
PD 06-MAR-1997.			
PA (LUDW-) LUDWIG INST CANCER RES.			
Percent Similarity:	45.6%	Conservative:	42
Best Local Similarity:	29.0%	Mismatches:	95
Query Match:	14.8%	Indels:	42
RESULT 1222			
ID ABL56524 standard; DNA; 435 BP.			
DE Human T87045 DNA fragment.			
PN WO9914241-A2.			
PD 25-MAR-1999.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	61.6%	Conservative:	13
Best Local Similarity:	48.5%	Mismatches:	38
Query Match:	14.7%	Indels:	0
RESULT 1223			
ID ABL37719 standard; DNA; 293 BP.			
DE Human clone T87045 DNA.			
PN WO9914241-A2.			
PD 25-MAR-1999.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	62.5%	Conservative:	13
Best Local Similarity:	49.0%	Mismatches:	36
Query Match:	14.4%	Indels:	0
RESULT 1224			
ID ABL65580 standard; DNA; 427 BP.			
DE Lung cancer related gene sequence SEQ ID NO:3917.			
PN WO200194629-A2.			
PD 13-DEC-2001.			
PA (AVAL-) AVALON PHARM.			
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	14.4%	Indels:	0
RESULT 122			

Percent Similarity: 41.5% Conservative: 37
Best Local Similarity: 26.9% Mismatches: 108
Query Match: 13.6% Indels: 40
RESULT 1229
ID ADH97307 standard; cDNA; 1393 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 40.2% Conservative: 48
Best Local Similarity: 26.3% Mismatches: 130
Query Match: 13.4% Indels: 77
RESULT 1230
ID ADO43534 standard; DNA; 1045 BP.
DE Nucleotide sequence of an additional human A34 clone.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Percent Similarity: 43.9% Conservative: 49
Best Local Similarity: 25.8% Mismatches: 89
Query Match: 13.2% Indels: 63
RESULT 1231
ID ADO43532 standard; DNA; 1910 BP.
DE Nucleotide sequence of a human A34 protein.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Percent Similarity: 43.9% Conservative: 49
Best Local Similarity: 25.8% Mismatches: 89
Query Match: 13.2% Indels: 63
RESULT 1232
ID AAX77525 standard; cDNA; 2166 BP.
DE Human secreted protein Auz26_3 cDNA.
PN WO9926972-A1.
PD 03-JUN-1999.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 43.9% Conservative: 49
Best Local Similarity: 25.8% Mismatches: 89
Query Match: 13.2% Indels: 63
RESULT 1233
ID AAZ59467 standard; cDNA; 2166 BP.
DE Human secreted protein Auz26_3 polynucleotide sequence.
PN WO960020-A1.
PD 25-NOV-1999.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 43.9% Conservative: 49
Best Local Similarity: 25.8% Mismatches: 89
Query Match: 13.2% Indels: 63
RESULT 1234
ID ADC38774 standard; cDNA; 2166 BP.
DE Human cDNA encoding a secreted protein #62.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 43.9% Conservative: 49
Best Local Similarity: 25.8% Mismatches: 89
Query Match: 13.2% Indels: 63
RESULT 1235
ID ADP55947 standard; cDNA; 2166 BP.
DE Human PRO cDNA sequence SEQ ID NO:1923.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.9% Conservative: 49
Best Local Similarity: 25.8% Mismatches: 89
Query Match: 13.2% Indels: 63
RESULT 1236
ID ADO43578 standard; DNA; 3017 BP.
DE Nucleotide sequence of a human A34 protein.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Percent Similarity: 43.9% Conservative: 49

Best Local Similarity: 25.8% Mismatches: 89
Query Match: 13.2% Indels: 63
RESULT 1237
ID ADC42864 standard; DNA; 1748 BP.
DE REMAP encoding sequence #1.
PN WO2003027228-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 42.2% Conservative: 49
Best Local Similarity: 24.5% Mismatches: 98
Query Match: 13.1% Indels: 62
RESULT 1238
ID AAH02949 standard; DNA; 1827 BP.
DE Human ehear stress-response coding sequence SEQ ID NO: 143.
PN WO200125427-A1.
PD 12-APR-2001.
PA (KYOY) KYOWA HAKKO KOGYO KK.
Percent Similarity: 40.6% Conservative: 49
Best Local Similarity: 26.3% Mismatches: 124
Query Match: 13.1% Indels: 79
RESULT 1239
ID AEA54216 standard; DNA; 1333 BP.
DE Viral receptor protein (ACVRP) nucleotide sequence #2.
PN US2005142538-A1.
PD 30-JUN-2005.
PA (INCY-) INCYTE CORP.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1240
ID AAX87000 standard; cDNA; 1387 BP.
DE Human viral receptor protein (ACVRP) nucleotide sequence.
PN US5942606-A.
PD 24-AUG-1999.
PA (INCY-) INCYTE PHARM INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1241
ID AAX28436 standard; DNA; 1813 BP.
DE EGF-like homologue PRO246 coding sequence.
PN WO9914327-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1242
ID AAX52221 standard; DNA; 1813 BP.
DE Protein PRO246 cDNA clone DNA35639-1172.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1243
ID AAA30052 standard; cDNA; 1813 BP.
DE Human PRO246 nucleotide sequence.
PN WO20015666-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1244
ID AAF72379 standard; cDNA; 1813 BP.
DE Human PRO246 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43

Best Local Similarity: 27.9% Mismatches: 105
 Query Match: 13.1% Indels: 54
 RESULT 1245
 ID AAC87040 standard; cDNA; 1813 BP.
 DE Novel human secreted and transmembrane protein PRO246.
 PN US2003032063-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1246
 ID AAS21412 standard; cDNA; 1813 BP.
 DE Human cDNA sequence encoding for PRO246 polypeptide.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1247
 ID RAC97441 standard; cDNA; 1813 BP.
 DE Human angiogenesis-associated protein PRO246 cDNA, SEQ ID NO:95.
 PN WO200053753-A2.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1248
 ID AAF60372 standard; cDNA; 1813 BP.
 DE PRO246 coding sequence.
 PN WO200105836-A1.
 PD 25-JAN-2001.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1249
 ID ACA60030 standard; cDNA; 1813 BP.
 DE Human cDNA for secreted/transmembrane protein PRO246.
 PN US200303530-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1250
 ID ACD07430 standard; cDNA; 1813 BP.
 DE Novel human secreted and transmembrane protein PRO246 cDNA.
 PN US2002197671-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1251
 ID ACA03771 standard; cDNA; 1813 BP.
 DE cDNA encoding human PRO polypeptide #169.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1252
 ID ASX71478 standard; cDNA; 1813 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO246.
 PN US2002132240-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%

Query Match: 13.1% Indels: 54
 RESULT 1253
 ID ACA04999 standard; cDNA; 1813 BP.
 DE Novel human secreted and transmembrane protein PRO246 cDNA.
 PN US2003032063-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1254
 ID ACH06810 standard; cDNA; 1813 BP.
 DE Human secreted/transmembrane polypeptide PRO246 cDNA.
 PN US2003044839-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1255
 ID ABX89309 standard; cDNA; 1813 BP.
 DE DNA encoding novel secreted and transmembrane protein PRO246.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1256
 ID ACD41963 standard; cDNA; 1813 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #169.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1257
 ID ABX96047 standard; cDNA; 1813 BP.
 DE Human secreted/transmembrane protein cDNA, #9.
 PN US2002160374-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1258
 ID ACA60529 standard; cDNA; 1813 BP.
 DE Novel human secreted and transmembrane protein PRO246 cDNA.
 PN US2002177165-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1259
 ID ACA05368 standard; cDNA; 1813 BP.
 DE cDNA encoding human secreted protein PRO246.
 PN US2003023054-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%
 RESULT 1260
 ID ACA04519 standard; cDNA; 1813 BP.
 DE Novel human secreted and transmembrane protein PRO246 DNA.
 PN US2003032062-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 43.2%
 Best Local Similarity: 27.9% Mismatches: 105
 Indels: 54
 Query Match: 13.1%

DE Human cDNA encoding secreted/transmembrane protein PRO246.
FN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1278
ID ADA67510 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
FN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1279
ID ADB30517 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
FN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1280
ID ADA85813 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
FN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1281
ID ADA97025 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
FN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1282
ID ADA79329 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
FN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1283
ID ADA7468 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
FN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1284
ID ADB16670 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
FN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1285
ID ACD82981 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #8.

FN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1286
ID ADA16074 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
FN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1287
ID ADA91762 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
FN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1288
ID ADB14825 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
FN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1289
ID ADA47281 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane polypeptide PRO246 cDNA.
FN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1290
ID ADB18786 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
FN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1291
ID ADA94001 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
FN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1292
ID ADB19897 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
FN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1293
ID ADB13209 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
FN US2003082710-A1.


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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1294
ID ACD98592 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1295
ID ADA74463 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1296
ID ADA42219 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1297
ID ADB24696 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1298
ID ADA82220 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1299
ID ADA75183 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1300
ID ADA85261 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1301
ID ADA84709 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1302
ID ACD23159 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #8.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1303
ID ADB25256 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1304
ID ADA80493 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1305
ID ADA75735 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1306
ID ADA46960 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1307
ID ADB25256 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1308
ID ADA93432 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1309
ID ADB26782 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
```


Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1310
ID ADA31069 standard; cDNA; 1813 BP.
DE Human PRO polypeptide #169.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1311
ID ADA60997 standard; cDNA; 1813 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1312
ID ADB24144 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1313
ID ADA96473 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1314
ID ADA81045 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1315
ID ADA95921 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1316
ID ADB26230 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1317
ID ADB21715 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Conservative: 43
Mismatch: 105
Indels: 54

Best Local Similarity: 27.9%
Query Match: 13.1%
Mismatch: 105
Indels: 54
RESULT 1318
ID ADA77494 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1319
ID ADB18234 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1320
ID ADA86917 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1321
ID ADA16498 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1322
ID ADA12927 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1323
ID ADA41795 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1324
ID ADA8020 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1325
ID ADA46408 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54


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Query Match: 13.1% Indels: 54
RESULT 1326
ID ADA17142 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1327
ID ADA42645 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1328
ID ADB28438 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1329
ID ADB28990 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1330
ID ADA76942 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1331
ID ADA88572 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1332
ID ADA97577 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1333
ID ADB27334 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1334
ID ADB38629 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
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ID ADB2267 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1335
ID ACD30276 standard; cDNA; 1813 BP.
DE Human cDNA encoding Pro246.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1336
ID ACD33521 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #8.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1337
ID ADA66958 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1338
ID ADB22819 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1339
ID ADB33592 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1340
ID ADA92314 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1341
ID ADB15377 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1342
ID ADB38629 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
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PN US2003082766-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1343
ID ADB38077 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1344
ID ADB66549 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1345
ID ADB89629 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1346
ID ADB90361 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1347
ID ADB77564 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1348
ID ADB39462 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1349
ID ADB74700 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1350
ID ADB47085 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082687-A1.

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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1351
ID ADB86692 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1352
ID ADB77297 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1353
ID ADB34454 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1354
ID ADB35558 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1355
ID ADB33902 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1356
ID ADB35006 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1357
ID ADB36110 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide SEQ ID NO 337.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 105
Indels: 54
Query Match:
RESULT 1358
ID ADB46505 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1359
ID ADC28346 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1360
ID ADC39546 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1361
ID ADC40060 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1362
ID ADC18888 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1363
ID ADC34184 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1364
ID ADC29239 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1365
ID ADC28770 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1366
ID ADC40655 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1367
ID ADC19312 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1368
ID ADC33760 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1369
ID ADC12830 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1370
ID ADC50378 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1371
ID ADC71925 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1372
ID ADC59904 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1373
ID ADC52911 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID337.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1374
ID ADC57265 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID337.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
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Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1375			
ID ADC60456 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein PRO246 cDNA.			
PN US2003087367-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1376			
ID ADC50931 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein PRO246 cDNA.			
PN US2003087361-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1377			
ID ADC65458 standard; cDNA; 1813 BP.			
DE Human PRO polynucleotide #169.			
PN US2003087362-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1378			
ID ADC54556 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein cDNA Seq ID337.			
PN US2003087363-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1379			
ID ADC53517 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein cDNA Seq ID337.			
PN US2003087364-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1380			
ID ADC59040 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein cDNA Seq ID337.			
PN US2003087359-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1381			
ID ADC55918 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein cDNA Seq ID337.			
PN US2003087360-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1382			
ID ADC58488 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein cDNA Seq ID337.			
PN US2003087346-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1383			
ID ADC58488 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein cDNA Seq ID337.			
PN US2003087346-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1384			
ID ADD03162 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein PRO246 cDNA.			
PN US2003092104-A1.			
PD 15-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1385			
ID ADC90154 standard; cDNA; 1813 BP.			
DE Novel human secreted and transmembrane protein PRO246 cDNA.			
PN US2003087348-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1386			
ID ADC69573 standard; cDNA; 1813 BP.			
DE cDNA encoding human PRO polypeptide #169.			
PN US2003194770-A1.			
PD 16-OCT-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1387			
ID ADC48462 standard; cDNA; 1813 BP.			
DE Human PRO polynucleotide #169.			
PN US2003194773-A1.			
PD 16-OCT-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	43.2%	Conservative:	43
Best Local Similarity:	27.9%	Mismatches:	105
Query Match:	13.1%	Indels:	54
RESULT 1388			
ID ADD09991 standard; cDNA; 1813 BP.			


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RESULT 1391
ID ADD11029 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1392
ID ADC47910 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1393
ID ADD04837 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1394
ID ADC79970 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1395
ID ADD09439 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1396
ID ADD03843 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1397
ID ADD03419 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1398
ID ADD41152 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1399
ID ADD091367 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1400
ID ADD53031 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1401
ID ADD53583 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1402
ID ADD51739 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1403
ID ADD02538 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1404
ID ADD01972 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1405
ID ADD54154 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1406
ID ADD92471 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
RESULT 1407
ID ADD91367 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Conservative: 43
Mismatches: 105
Indels: 54
Query Match: 13.1%
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DE Human PRO polynucleotide #169.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1408
ID ADE03981 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1409
ID ADE03981 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1410
ID ADE22210 standard; cDNA; 1813 BP.
DE ADE22210 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1411
ID ADE22210 standard; cDNA; 1813 BP.
DE ADE22210 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1412
ID ADE41970 standard; cDNA; 1813 BP.
DE ADE41970 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1413
ID ADE17787 standard; cDNA; 1813 BP.
DE ADE17787 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1414
ID ADE91919 standard; cDNA; 1813 BP.
DE ADE91919 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1415
ID ADE33382 standard; cDNA; 1813 BP.
DE ADE33382 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1416
ID ADE33934 standard; cDNA; 1813 BP.
DE ADE33934 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1417
ID ADD79986 standard; cDNA; 1813 BP.
DE ADD79986 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1418
ID ADD93023 standard; cDNA; 1813 BP.
DE ADD93023 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1419
ID ADE19443 standard; cDNA; 1813 BP.
DE ADE19443 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1420
ID ADE34671 standard; cDNA; 1813 BP.
DE ADE34671 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1421
ID ADE18891 standard; cDNA; 1813 BP.
DE ADE18891 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1422
ID ADE43087 standard; cDNA; 1813 BP.
DE ADE43087 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1423
ID ADD95876 standard; cDNA; 1813 BP.
DE ADD95876 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199059-A1.
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PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1424
ID ADE22762 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1425
ID ADD78880 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1426
ID ADE32830 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1427
ID ADE42522 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1428
ID ADD80538 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1429
ID ADD89566 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1430
ID ADE40850 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1431
ID ADE04649 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1432
ID ADE92778 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1433
ID ADG21487 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1434
ID ADG23128 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1435
ID ADF97463 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1436
ID ADG80527 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1437
ID ADG79975 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1438
ID ADG63790 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane polypeptide PRO246 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1439
ID ADH59154 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1440	
ID ADH55267 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003207381-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1441	
ID ADH55819 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003207379-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1442	
ID ADI37933 standard; cDNA; 1813 BP.	
DE Human secreted/transmembrane protein cDNA, #9.	
PN US2003054352-A1.	
PD 20-MAR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1443	
ID ADI64038 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003207385-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1444	
ID ADI64987 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003207386-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1445	
ID ADI63486 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003207387-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1446	
ID ADH81900 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003207388-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1447	
ID ADH81348 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003207377-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1448	
ID ADH82517 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003087355-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1449	
ID ACD24021 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003032156-A1.	
PD 13-FEB-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1450	
ID ACA58323 standard; cDNA; 1813 BP.	
DE cDNA encoding human PRO polypeptide #8.	
PN US2002192659-A1.	
PD 19-DEC-2002.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1451	
ID ACD42390 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003040014-A1.	
PD 27-FEB-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1452	
ID ACA67162 standard; cDNA; 1813 BP.	
DE cDNA encoding human PRO polypeptide #169.	
PN US2003004311-A1.	
PD 02-JAN-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1453	
ID ADJ26201 standard; cDNA; 1813 BP.	
DE Human secreted/transmembrane protein cDNA, #9.	
PN US2003054349-A1.	
PD 20-MAR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1454	
ID ADM82517 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003087355-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1455	
ID ADN15916 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003087353-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54
RESULT 1456	
ID ADH81348 standard; cDNA; 1813 BP.	
DE Novel human secreted and transmembrane protein PRO246 cDNA.	
PN US2003207377-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 43.2%	Conservative: 43
Best Local Similarity: 27.9%	Mismatches: 105
Query Match: 13.1%	Indels: 54


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Query Match: 13.1% Indels: 54
RESULT 1456
ID ADN16545 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1457
ID ADN15364 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1458
ID ADN14812 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1459
ID ADC81074 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1460
ID ADE79116 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1461
ID ADD76522 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US200310087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1462
ID ADD87886 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1463
ID ADD86290 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1464
ID ADE79540 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1465
ID ADE75738 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1466
ID ADE73216 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1467
ID ADE23314 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1468
ID ADE23866 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1469
ID ADE24509 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1470
ID ADD87334 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1471
ID ADE89200 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
RESULT 1472
ID ADE79116 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.2% Conservative: 43
Best Local Similarity: 27.9% Mismatches: 105
Query Match: 13.1% Indels: 54
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ID ADE41204 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane polypeptide PRO246 cDNA.
PN US2003104558-A1.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1473
ID ADE73751 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1474
ID ADE18339 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1475
ID ADE88648 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1476
ID ADE9305 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1477
ID ADE94668 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1478
ID ADE91079 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1479
ID ADE95220 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1480
ID ADE93330 standard; cDNA; 1813 BP.

DE Human PRO polynucleotide #169.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1481
ID ADE34911 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1482
ID ADE98424 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1483
ID ADE92226 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1484
ID ADE90527 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1485
ID ADE91674 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1486
ID ADE98851 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatch: 105
Indels: 54
RESULT 1487
ID ADG40321 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1488
ID ADF73715 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1489
ID ADG02253 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1490
ID ADG22039 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1491
ID ADG20109 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1492
ID ADF98015 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1493
ID ADG24232 standard; cDNA; 1813 BP.
DE Novel human secreted and transmembrane protein PRO246 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1494
ID ADF98586 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1495
ID ADG03417 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Conservative: 43

Percent Similarity: 27.9%
Best Local Similarity: 13.1%
Query Match: 13.1%
Mismatches: 105
Indels: 54
RESULT 1496
ID ADF99138 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1497
ID ADG16723 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1498
ID ADG05182 standard; cDNA; 1813 BP.
DE Human PRO polynucleotide #169.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1499
ID ADG19449 standard; cDNA; 1813 BP.
DE cDNA encoding human PRO polypeptide #169.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54
RESULT 1500
ID ADF73291 standard; cDNA; 1813 BP.
DE Human secreted/transmembrane protein cDNA, #9.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.2%
Best Local Similarity: 27.9%
Mismatches: 43
Indels: 105
Query Match: 13.1%
Conservative: 43
Mismatches: 105
Indels: 54

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OM protein - nucleic search, using frame plus p2n model

Run on: May 17, 2006, 14:58:23 ; Search time 228 Seconds
(without alignments) 3840.697 Million cells

Title: US-10-785-221-9

Perfect score:

Sequence: 1 MARRSRHRLLLLLRVLVVA.....TPVIPALWKAAGSGRQGF 312

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Угәрҙең 10.0 , Угәрҙең 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delect 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length:	200000000
Maximum DB seq length:	200000000

Post-processing: Minimum March 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

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-MODEL=frame+ p2n.model -DEV=x1h
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-Q=/abss/ABSSWEB_spool/US10785221/runat_16052006_083854_19475/app_query.fasta_1

-DB=Issued_Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40
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-MODE=LOCAL -QUITEMT=ptc -NORM=ext -HEADSIZE=500 -MINI EN=0 -MAYI EN=200000
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-HOST=abbs08 -USER=JIS10785221 @CGN 1 1 193 @rnat 16052006 083854 19475
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-NCPU=6 -ICPU=3 -NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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8: /EMC_Celerra_SIDS3/ptodata/2/ina/pp COMB.seq:

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SUMMARIES

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5	1605	100.0	1295	3	US-09-306-700-63	Sequence 63, Appl
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7	1605	100.0	1295	3	US-09-304-920A-63	Sequence 63, Appl
8	1605	100.0	1295	3	US-09-309-064-63	Sequence 63, Appl

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132	170.5	10.6	5406	2	US-07-813-593-3	Sequence 3, Appl1	205	155	9.7	994	3	US-09-864-675-1	Sequence 1, Appl1
133	170.5	10.6	5406	2	US-07-977-451-5	Sequence 5, Appl1	206	154.5	9.6	1339	3	US-08-468-858B-3	Sequence 3, Appl1
134	170.5	10.6	5406	2	US-07-946-507-3	Sequence 3, Appl1	207	154.5	9.6	1339	3	US-08-468-859A-3	Sequence 3, Appl1
135	170.5	10.6	5406	2	US-08-252-517-5	Sequence 5, Appl1	208	153	9.5	2839	3	US-08-468-856B-5	Sequence 5, Appl1
136	170.5	10.6	5406	2	US-07-906-397A-5	Sequence 5, Appl1	209	153	9.5	2839	3	US-08-468-859A-5	Sequence 5, Appl1
137	170.5	10.6	5406	2	US-08-601-891-5	Sequence 5, Appl1	210	152.5	9.5	1273	3	US-09-778-510-3	Sequence 3, Appl1
138	170.5	10.6	5406	2	US-09-021-324-5	Sequence 5, Appl1	211	151.5	9.4	2999	3	US-09-949-016-4676	Sequence 4676, Ap
139	170.5	10.6	5406	3	US-09-872-136B-5	Sequence 5, Appl1	212	151.5	9.4	3309	4	US-10-094-743-1553	Sequence 1553, Ap
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141	170.5	10.6	5406	7	PCT-US92-02750-7	Sequence 7, Appl1	214	150.5	9.4	24120	5	US-10-077-130-4	Sequence 4, Appl1
142	170.5	10.6	5406	7	PCT-US92-05401-5	Sequence 5, Appl1	215	150	9.3	1364	3	US-09-924-103-3	Sequence 3, Appl1
143	170.5	10.6	5406	7	PCT-US92-09893-5	Sequence 5, Appl1	216	150	9.3	2287	2	US-09-023-655-1216	Sequence 1216, Ap
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232	148	9.2	1103	2	US-08-602-725-33	Sequence 33, Appl	305	143	8.9	4277	3	US-10-015-393A-57	Sequence 57, Appl
233	148	9.2	1476	3	US-08-753-007A-7	Sequence 7, Appl	306	143	8.9	4277	3	US-10-011-833A-57	Sequence 57, Appl
234	148	9.2	1476	3	US-09-398-496-7	Sequence 7, Appl	307	143	8.9	4277	3	US-10-006-041A-57	Sequence 57, Appl
235	148	9.2	2099	3	US-09-949-016-5169	Sequence 5169, Appl	308	143	8.9	4277	3	US-10-012-064A-57	Sequence 57, Appl
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238	148	9.2	2268	3	US-09-398-496-31	Sequence 31, Appl	311	143	8.9	4277	5	US-10-015-386A-57	Sequence 57, Appl
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241	147.5	9.2	6263	3	US-09-023-655-1473	Sequence 1473, Appl	314	143	8.9	4277	5	US-10-006-746A-57	Sequence 57, Appl
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244	146	9.1	1473	3	US-09-949-016-245	Sequence 245, Appl	317	143	8.9	4277	5	US-10-015-519A-57	Sequence 57, Appl
245	146	9.1	1475	3	US-09-949-016-1654	Sequence 1654, Appl	318	143	8.9	4277	5	US-10-015-715A-57	Sequence 57, Appl
246	146	9.1	23218	3	US-09-949-016-11987	Sequence 11987, Appl	319	143	8.9	4277	5	US-10-007-236A-57	Sequence 57, Appl
247	146	9.1	23219	3	US-09-949-016-13396	Sequence 13396, Appl	320	142.5	8.9	6363	3	US-09-023-655-879	Sequence 879, Appl
248	145.5	9.1	2633	3	US-09-023-655-950	Sequence 950, Appl	321	142	8.8	534	3	US-09-702-705-1325	Sequence 1325, Appl
249	145.5	9.1	3384	4	US-10-094-749-992	Sequence 992, Appl	322	142	8.8	534	3	US-09-736-457-1325	Sequence 1325, Appl
250	145.5	9.1	4956	5	US-09-131-651-7	Sequence 7, Appl	323	142	8.8	534	3	US-09-614-124B-1325	Sequence 1325, Appl
251	145.5	9.1	6718	3	US-09-949-016-4632	Sequence 4632, Appl	324	142	8.8	534	3	US-09-671-325-1325	Sequence 1325, Appl
252	145	9.0	4188	5	US-09-191-651-1	Sequence 1, Appl	325	142	8.8	534	3	US-09-658-824-1325	Sequence 1325, Appl
253	145	9.0	107820	5	US-09-792-616-1	Sequence 1, Appl	326	142	8.8	534	3	US-10-017-754-1325	Sequence 1325, Appl
254	144.5	9.0	2058	5	US-10-162-335-45	Sequence 45, Appl	327	142	8.8	534	3	US-09-651-563-1325	Sequence 1325, Appl
255	144.5	9.0	3173	3	US-08-468-856B-1	Sequence 1, Appl	328	142	8.8	2598	3	US-09-949-016-3414	Sequence 3414, Appl
256	144.5	9.0	3173	3	US-08-468-859A-1	Sequence 1, Appl	329	142	8.8	3260	3	US-09-949-002-42	Sequence 42, Appl
257	144.5	9.0	3894	5	US-09-191-651-5	Sequence 5, Appl	330	142	8.8	3287	3	US-09-949-002-141	Sequence 141, Appl
258	144	9.0	1630	3	US-08-468-856B-2	Sequence 2, Appl	331	141.5	8.8	2876	3	US-09-489-847-22	Sequence 22, Appl
259	144	9.0	1630	3	US-08-468-859A-2	Sequence 2, Appl	332	141	8.8	2116	3	US-09-023-655-1256	Sequence 1256, Appl
260	144	9.0	4078	3	US-09-016-434-1132	Sequence 1132, Appl	333	140.5	8.8	3398	7	PCT-US95-08493-12	Sequence 12, Appl
261	144	9.0	6000	2	US-08-348-006B-6	Sequence 6, Appl	334	140	8.7	2166	2	US-08-408-095-30	Sequence 30, Appl
262	144	9.0	6000	2	US-08-800-825A-6	Sequence 6, Appl	335	140	8.7	2481	3	US-09-877-730-15	Sequence 15, Appl
263	144	9.0	6000	3	US-09-158-657-6	Sequence 6, Appl	336	140	8.7	2715	3	US-09-877-730-5	Sequence 5, Appl
264	144	9.0	6000	7	PCT-US94-10166-6	Sequence 6, Appl	337	140	8.7	2724	3	US-09-877-730-19	Sequence 19, Appl
265	144	9.0	325791	3	US-09-768-185A-1	Sequence 1, Appl	338	140	8.7	2958	3	US-09-877-730-9	Sequence 9, Appl
266	143.5	8.9	1542	3	US-09-205-258-123	Sequence 123, Appl	339	140	8.7	2976	3	US-09-877-730-11	Sequence 11, Appl
267	143.5	8.9	1542	3	US-10-004-860-123	Sequence 123, Appl	340	140	8.7	3210	3	US-09-877-730-1	Sequence 1, Appl
268	143.5	8.9	1685	3	US-09-907-794A-83	Sequence 83, Appl	341	140	8.7	3219	3	US-09-877-730-17	Sequence 17, Appl
269	143.5	8.9	1685	3	US-09-905-125A-83	Sequence 83, Appl	342	140	8.7	3874	3	US-09-877-730-31	Sequence 31, Appl
270	143.5	8.9	1685	3	US-09-902-775A-83	Sequence 83, Appl	343	140	8.7	4608	3	US-09-041-886-24	Sequence 24, Appl
271	143.5	8.9	1685	3	US-09-906-700-83	Sequence 83, Appl	344	140	8.7	4608	7	PCT-US94-05277-1	Sequence 1, Appl
272	143.5	8.9	1685	3	US-09-903-603A-83	Sequence 83, Appl	345	139.5	8.7	601	3	US-09-949-016-139578	Sequence 139578
273	143.5	8.9	1685	3	US-09-904-320A-83	Sequence 83, Appl	346	139.5	8.7	3453	3	US-09-877-730-7	Sequence 7, Appl
274	143.5	8.9	1685	3	US-09-909-064-83	Sequence 83, Appl	347	139.5	8.7	34314	3	US-09-949-016-12031	Sequence 12031, A
275	143.5	8.9	1685	3	US-09-905-381A-83	Sequence 83, Appl	348	139.5	8.7	34314	3	US-09-949-016-15686	Sequence 15686, A
276	143.5	8.9	1685	3	US-09-906-618-83	Sequence 83, Appl	349	139	8.7	1870	2	US-08-359-705B-3	Sequence 3, Appl
277	143.5	8.9	1685	3	US-09-906-646-83	Sequence 83, Appl	350	139	8.7	1870	2	US-08-286-846A-3	Sequence 3, Appl
278	143.5	8.9	1685	3	US-09-904-462-83	Sequence 83, Appl	351	139	8.7	1870	2	US-08-457-880A-3	Sequence 3, Appl
279	143.5	8.9	1685	3	US-09-902-736A-83	Sequence 83, Appl	352	139	8.7	1870	3	US-08-444-622A-3	Sequence 3, Appl
280	143.5	8.9	1685	3	US-09-906-722A-83	Sequence 83, Appl	353	139	8.7	1870	3	US-08-942-562-3	Sequence 3, Appl
281	143.5	8.9	1685	4	US-09-905-449-83	Sequence 83, Appl	354	139	8.7	1870	3	US-09-156-923-3	Sequence 3, Appl
282	143.5	8.9	1685	4	US-09-903-562B-83	Sequence 83, Appl	355	139	8.7	2052	3	US-10-012-231A-147	Sequence 147, Appl
283	143.5	8.9	1685	4	US-09-906-679A-83	Sequence 83, Appl	356	139	8.7	2052	3	US-10-015-389A-147	Sequence 147, Appl
284	143.5	8.9	1685	5	US-09-907-841-83	Sequence 83, Appl	357	139	8.7	2052	3	US-10-006-768A-147	Sequence 147, Appl
285	143.5	8.9	1718	3	US-09-778-510-5	Sequence 5, Appl	358	139	8.7	2052	3	US-10-015-671A-147	Sequence 147, Appl
286	143.5	8.9	1820	3	US-09-778-510-1	Sequence 1, Appl	359	139	8.7	2052	3	US-10-015-393A-147	Sequence 147, Appl
287	143	8.9	2031	2	US-08-217-299-2	Sequence 2, Appl	360	139	8.7	2052	3	US-10-011-833A-147	Sequence 147, Appl
288	143	8.9	2097	2	US-08-602-725-35	Sequence 35, Appl	361	139	8.7	2052	3	US-10-006-041A-147	Sequence 147, Appl
289	143	8.9	2220	2	US-08-389-459A-16	Sequence 16, Appl	362	139	8.7	2052	4	US-10-012-064A-147	Sequence 147, Appl
290	143	8.9	2220	3	US-08-987-867A-16	Sequence 16, Appl	363	139	8.7	2052	4	US-10-015-392A-147	Sequence 147, Appl
291	143	8.9	2349	2	US-08-184-009-145	Sequence 145, Appl	364	139	8.7	2052	5	US-10-011-795B-147	Sequence 147, Appl
292	143	8.9	2349	2	US-08-458-356-145	Sequence 145, Appl	365	139	8.7	2052	5	US-10-015-386A-147	Sequence 147, Appl
293	143	8.9	2349	3	US-08-460-736-145	Sequence 145, Appl	366	139	8.7	2052	5	US-10-012-121A-147	Sequence 147, Appl
294	143	8.9	2349	3	US-09-535-370-145	Sequence 145, Appl	367	139	8.7	2052	5	US-10-006-485A-147	Sequence 147, Appl
295	143	8.9	2349	3	US-09-663-667-145	Sequence 145, Appl	368	139	8.7	2052	5	US-10-006-746A-147	Sequence 147, Appl
296	143	8.9	2434	2	US-08-184-009-144	Sequence 144, Appl	369	139	8.7	2052	5	US-10-012-752A-147	Sequence 147, Appl
297	143	8.9	2434	2	US-08-458-356-144	Sequence 144, Appl	370	139	8.7	2052	5	US-10-017-253A-147	Sequence 147, Appl
298	143	8.9	2434	3	US-08-460-736-144	Sequence 144, Appl	371	139	8.7	2052	5	US-10-015-519A-147	Sequence 147, Appl
299	143	8.9	2434	3	US-09-535-370-144	Sequence 144, Appl	372	139	8.7	2052	5	US-10-015-715A-147	Sequence 147, Appl
300	143	8.9	2434	3	US-09-663-667-144	Sequence 144, Appl	373	139	8.7	2052	5	US-10-007-236A-147	Sequence 147, Appl

374	139	8.7	2256	3	US-10-104-047-1425	Sequence 1425, Ap	447	134	8.3	8578	3	US-09-784-358-17	Sequence 17, Appl
375	139	8.7	3060	2	US-08-286-305A-6	Sequence 6, Appl	448	133.5	8.3	601	3	US-09-949-016-124514	Sequence 124514, A
376	139	8.7	3060	2	US-08-441-104A-6	Sequence 6, Appl	449	133.5	8.3	1759	3	US-09-667-135-3	Sequence 3, Appl
377	139	8.7	3060	2	US-08-440-816A-6	Sequence 6, Appl	450	133.5	8.3	2118	3	US-09-270-767-11659	Sequence 11659, A
378	139	8.7	3060	2	US-09-417-381A-6	Sequence 6, Appl	451	133.5	8.3	3556	3	US-09-270-767-10439	Sequence 10439, A
379	139	8.7	3194	2	US-08-359-705B-1	Sequence 1, Appl	452	133.5	8.3	64984	3	US-09-949-016-15254	Sequence 15254, A
380	139	8.7	3194	2	US-08-286-846A-1	Sequence 1, Appl	453	133	8.3	1014	2	US-08-414-657D-5	Sequence 5, Appl
381	139	8.7	3194	2	US-08-457-880A-1	Sequence 1, Appl	454	133	8.3	1014	2	US-09-135-080-7	Sequence 7, Appl
382	139	8.7	3194	3	US-08-444-622A-1	Sequence 1, Appl	455	133	8.3	1238	2	US-08-414-657D-3	Sequence 3, Appl
383	139	8.7	3194	3	US-08-942-562-1	Sequence 1, Appl	456	133	8.3	1238	3	US-09-135-080-3	Sequence 3, Appl
384	139	8.7	3194	3	US-09-156-923-1	Sequence 1, Appl	457	133	8.3	1780	5	US-10-162-335-93	Sequence 93, Appl
385	139	8.7	3707	2	US-08-271-454-1	Sequence 1, Appl	458	133	8.3	2580	3	US-09-774-528-327	Sequence 327, App
386	139	8.7	3707	2	US-09-949-016-827	Sequence 827, App	459	133	8.3	2580	3	US-10-120-988-327	Sequence 327, App
387	139	8.7	3707	7	PCT-US95-08180-1	Sequence 1, Appl	460	133	8.3	2685	3	US-09-949-016-4734	Sequence 4734, Ap
388	138.5	8.6	1046	3	US-09-799-451-332	Sequence 332, App	461	133	8.3	11939	3	US-09-949-016-13232	Sequence 13232, A
389	138.5	8.6	1896	3	US-09-412-554A-8	Sequence 8, Appl	462	132.5	8.3	576	3	US-09-270-767-2049	Sequence 2049, Ap
390	138.5	8.6	2463	2	US-08-339-578-1	Sequence 1, Appl	463	132.5	8.3	576	3	US-09-270-767-17331	Sequence 17331, A
391	138.5	8.6	3192	3	US-09-412-554A-1	Sequence 1, Appl	464	132.5	8.3	8083	3	US-09-383-630-4	Sequence 4, Appl
392	138.5	8.6	5830	3	US-09-967-655-3	Sequence 3, Appl	465	132.5	8.3	8083	3	US-09-383-630-5	Sequence 5, Appl
393	138.5	8.6	5830	3	US-09-949-016-327	Sequence 327, App	466	132.5	8.3	25249	3	US-09-949-016-17444	Sequence 17444, A
394	138.5	8.6	5831	3	US-09-949-016-3982	Sequence 3982, Ap	467	132.5	8.3	65902	3	US-09-949-002-609	Sequence 609, App
395	138.5	8.6	44430	3	US-09-949-016-12468	Sequence 12468, A	c	468	132	6055	3	US-09-953-318-10	Sequence 10, Appl
396	138.5	8.6	44431	3	US-09-949-016-15882	Sequence 15882, A	468	132	8.2	7718	3	US-09-976-594-244	Sequence 244, App
397	138	8.6	1288	3	US-09-724-864-16	Sequence 16, Appl	469	132	8.2	51620	3	US-09-949-016-12848	Sequence 12848, A
398	138	8.6	4441	3	US-09-949-016-15325	Sequence 15325, A	470	132	8.2	51621	3	US-09-949-016-16503	Sequence 16503, A
399	137.5	8.6	2184	3	US-09-484-970B-161	Sequence 161, App	471	132	8.2	67386	3	US-09-949-016-16519	Sequence 16519, A
400	137.5	8.6	2430	3	US-09-620-312D-176	Sequence 176, App	472	132	8.2	75799	3	US-09-949-016-15231	Sequence 15231, A
401	137.5	8.6	4071	3	US-09-098-707A-1	Sequence 1, Appl	c	473	132	939	3	US-09-700-397-5	Sequence 5, Appl
402	137.5	8.6	4071	3	US-09-483-539-1	Sequence 1, Appl	474	131.5	8.2	1032	3	US-09-700-397-1	Sequence 1, Appl
403	137.5	8.6	4071	3	US-10-100-405A-1	Sequence 1, Appl	475	131.5	8.2	1151	2	US-08-456-104-3	Sequence 3, Appl
404	137.5	8.6	4071	3	US-10-022-939-1	Sequence 1, Appl	476	131.5	8.2	1151	3	US-08-205-697A-20	Sequence 20, Appl
405	137.5	8.6	37155	3	US-09-949-016-16945	Sequence 16945, A	477	131.5	8.2	1151	3	US-08-702-525-20	Sequence 20, Appl
406	137.5	8.6	40181	3	US-09-949-016-17016	Sequence 17016, A	478	131.5	8.2	1151	3	US-09-837-867A-20	Sequence 20, Appl
407	137	8.5	1024	10	5169835-16	Patent No. 5169835	479	131.5	8.2	1151	3	US-09-206-132-3	Sequence 3, Appl
408	137	8.5	1553	3	US-09-645-069-3	Sequence 3, Appl	480	131.5	8.2	1151	7	PCT-US95-02576-20	Sequence 20, Appl
409	137	8.5	1553	3	US-09-644-934-3	Sequence 3, Appl	481	131.5	8.2	1151	3	US-08-479-744A-22	Sequence 22, Appl
410	137	8.5	1553	5	US-10-115-609-3	Sequence 3, Appl	482	131.5	8.2	1163	3	US-08-280-757B-22	Sequence 22, Appl
411	137	8.5	1604	4	US-09-875-338-1	Sequence 1, Appl	483	131.5	8.2	1163	3	US-09-425-762-22	Sequence 22, Appl
412	137	8.5	3600	4	US-09-875-338-3	Sequence 3, Appl	484	131.5	8.2	1163	3	US-09-425-516-22	Sequence 22, Appl
413	137	8.5	3616	3	US-09-451-291-5	Sequence 5, Appl	485	131.5	8.2	1163	3	US-09-441-411-23	Sequence 23, Appl
414	137	8.5	14261	3	US-09-949-016-15528	Sequence 15528, A	486	131.5	8.2	1261	3	US-08-205-697A-12	Sequence 12, Appl
415	137	8.5	27463	3	US-09-949-016-11876	Sequence 11876, A	487	131.5	8.2	1261	3	US-08-702-525-12	Sequence 12, Appl
c	416	136.5	8.5	439	Sequence 1558, Ap	488	131.5	8.2	1261	3	US-09-837-867A-12	Sequence 12, Appl	
c	417	136.5	8.5	439	US-09-270-767-1558	Sequence 1558, Ap	489	131.5	8.2	1261	7	PCT-US95-02576-12	Sequence 12, Appl
c	418	136.5	8.5	439	US-09-270-767-16840	Sequence 16840, A	490	131.5	8.2	1261	3	US-09-999-833A-522	Sequence 522, App
c	419	136.5	8.5	4236	US-08-810-116-7	Sequence 7, Appl	491	131.5	8.2	1679	3	US-10-020-445A-522	Sequence 522, App
c	420	136	8.5	3159	US-07-930-548A-7	Sequence 7, Appl	492	131.5	8.2	1679	4	US-09-978-189-522	Sequence 522, App
c	421	136	8.5	17198	US-08-986-485-3	Sequence 3, Appl	493	131.5	8.2	1679	4	US-10-017-085A-522	Sequence 522, App
c	422	136	8.5	188504	US-09-949-016-13776	Sequence 13776, A	494	131.5	8.2	1679	5	US-10-145-129A-522	Sequence 522, App
c	423	136	8.5	200918	US-09-949-002-711	Sequence 711, App	495	131.5	8.2	1679	5	US-10-013-929A-522	Sequence 522, App
c	424	135.5	8.4	601	US-09-949-002-647	Sequence 647, App	496	131.5	8.2	1679	5	US-10-013-917A-522	Sequence 522, App
c	425	135	8.4	1195	US-09-949-016-124513	Sequence 124513, A	497	131.5	8.2	1679	5	US-10-013-917A-522	Sequence 522, App
c	426	135	8.4	1195	US-09-976-594-403	Sequence 403, App	498	131.5	8.2	1693	3	US-09-700-397-2	Sequence 2, Appl
c	427	135	8.4	3527	US-10-104-047-225	Sequence 225, App	499	131.5	8.2	2264	2	US-08-232-538-16	Sequence 16, Appl
c	428	134.5	8.4	870	US-09-451-291-2	Sequence 2, Appl	500	131.5	8.2	2264	2	US-08-786-164-16	Sequence 16, Appl
c	429	134.5	8.4	873	US-09-910-174B-22	Sequence 22, Appl	501	131.5	8.2	24154	3	US-09-949-016-16374	Sequence 16374, A
c	430	134.5	8.4	873	US-09-620-461-22	Sequence 22, Appl	502	131.5	8.2	135030	3	US-09-949-016-14896	Sequence 14896, A
c	431	134.5	8.4	2292	US-09-142-956B-1	Sequence 1, Appl	503	131.5	8.2	425592	3	US-09-949-016-14182	Sequence 14182, A
c	432	134.5	8.4	2378	US-09-949-016-2703	Sequence 2703, Ap	504	131	8.2	4014	3	US-09-119-014D-5	Sequence 5, Appl
c	433	134.5	8.4	2383	US-08-232-538-18	Sequence 18, Appl	505	131	8.2	7680	3	US-09-953-318-3	Sequence 3, Appl
c	434	134.5	8.4	2383	US-08-786-164-18	Sequence 18, Appl	506	131	8.2	12797	3	US-09-949-016-13123	Sequence 13123, A
c	435	134.5	8.4	2718	US-09-667-135-1	Sequence 1, Appl	507	131	8.2	12797	3	US-09-949-016-12013	Sequence 12013, A
c	436	134.5	8.4	18291	US-09-949-016-14787	Sequence 14787, A	508	130.5	8.1	854	5	US-09-191-651-9	Sequence 9, Appl
c	437	134.5	8.4	36952	US-09-949-016-14786	Sequence 14786, A	509	130.5	8.1	2142	3	US-09-774-528-100	Sequence 100, App
c	438	134	8.3	1199	US-09-270-767-13050	Sequence 13050, A	510	130.5	8.1	2142	3	US-10-120-988-100	Sequence 100, App
c	439	134	8.3	2869	US-08-374-834-2	Sequence 2, Appl	511	130.5	8.1	2142	3	US-10-120-988-100	Sequence 100, App
c	440	134	8.3	2869	US-08-644-271-2	Sequence 2, Appl	512	130.5	8.1	2163	3	US-09-774-528-99	Sequence 99, Appl
c	441	134	8.3	2869	US-09-077-955-2	Sequence 2, Appl	513	130.5	8.1	2163	3	US-10-120-988-99	Sequence 99, Appl
c	442	134	8.3	2869	US-10-016-283-2	Sequence 2, Appl	514	130.5	8.1	22400	3	US-10-143-266-1	Sequence 1, Appl
c	443	134	8.3	3095	US-08-434-000A-7	Sequence 7, Appl	515	130.5	8.1	51336	3	US-09-949-016-16054	Sequence 16054, A
c	444	134	8.3	3095	US-09-312-157-7	Sequence 7, Appl	516	130	8.1	945	3	US-09-445-375A-7	Sequence 7, Appl
c	445	134	8.3	3095	US-09-717-888-7	Sequence 7, Appl	517	130	8.1	968	3	US-09-645-069-1	Sequence 1, Appl
c	446	134	8.3	4854	US-09-784-358-15	Sequence 15, Appl	518	130	8.1	968	3	US-09-644-934-1	Sequence 1, Appl
c	447	134	8.3	5076	US-09-784-358-1	Sequence 1, Appl	519	130	8.1	968	5	US-10-115-609-1	Sequence 1, Appl

520	129.5	8.1	409	3	US-09-702-705-1328	Sequence 1328, Ap	593	127	7.9	3145	3	US-09-949-016-1149	Sequence 1149, Ap
521	129.5	8.1	409	3	US-09-736-457-1328	Sequence 1328, Ap	594	127	7.9	3402	3	US-09-991-181-118	Sequence 118, App
522	129.5	8.1	409	3	US-09-614-1248-1328	Sequence 1328, Ap	595	127	7.9	3402	3	US-09-990-444-118	Sequence 118, App
523	129.5	8.1	409	3	US-09-671-325-1328	Sequence 1328, Ap	596	127	7.9	3402	3	US-09-997-333-118	Sequence 118, App
524	129.5	8.1	409	3	US-09-658-824-1328	Sequence 1328, Ap	597	127	7.9	3402	3	US-09-992-598-118	Sequence 118, App
525	129.5	8.1	409	3	US-10-017-754-1328	Sequence 1328, Ap	598	127	7.9	3402	4	US-09-989-735-118	Sequence 118, App
526	129.5	8.1	409	3	US-09-651-653-1328	Sequence 1328, Ap	599	127	7.9	3402	5	US-09-989-726-118	Sequence 118, App
527	129.5	8.1	756	2	US-08-414-657D-17	Sequence 17, Appl	600	127	7.9	3402	5	US-09-997-514-118	Sequence 118, App
528	129.5	8.1	756	2	US-08-414-657D-18	Sequence 18, Appl	601	127	7.9	3402	5	US-09-989-728-118	Sequence 118, App
529	129.5	8.1	861	2	US-08-414-657D-9	Sequence 9, Appli	602	127	7.9	3402	5	US-09-997-349-118	Sequence 118, App
530	129.5	8.1	861	2	US-08-414-657D-10	Sequence 10, Appl	603	127	7.9	3402	5	US-09-997-653-118	Sequence 118, App
531	129.5	8.1	942	2	US-08-414-657D-6	Sequence 6, Appli	604	127	7.9	3402	5	US-09-989-293A-118	Sequence 118, App
532	129.5	8.1	924	2	US-08-414-657D-7	Sequence 7, Appli	605	127	7.9	7659	5	US-09-543-679A-2501	Sequence 2501, Ap
533	129.5	8.1	945	2	US-08-414-657D-8	Sequence 8, Appli	606	127	7.9	17337	2	US-07-906-871-15	Sequence 15, Appl
534	129.5	8.1	977	2	US-08-414-657D-1	Sequence 1, Appli	607	127	7.9	21742	5	US-09-543-679A-2505	Sequence 2505, Ap
535	129.5	8.1	977	3	US-09-135-080-1	Sequence 1, Appli	c 608	127	7.9	24405	3	US-09-949-016-12040	Sequence 12040, A
536	129.5	8.1	1004	3	US-09-383-586-24	Sequence 24, Appl	c 609	127	7.9	24405	3	US-09-949-016-17346	Sequence 17346, A
537	129.5	8.1	1004	3	US-09-823-038A-24	Sequence 24, Appl	c 610	127	7.9	24482	3	US-09-949-016-13391	Sequence 13391, A
538	129.5	8.1	2181	3	US-09-254-465A-7	Sequence 7, Appli	c 611	127	7.9	26664	3	US-09-564-805-28	Sequence 28, Appl
539	129.5	8.1	2181	3	US-09-254-465A-11	Sequence 11, Appl	612	127	7.9	26664	3	US-09-434-382-28	Sequence 28, Appl
540	129.5	8.1	2181	3	US-09-953-499-7	Sequence 7, Appli	613	127	7.9	29558	3	US-09-949-016-15607	Sequence 15607, A
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542	129.5	8.1	2181	3	US-09-999-833A-51	Sequence 51, Appl	c 615	127	7.9	31035	3	US-09-949-016-17466	Sequence 17466, A
543	129.5	8.1	2181	3	US-10-020-445A-51	Sequence 51, Appl	c 616	127	7.9	36679	3	US-09-949-016-12732	Sequence 12732, A
544	129.5	8.1	2181	4	US-09-978-189-51	Sequence 51, Appl	c 617	127	7.9	38207	3	US-09-949-016-17274	Sequence 17274, A
545	129.5	8.1	2181	5	US-10-017-085A-51	Sequence 51, Appl	c 618	127	7.9	71863	3	US-09-949-016-15112	Sequence 15112, A
546	129.5	8.1	2181	4	US-10-145-128A-51	Sequence 51, Appl	619	127	7.9	112112	3	US-09-949-016-15639	Sequence 15639, A
547	129.5	8.1	2181	5	US-10-013-929A-51	Sequence 51, Appl	620	127	7.9	117608	5	US-09-543-679A-3002	Sequence 3002, Ap
548	129.5	8.1	2181	5	US-10-013-917A-51	Sequence 51, Appl	621	127	7.9	154600	3	US-09-949-016-14757	Sequence 14757, A
549	129.5	8.1	4059	3	US-09-799-451-560	Sequence 560, App	c 622	127	7.9	264358	3	US-09-949-016-15725	Sequence 15725, A
550	129	8.0	3269	3	US-08-434-000A-9	Sequence 9, Appli	623	126.5	7.9	409	3	US-09-702-705-1040	Sequence 1040, Ap
551	129	8.0	3269	3	US-09-312-157-9	Sequence 9, Appli	624	126.5	7.9	409	3	US-09-702-705-1462	Sequence 1462, Ap
552	129	8.0	3269	3	US-09-717-888-9	Sequence 9, Appli	625	126.5	7.9	409	3	US-09-736-457-1040	Sequence 1040, Ap
553	129	8.0	89210	3	US-09-949-016-16988	Sequence 16988, A	c 626	126.5	7.9	409	3	US-09-736-457-1462	Sequence 1462, Ap
554	128.5	8.0	601	3	US-09-949-016-71335	Sequence 71335, A	627	126.5	7.9	409	3	US-09-614-1248-1040	Sequence 1040, Ap
555	128.5	8.0	2768	3	US-09-774-528-426	Sequence 426, App	c 628	126.5	7.9	409	3	US-09-614-1248-1462	Sequence 1462, Ap
556	128.5	8.0	2768	3	US-10-120-988-426	Sequence 426, App	629	126.5	7.9	409	3	US-09-671-325-1040	Sequence 1040, Ap
557	128.5	8.0	4078	3	US-09-016-434-1120	Sequence 1120, Ap	c 630	126.5	7.9	409	3	US-09-671-325-1462	Sequence 1462, Ap
558	128.5	8.0	5926	3	US-09-917-254-41	Sequence 41, Appl	c 631	126.5	7.9	409	3	US-09-658-824-1040	Sequence 1040, Ap
559	128.5	8.0	5926	4	US-09-880-107-3371	Sequence 3371, Ap	c 632	126.5	7.9	409	3	US-09-658-824-1462	Sequence 1462, Ap
560	128.5	8.0	36221	3	US-09-954-556-29	Sequence 29, Appl	633	126.5	7.9	409	3	US-10-017-754-1040	Sequence 1040, Ap
561	128.5	8.0	67386	3	US-09-949-016-16519	Sequence 16519, A	c 634	126.5	7.9	409	3	US-10-017-754-1462	Sequence 1462, Ap
562	128.5	8.0	69909	3	US-09-949-016-13423	Sequence 13423, A	635	126.5	7.9	409	3	US-09-651-563-1040	Sequence 1040, Ap
563	128.5	8.0	129554	3	US-09-949-002-765	Sequence 765, App	c 636	126.5	7.9	409	3	US-09-651-563-1462	Sequence 1462, Ap
564	128.5	8.0	152132	3	US-09-949-016-13845	Sequence 13845, A	637	126.5	7.9	601	3	US-09-949-016-20467	Sequence 20467, A
565	128.5	8.0	152143	5	US-09-949-016-12371	Sequence 2371, A	c 638	126.5	7.9	601	3	US-09-949-016-135189	Sequence 135189, A
566	128	8.0	1263	5	US-10-162-335-99	Sequence 99, Appl	c 639	126.5	7.9	601	3	US-09-949-016-141714	Sequence 141714, A
567	128	8.0	2199	4	US-10-094-749-1302	Sequence 1302, Ap	640	126.5	7.9	921	2	US-08-184-009-202	Sequence 202, App
568	128	8.0	2607	3	US-09-715-249-7	Sequence 7, Appli	641	126.5	7.9	921	2	US-08-458-356-202	Sequence 202, App
569	128	8.0	2610	2	US-08-374-834-17	Sequence 17, Appl	642	126.5	7.9	921	3	US-08-460-736-202	Sequence 202, App
570	128	8.0	2610	2	US-08-644-271-28	Sequence 28, Appl	643	126.5	7.9	921	3	US-09-535-370-202	Sequence 202, App
571	128	8.0	2610	3	US-09-077-955-32	Sequence 32, Appl	644	126.5	7.9	921	3	US-09-663-667-202	Sequence 202, App
572	128	8.0	2610	3	US-10-016-283-32	Sequence 32, Appl	645	126.5	7.9	2043	4	US-09-880-107-2428	Sequence 2428, Ap
573	127.5	7.9	360	5	US-09-984-429-542	Sequence 542, App	646	126.5	7.9	6585	3	US-09-949-016-14470	Sequence 14470, A
574	127.5	7.9	601	3	US-09-949-016-152457	Sequence 152457, A	c 647	126.5	7.9	11879	3	US-09-949-016-14211	Sequence 14211, A
575	127.5	7.9	601	3	US-09-949-016-163561	Sequence 163561, A	648	126.5	7.9	20840	3	US-09-949-016-14115	Sequence 14115, A
576	127.5	7.9	18264	3	US-09-949-016-16469	Sequence 16469, A	c 649	126.5	7.9	24395	3	US-09-949-016-14758	Sequence 14758, A
577	127.5	7.9	23257	3	US-09-949-016-12894	Sequence 12894, A	c 650	126.5	7.9	40548	3	US-09-949-016-13317	Sequence 13317, A
578	127.5	7.9	33260	3	US-09-949-016-16327	Sequence 16327, A	651	126.5	7.9	40617	3	US-09-949-016-15197	Sequence 15197, A
579	127.5	7.9	33153	3	US-09-949-016-16337	Sequence 16337, A	652	126.5	7.9	63783	3	US-09-949-016-13576	Sequence 13576, A
580	127.5	7.9	33125	3	US-09-949-016-16436	Sequence 16436, A	653	126.5	7.9	363032	3	US-09-949-016-12415	Sequence 12415, A
581	127.5	7.9	33125	3	US-09-949-016-16437	Sequence 16437, A	654	126.5	7.9	363032	3	US-09-949-016-15754	Sequence 15754, A
582	127.5	7.9	39755	3	US-09-949-016-17352	Sequence 17352, A	655	126.5	7.9	363032	3	US-08-232-538-17	Sequence 17, Appl
583	127.5	7.9	59140	3	US-09-949-016-16023	Sequence 16023, A	656	126	7.9	2352	2	US-08-786-164-17	Sequence 17, Appl
584	127.5	7.9	117838	3	US-09-949-016-17595	Sequence 17595, A	657	126	7.9	2352	2	US-09-051-363-1	Sequence 1, Appli
585	127.5	7.9	162914	3	US-09-949-016-15578	Sequence 15578, A	658	126	7.9	2523	3	US-10-077-130-3	Sequence 3, Appli
586	127.5	7.9	247299	3	US-09-949-016-17590	Sequence 17590, A	659	126	7.9	7928	5	US-09-548-473B-5	Sequence 5, Appli
587	127	7.9	215	3	US-09-513-999C-2518	Sequence 2518, Ap	660	126	7.9	8106	5	US-10-077-130-1	Sequence 1, Appli
588	127	7.9	601	3	US-09-949-016-57021	Sequence 57021, A	661	126	7.9	16641	3	US-09-949-016-15826	Sequence 15826, A
589	127	7.9	601	3	US-09-949-016-121008	Sequence 121008, A	c 662	126	7.9	26433	3	US-09-949-016-15401	Sequence 15401, A
590	127	7.9	601	3	US-09-949-016-140669	Sequence 140669, A	c 663	126	7.9	31229	3	US-09-949-016-12619	Sequence 12619, A
591	127	7.9	3086	3	US-09-684-708A-20	Sequence 20, Appl	c 664	126	7.9	31229	3	US-09-949-016-15766	Sequence 15766, A
592	127	7.9	3093	3	US-09-949-016-4183	Sequence 4183, Ap	c 665	126	7.9	31231	3		

c 666	126	7.9	44378	3	US-09-949-016-12540	Sequence 12540, A	739	124.5	7.8	14207	3	US-09-949-016-13775	Sequence 13775, A
c 667	126	7.9	62327	3	US-09-949-016-16809	Sequence 16809, A	c 740	124.5	7.8	17132	3	US-09-949-016-15361	Sequence 15361, A
c 668	125.5	7.8	849	3	US-09-915-789A-6	Sequence 6, Appl1	c 741	124.5	7.8	17353	3	US-09-949-016-13437	Sequence 13437, A
669	125.5	7.8	1443	4	US-09-875-338-4	Sequence 4, Appl1	c 742	124.5	7.8	18456	3	US-09-949-016-13952	Sequence 13952, A
670	125.5	7.8	1658	3	US-09-991-181-290	Sequence 290, App	c 743	124.5	7.8	22539	3	US-09-949-016-15931	Sequence 15931, A
671	125.5	7.8	1658	3	US-09-929-769-4	Sequence 4, Appl1	c 744	124.5	7.8	24150	3	US-09-949-016-12438	Sequence 12438, A
672	125.5	7.8	1658	3	US-09-990-444-290	Sequence 290, App	c 745	124.5	7.8	27525	3	US-09-949-016-16835	Sequence 16835, A
673	125.5	7.8	1658	3	US-09-997-333-290	Sequence 290, App	746	124.5	7.8	27702	3	US-09-949-016-11795	Sequence 11795, A
674	125.5	7.8	1658	3	US-09-992-598-290	Sequence 290, App	747	124.5	7.8	27910	3	US-09-949-016-15020	Sequence 15020, A
675	125.5	7.8	1658	4	US-09-989-735-290	Sequence 290, App	748	124.5	7.8	27910	3	US-09-949-016-15021	Sequence 15021, A
676	125.5	7.8	1658	4	US-09-989-726-290	Sequence 290, App	749	124.5	7.8	27910	3	US-09-949-016-15022	Sequence 15022, A
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678	125.5	7.8	1658	5	US-09-989-728-290	Sequence 290, App	751	124.5	7.8	27910	3	US-09-949-016-15024	Sequence 15024, A
679	125.5	7.8	1658	5	US-09-997-349-290	Sequence 290, App	752	124.5	7.8	27910	3	US-09-949-016-15025	Sequence 15025, A
680	125.5	7.8	1658	5	US-09-997-653-290	Sequence 290, App	753	124.5	7.8	39176	3	US-09-949-016-17603	Sequence 17603, A
681	125.5	7.8	1658	5	US-09-989-293A-290	Sequence 290, App	c 754	124.5	7.8	47115	3	US-09-949-016-12278	Sequence 12278, A
682	125.5	7.8	1831	3	US-09-667-135-27	Sequence 27, Appl	c 755	124.5	7.8	47122	3	US-09-949-016-16520	Sequence 16520, A
683	125.5	7.8	2449	3	US-09-949-016-1248	Sequence 1248, Ap	c 756	124.5	7.8	56241	3	US-09-949-016-15174	Sequence 15174, A
684	125.5	7.8	2544	3	US-10-104-047-21	Sequence 21, Appl	c 757	124.5	7.8	56241	3	US-09-949-016-15175	Sequence 15175, A
685	125.5	7.8	2627	3	US-09-404-879A-391	Sequence 391, App	c 758	124.5	7.8	64137	3	US-09-949-016-14831	Sequence 14831, A
686	125.5	7.8	2627	3	US-09-667-857-391	Sequence 391, App	c 759	124.5	7.8	64171	3	US-09-949-016-12502	Sequence 12502, A
687	125.5	7.8	2627	3	US-10-198-053-391	Sequence 391, App	c 760	124.5	7.8	72128	3	US-09-949-016-16018	Sequence 16018, A
688	125.5	7.8	2627	3	US-09-827-271-391	Sequence 391, App	c 761	124.5	7.8	74962	3	US-09-685-853A-3	Sequence 3, Appl1
689	125.5	7.8	5933	3	US-09-383-630-1	Sequence 1, Appl1	c 762	124.5	7.8	74962	3	US-09-949-016-15532	Sequence 15532, A
690	125.5	7.8	5933	3	US-09-383-630-2	Sequence 2, Appl1	c 763	124.5	7.8	767677	3	US-09-949-016-11147	Sequence 12147, A
691	125.5	7.8	13193	3	US-09-949-016-17515	Sequence 17515, A	c 764	124.5	7.8	767677	3	US-09-949-016-17361	Sequence 17361, A
692	125.5	7.8	14079	3	US-09-949-016-11993	Sequence 11993, A	c 765	124	7.7	601	3	US-09-949-016-58383	Sequence 58383, A
693	125.5	7.8	26510	3	US-09-949-016-12408	Sequence 12408, A	766	124	7.7	601	3	US-09-949-016-124515	Sequence 124515, A
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696	125.5	7.8	150394	3	US-09-949-016-13042	Sequence 13042, A	769	124	7.7	1493	2	US-08-752-307B-6	Sequence 6, Appl1
697	125.5	7.8	784019	3	US-09-949-016-14033	Sequence 14033, A	770	124	7.7	1493	3	US-09-707-802-6	Sequence 6, Appl1
698	125.5	7.8	828152	3	US-09-949-016-12777	Sequence 12777, A	771	124	7.7	1493	3	US-09-991-326-6	Sequence 6, Appl1
c 699	125	7.8	601	3	US-09-949-016-125402	Sequence 125402, A	772	124	7.7	1716	2	US-08-147-772-3	Sequence 3, Appl1
c 700	125	7.8	601	3	US-09-949-002-3336	Sequence 3326, Ap	773	124	7.7	1716	2	US-08-456-104-7	Sequence 7, Appl1
c 701	125	7.8	601	3	US-09-949-002-9770	Sequence 9770, Ap	774	124	7.7	1716	2	US-08-101-624-24	Sequence 24, Appl
702	125	7.8	1581	7	PCT-US95-08493-14	Sequence 14, Appl	775	124	7.7	1716	3	US-08-153-262-3	Sequence 3, Appl1
703	125	7.8	2580	7	PCT-US95-08493-18	Sequence 18, Appl	776	124	7.7	1716	3	US-08-479-744A-30	Sequence 30, Appl
704	125	7.8	2604	7	PCT-US95-08493-20	Sequence 20, Appl	777	124	7.7	1716	3	US-08-280-757B-30	Sequence 30, Appl
705	125	7.8	4548	3	US-09-571-479C-5	Sequence 5, Appl1	778	124	7.7	1716	3	US-09-159-135-3	Sequence 3, Appl1
706	125	7.8	5905	3	US-09-949-016-5625	Sequence 5625, Ap	779	124	7.7	1716	3	US-08-205-697A-16	Sequence 16, Appl
707	125	7.8	6218	3	US-09-949-016-706	Sequence 706, App	780	124	7.7	1716	3	US-08-703-525-16	Sequence 16, Appl
708	125	7.8	6384	3	US-09-576-594-724	Sequence 724, App	781	124	7.7	1716	3	US-09-450-798-3	Sequence 3, Appl1
c 709	125	7.8	6384	3	US-09-319-039-279	Sequence 279, App	782	124	7.7	1716	3	US-09-425-762-30	Sequence 30, Appl
710	125	7.8	25656	3	US-09-949-016-13022	Sequence 13022, A	783	124	7.7	1716	3	US-09-837-867A-16	Sequence 16, Appl
711	125	7.8	36542	3	US-09-949-016-12149	Sequence 12149, A	784	124	7.7	1716	3	US-08-453-386A-3	Sequence 3, Appl1
712	125	7.8	36544	3	US-09-949-016-13434	Sequence 13434, A	785	124	7.7	1716	3	US-09-206-132-7	Sequence 7, Appl1
713	125	7.8	37269	3	US-09-949-016-16672	Sequence 16672, A	786	124	7.7	1716	3	US-09-425-516-30	Sequence 30, Appl
c 714	125	7.8	38619	3	US-09-949-002-669	Sequence 669, App	787	124	7.7	1716	7	PCT-US95-02576-16	Sequence 16, Appl
c 715	125	7.8	38619	3	US-09-949-002-833	Sequence 833, App	788	124	7.7	3943	3	US-08-506-296B-27	Sequence 27, Appl
716	125	7.8	43463	3	US-09-949-016-16341	Sequence 16341, A	c 789	124	7.7	21893	3	US-09-949-016-16407	Sequence 16407, A
c 717	125	7.8	46085	3	US-09-949-016-13547	Sequence 13547, A	c 790	124	7.7	26867	3	US-09-949-016-16332	Sequence 16332, A
c 718	125	7.8	46085	3	US-09-949-016-13548	Sequence 13548, A	c 791	124	7.7	26867	3	US-09-949-016-16333	Sequence 16333, A
c 719	125	7.8	52789	3	US-09-949-016-12130	Sequence 12130, A	c 792	124	7.7	28315	3	US-09-949-016-16333	Sequence 16333, A
c 720	125	7.8	52790	3	US-09-949-016-16641	Sequence 16641, A	793	124	7.7	29485	3	US-09-785-381-6	Sequence 6, Appl1
c 721	125	7.8	54000	3	US-09-843-377-11	Sequence 11, Appl	c 794	124	7.7	60489	3	US-09-949-016-16287	Sequence 16287, A
c 722	125	7.8	114793	3	US-10-148-806-3	Sequence 3, Appl1	c 795	124	7.7	68436	3	US-09-949-016-12943	Sequence 12943, A
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c 729	124.5	7.8	601	3	US-09-949-016-148889	Sequence 148889, A	802	124	7.7	325791	3	US-09-768-185A-1	Sequence 1, Appl1
c 730	124.5	7.8	2991	3	US-08-795-430-48	Sequence 48, Appl	803	123.5	7.7	575	3	US-09-385-982-473	Sequence 473, App
c 731	124.5	7.8	2991	3	US-09-355-700-48	Sequence 48, Appl	c 804	123.5	7.7	601	3	US-09-949-016-45626	Sequence 45626, A
c 732	124.5	7.8	2991	3	US-09-534-376A-48	Sequence 48, Appl	805	123.5	7.7	849	3	US-10-198-053-621	Sequence 621, App
733	124.5	7.8	4285	3	US-09-040-774-1	Sequence 1, Appl1	806	123.5	7.7	900	3	US-09-495-052-61	Sequence 61, Appl
734	124.5	7.8	5207	3	US-09-858-664A-1	Sequence 1, Appl1	807	123.5	7.7	1958	10	5169835-1	Patent No. 5169835
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736	124.5	7.8	5207	3	US-10-274-978-3	Sequence 3, Appl1	809	123.5	7.7	3630	3	US-09-312-157-5	Sequence 5, Appl1
737	124.5	7.8	5207	3	US-10-697-263-1	Sequence 1, Appl1	810	123.5	7.7	3630	3	US-09-717-888-5	Sequence 5, Appl1
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834	123	7.7	601	3	US-09-949-016-202731	Sequence 202731, A	907	122.5	7.6	118868	3	US-09-949-016-15746	Sequence 15746, A
835	123	7.7	785	3	US-09-270-767-1269	Sequence 1269, App	908	122.5	7.6	135476	3	US-09-949-016-12611	Sequence 12611, A
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842	123	7.7	2487	2	US-08-261-304-1	Sequence 1, Appl	915	122	7.6	2830	3	US-09-646-561-3	Sequence 3, Appl
843	123	7.7	11437	3	US-09-949-002-587	Sequence 587, App	916	122	7.6	3025	3	US-09-954-556-23	Sequence 23, Appl
844	123	7.7	11589	3	US-09-949-002-826	Sequence 826, App	917	122	7.6	4615	3	US-09-949-016-15282	Sequence 15282, A
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858	123	7.7	161607	3	US-09-949-016-12110	Sequence 12110, A	931	122	7.6	79351	3	Sequence 12675, A	Sequence 12675, A
859	123	7.7	194915	3	US-09-949-016-15584	Sequence 15584, A	932	122	7.6	80357	3	Sequence 13572, A	Sequence 13572, A
860	123	7.7	198632	3	US-09-949-016-12781	Sequence 12781, A	933	122	7.6	80357	3	Sequence 13747, A	Sequence 13747, A
861	123	7.7	198637	3	US-09-949-016-17393	Sequence 17393, A	934	122	7.6	85963	3	Sequence 13804, A	Sequence 13804, A
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874	122.5	7.6	601	3	US-09-949-016-127033	Sequence 127033, A	947	122	7.6	275110	3	Sequence 16070, A	Sequence 16070, A
875	122.5	7.6	601	3	US-09-949-016-127034	Sequence 127034, A	948	121.5	7.6	415	3	US-09-736-457-435	Sequence 435, App
876	122.5	7.6	601	3	US-09-949-016-135192	Sequence 135192, A	949	121.5	7.6	415	3	US-09-614-124B-435	Sequence 435, App
877	122.5	7.6	601	3	US-09-949-016-141281	Sequence 141281, A	950	121.5	7.6	415	3	US-09-736-457-435	Sequence 435, App
878	122.5	7.6	601	3	US-09-949-016-141282	Sequence 141282, A	951	121.5	7.6	415	3	US-09-614-124B-435	Sequence 435, App
879	122.5	7.6	1714	3	US-09-949-016-141282	Sequence 141282, A	952	121.5	7.6	415	3	US-09-589-184-435	Sequence 435, App
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882	122.5	7.6	1714	4	US-09-978-189-84	Sequence 84, Appl	955	121.5	7.6	415	3	US-10-017-754-435	Sequence 435, App
883	122.5	7.6	1714	5	US-10-017-085A-84	Sequence 84, Appl	956	121.5	7.6	415	3	US-09-651-563-435	Sequence 435, App
884	122.5	7.6	1714	5	US-10-145-129A-84	Sequence 84, Appl	957	121.5	7.6	415	3	US-09-519-642-435	Sequence 435, App
					US-10-013-929A-84	Sequence 84, Appl						US-09-949-016-86063	Sequence 86063, A

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1116	120	7.5	3944	3	US-09-949-016-1879	Sequence 1879, Ap	c1189	119.5	7.4	46940	3	US-09-949-016-16252	Sequence 16252, A
1117	120	7.5	3944	3	US-09-949-016-1880	Sequence 1880, Ap	c1190	119.5	7.4	54161	3	US-09-949-016-11905	Sequence 11905, A
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1137	120	7.5	53332	3	US-09-801-861-3	Sequence 3, Appl	1210	119.5	7.4	601	3	US-09-949-016-154185	Sequence 154185, A
1138	120	7.5	53332	3	US-10-224-562-3	Sequence 3, Appl	1211	119.5	7.4	601	3	US-09-949-016-161295	Sequence 161295, A
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1140	120	7.5	59977	3	US-09-949-016-12259	Sequence 12259, A	c1213	119.5	7.4	601	3	US-09-949-016-195490	Sequence 195490, A
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1142	120	7.5	79988	3	US-09-949-016-12274	Sequence 12274, A	1215	119.5	7.4	1452	3	US-09-949-016-5250	Sequence 5250, Ap
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[illegible]

! TYPE: DNA
! ORGANISM: Homo sapiens
US-09-905-125A-63

Alignment Scores:
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US-10-785-221-9 (1-312) x US-09-905-125A-63 (1-1295)

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Qy 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
Db 449 CTGGAGAGGATACAGTCACTCTGGAAGTATTTAGTGGCTCCAGCAGTTCATCATGTAA 508
Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
Db 509 GTACCTCTCTGCTCTGAGTGAAGTCTGTGAGAGCTAGATGTCAGACAAAGAGGG 568
Qy 161 AsnProAlaProGluTyrThrTrpPheLysAspGlyIleArgLeuLeuGluAenProArg 180
Db 569 AATCCAGCTCTCAATACACATGTTTAAAGGATGGCATCGTTTGTAGAAAATCCACA 628
Qy 181 LeuGlySerGlnSerThrAenSerSerTyrThrMetAsnThrLysThrGlyThrLeuGln 200
Db 629 CTTGGCTCCCAAGACCAACAGCTCATACACAATGAATACAAAACTGGAACTCTGCAA 688
Qy 201 PheAsnThrValSerLysLeuAspThrGlyGluTyrSerCysGluAlaArgAenSerVal 220
Db 689 TTTAACTGTTTCCAACTGGACACTGGAGAAATATCTCTGGAAGCCCGCAATCTGT 748
Qy 221 GlyTyrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
Db 749 GGATATCGCAGGTGCTCTGGAAACCAATGCAAGTAGATGATCTCAACATAAGTGGCATC 808
Qy 241 IleAlaValValValValAlaLeuValIleSerValCysGlyLeuGlyValCysTyr 260
Db 809 ATAGCAGCGCTAGTAGTTGGGCTTTAGTGATTTCCGTTTGTGGCCTTGTGTATGCTAT 868
Qy 261 AlaGlnArgLysGlyTyrPheSerLysGluThrSerPheGlnLysSerAenSerSer 280
Db 869 GCTCAGAGGAAGGCTACTTTTCAAAGAAACCTCTCTCCAGAAAGTAGTAATCTTCATCT 928
Qy 281 LysAlaThrThrMetSerGluAenValGlnTrpLeuThrProValIleProAlaLeuTrp 300
Db 929 AAAGCCACGACATGATGAAATGTGCAGTGGCTCAGCGCTGTAAATCCAGCAGCTTTGG 988

Qy 301 LysAlaAlaAlaGlyGlySerArgGlyGlnGluPhe 312
Db 989 AAGGCCGCGCGCGGATCACGAGTCCAGGAGTTC 1024

RESULT 4

US-09-902-775A-63
; Sequence 63, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219


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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-63

Alignment Scores:
Pred. No.: 1.6e-183 Length: 1295
Score: 1605.00 Matches: 312
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-785-221-9 (1-312) x US-09-902-775A-63 (1-1295)

Qy 1 MetAlaArgSerArgHisArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuValAla 20
Db 89 ATGCGAGGAGGAGCGCCACCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
Qy 21 LeuGlyThrHisLysAlaLysArgPheSerAlaProLysAspGlnGlnValThrAla 40
Db 149 CTGGGCTATCATAGGCTATGGGTTTTCTGCCCAAAAGACCAACCAAGTAGTCACAGCA 208
Qy 41 ValGluThrGlnGluAlaLeuAlaCysLysThrProLysLysThrValSerSerArg 60
Db 209 GTAGAGTACCAAGAGGCTATTTAGCTGCAAAACCCCAAGAAAGACTGTTTCTCCAGA 268
Qy 61 LeuGluThrLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
Db 269 TTAGAGTGGAAAGAACTGGGTGCGAGTGCTCTCTTTGCTACTATCAACAGACTCTTCAA 328
Qy 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgLleLysAsnValThr 100
Db 329 GGTGATTTTAAAAATCAGAGCTGAGATGATAGATTCAATATCCGATCAAAAATGTGACA 388
Qy 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlyAsn 120
Db 389 AGAAGTATCGGGGAATATCGTGTGAAGTTAGTGCCCTATGAGCAAGGCCAAAC 448
Qy 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
Db 449 CTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCATCATGTGAA 508
Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
Db 509 GTACCTCTTCTGCTCTGAGTGGAACTGTGTAGAGCTACGATGTCAGACAAAGAGGG 568
Qy 161 AsnProAlaProGluTyrThrTrpPheLysAspGlyIleArgLeuLeuGluAsnProArg 180
Db 569 AATCAGCTCTGTAATACATGTTTAAAGATGGCATCCGTTTGTAGAAATATCCAGA 628
Qy 181 LeuGlySerGlnSerThrAsnSerSerTyrThrMetAsnThrLysThrGlyThrLeuGln 200
Db 629 CTTGGCTCCCAAGCACCAACAGCTCATACACATGAATACAAAATCGAATCTGCAA 688
Qy 201 PheAsnThrValSerLysLeuAspThrGlyLysTyrSerCysGluAlaArgAsnSerVal 220
Db 689 TTTAATACTGTTTCCAAACTGGACACTGGAGATATTCTGTGAAGCCCGCAATTCGTGT 748
Qy 221 GlyTyrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
Db 749 GGATATCGCAGGTGCTCGGGAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATC 808
Qy 241 IleAlaAlaValValValAlaLeuValIleSerValCysGlyLeuGlyValCysTyr 260
Db 809 ATACACCGGTAGTAGTTGTGGCCCTTAGTGATTTCCGTTTGTGGCCCTGGTGTATGCTAT 868
Qy 261 AlaGlnArgLysGlyTyrPheSerLysGluThrSerPheGlnLysSerAsnSerSer 280
Db 869 GCTCAGAGGAAGGCTACTTTTCAAAAGAAACCTCTCTCCAGAGAGAGTAAATCTTCATCT 928
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Qy 281 LyeAlaThrThrMetSerGluAsnValGlnTrpLeuThrProValIleProAlaLeuTrp 300
Db 929 AAAGCCACGACAAATGAGTGAATAATGTGCAGTGGCTCAGCGCTGTATATCCAGCACTTTGG 988
Qy 301 LyeAlaAlaAlaGlyLysArgGlyGlnGluPhe 312
Db 989 AAGCGCGCGCGCGCGGATCAGGAGGTCCAGAGTTC 1024

RESULT 5
US-09-906-700-63
; Sequence 63, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-906-700-63

Alignment Scores:
Pred. No.: 1,6e-183 Length: 1295
Score: 1605.00 Matches: 312
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-785-221-9 (1-312) x US-09-906-700-63 (1-1295)

QY 1 MetAlaArgSerArgHisArgLeuLeuLeuLeuLeuLeuLeuValValAla 20
DB 89 ATGGCGAGGAGGAGCGCCACCGCTCTCTGCTGCTGCTGCTGCTGCTGCTG 148
QY 21 LeuGlyTyrHisLysAlaTyrGlyPheSerAlaProLysAspGlnGlnValThAla 40
DB 149 CTGGGCTATCATAGGCTATGGTCTTCTGCCCAAGACCAACAAGTAGTCACAGCA 208
QY 41 ValGluTyrGlnGluAlaLeuAlaCysLysThrProLysLysThrValSerSerArg 60
DB 209 GTAGAGTACCAAGAGGCTATTTAGGCTGCAAAACCCCAAGAAAGACTGTTCCTCCAGA 268
QY 61 LeuGluTyrLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
DB 269 TTAGAGTGGAGAAACTGGGTGGAGTGCTCTCTTTGCTCTACTATCAACAGACTCTTCAA 328
QY 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
DB 329 GGTGATTTAAATAATCGAGCTGAGATGATAGATTTCATATCCGATCAAAATGTGACA 388
QY 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlnAan 120
DB 389 AGAAGTGATCGGGGAAATATCGTTGTGAAGTTAGTGCCCATCTGAGCAAGGCCAAAC 448
QY 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
DB 449 CTGGAAGAGGATACAGTCACTCTGGAGATATTAGTGGCTCCAGCAGTTCCATCATGTGAA 508
QY 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
DB 509 GTACCTCTCTCTCTGAGTGAACTGTGGTAGAGTACGATGTCAAGACAAAGAGGG 568
QY 161 AsnProAlaProGluTyrThrTrpPheLysAspGlyIleArgLeuLeuGluAanProArg 180
DB 569 AATCCAGCTCTCTGAATACATCGTTTAAAGGATGGCATCCGTTGTGTAGAAAATCCAGA 628
QY 181 LeuGlySerGlnSerThrAsnSerSerTyrThrMetAsnThrLysThrGlyThrLeuGln 200
DB 629 CTTGGCTCCCAAGACCAACAGCTCATACACATGATGATCAAAAACTGGAACTCTGCAA 688
QY 201 PheAsnThrValSerLysLeuAspThrGlyGluTyrSerCysGluAlaArgAsnSerVal 220
DB 689 TTTAATACTGTTTCCAAACTGGACACTGGAGATATTCTCTGTGAAGCCCGCAATTCGTGT 748
QY 221 GlyTyrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
DB 749 GGATATCGCAGGTTCTCTCGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATC 808
QY 241 IleAlaAlaValValValValAlaLeuValIleSerValCysGlyLeuGlyValCysTyr 260
DB 809 ATAGCAGCCGTAGTTGTGGCTTAGTGATTTCCGTTTGTGGCTTGTGTATGCTAT 868
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QY 261 AlaGlnArgLysGlyTyrPheSerLysGluThrSerPheGlnLysSerAsnSerSerSer 280
DB 869 GCTCAGAGAAAGGCTACTTTTCAAAGAAACCTCTTCCAGAAAGATATTTCTCATCT 928
QY 281 LysAlaThrThrMetSerGluAanValGlnThrLeuThrProValIleProAlaLeuTyr 300
DB 929 AAAGCCACGACATGAGTGAAAATGTGCAGTGGCTCAGCGCTGTATCCAGCAGCTTGG 988
QY 301 LysAlaAlaAlaGlyGlySerArgGlyGlnGluPhe 312
DB 989 AAGGCCGCGCGCGCGGATCAGAGGTCAGGAGTTC 1024

RESULT 6
US-09-903-603A-63
; Sequence 63, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; PRIOR FILING DATE: 2001-07-11
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-903-603A-63

Alignment Scores:
Pred. No.: 1.6e-183 Length: 1295
Score: 1605.00 Matches: 312
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-785-221-9 (1-312) x US-09-903-603A-63 (1-1295)

Qy 1 MetAlaArgSerArgHisArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuValVala 20
Db 89 ATGCGAGAGAGAGCGCCGCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
Qy 21 LeuGlyTyrHisLysAlaTyrGlyPheSerAlaProLysAspGlnGlnValValThrAla 40
Db 149 CTGGGCTATCATAGGCTATGGTCTTCTGCCCCCAAGACCAACCAAGTAGTCACAGCA 208
Qy 41 ValGluTyrGlnGluAlaLeuLeuAlaCysLysThrProLysLysThrValSerSerArg 60
Db 209 GTAGAGTACCAAGAGGCTATTATTAGCTGCGCAAAACCCCAAGAAAGACTGTTTCTCTCCAGA 268
Qy 61 LeuGluTrpLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
Db 269 TTAGAGTGGAAAGAACTGGGTCGGAGTGTCTCTTGTGTACTATCAACAGACTCTTCAA 328
Qy 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
Db 329 GGTGATTTTAAATATCGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 388
Qy 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlnAsn 120
Db 389 AGAAGTGTATGCGGGAATATCGTTGTGAAAGTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 448
Qy 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
Db 449 CTGGAAGAGGATACAGTCACTCTGGAAGATATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 508
Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
Db 509 GTACCTCTTCTGCTGAGTGGAACTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 568
Qy 161 AsnProAlaProGluTyrThrTyrPheLysAspGlyIleArgLeuLeuGluAsnProArg 180
Db 569 AATCAGCTCTGAATACACATCGTTTAAAGATGGCATCCGTTTGTAGTAAATATCCAGA 628
Qy 181 LeuGlySerGlnSerThrAsnSerSerTyrThrMetAsnThrLysThrGlyThrLeuGln 200
Db 629 CTTGGCTCCCAAGACCAACAGCTCATACAAATGAAATACAAAATATGGAATCTGCA 688
Qy 201 PheAsnThrValSerLysLeuAspThrGlyGluTyrSerCysGluAlaArgAsnSerVal 220
Db 689 TTTAATACTGTTTCAAACTGGACACTGGAGAAATATCTCTGTAAGCCCGCAATCTGTT 748
Qy 221 GlyTyrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
Db 749 GGATATCGCAGTGTCTCTGGGAACGAATGCAAGTAGATGATCTCAACATAGTGGCATC 808
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241 IleAlaAlaValValValValValValValValValValValValValValValValValValValVal 260
Db 809 ATAGCAGCCGTAGTAGTTGGCCTTAGTAGTTCCGTTTGTGGCCTTGGTGTATGCTAT 868
Qy 261 AlaGlnArgLysGlyTyrPheSerLysGluThrSerPheGlnLysSerAsnSerSerSer 280
Db 869 GCTCAGAGGAAGGCTACTATTTTCAAAAGAAACCTCTTCCAGAGAGAGTAATTTCTTCATCT 928
Qy 281 LysAlaThrThrMetSerGluAsnValGlnTrpLeuThrProValIleProAlaLeuTrp 300
Db 929 AAGCCACGACAATGAGTGAATGTCAGTGGCTCAGCTGTATATCCCGACACTTGG 988
Qy 301 LysAlaAlaAlaGlyGlySerArgGlyGlnGluPhe 312
Db 989 AAGGCCGCGCGCGCGGATCACGAGGTTCAGAGTTC 1024

RESULT 7
US-09-904-920A-63
; Sequence 63, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-920A-63

Alignment Scores:
Pred. No.: 1.6e-183 Length: 1295
Score: 1605.00 Matches: 312
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-785-221-9 (1-312) x US-09-904-920A-63 (1-1295)

Qy 1 MetAlaArgSerArgHisArgLeuLeuLeuLeuLeuLeuLeuLeuLeuValAla 20
Db 89 ATGGCGAGGAGGAGCGCCACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGCC 148

Qy 21 LeuGlyTyRHisLysAlaTyRGLyPheSerAlaProLysAspGlnGlnValThraLa 40
Db 149 CTGGGCTATCATAGGCGCTATGGTTTCTGCCCAAGAACCCAAAGACCAACAGTAGTACAGCA 208

Qy 41 ValGluTyRGLnGluAlaLeuLeuAlaCysLysThrProLysLysThrValSerSerArg 60
Db 209 GTAGAGTACCAGAGGCTATTTAGCTCGCAAAACCCCAAGAAAGACTGTTCTCTCAGA 268

Qy 61 LeuGluTrpLysLysLeuGlyArgSerValSerPheValTyRtyrGlnGlnThrLeuGln 80
Db 269 TTAGAGTGGGAAGAAACTGGGTCGGAGTGTCTCTTTGTCTACTATCAACAGACTCTTCAA 328

Qy 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
Db 329 GGTGATTTTAAATTCAGCTGAGATGATAGATTTCATATCCGGATCAAAATGTGACA 388

Qy 101 ArgSerAspAlaGlyLysTyRArgCysGluValSerAlaProSerGluGlnGlyGlnAsn 120
Db 389 AGAAGTGATCGGGGAAATATCTGTGAAGTGTAGTGCCCATCTGAGCAAGGCCAAAC 448

Qy 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProLysCysGlu 140
Db 449 CTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGCTCCACAGTTCATCATGTGAA 508

Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
Db 509 GTACCTCTCTCTCTCTGAGTGAGACTGTGTGTAGAGTACGATGTCAAGCAAGAGGG 568

Qy 161 AsnProAlaProGluTyRThrTrpPheLysAspGlyIleArgLeuLeuGluAsnProArg 180
Db 569 AATCCAGCTCTGAATACATCGTTTAAAGATGGCATCGTTTGTAGAAAATCCAGA 628

Qy 181 LeuGlySerGlnSerThrAsnSerSerTyRThrMetAsnThrLysThrGlyThrLeuGln 200
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Qy 201 PheAsnThrValSerLysLeuAspThrGlyGlyTyR-SerCysGluAlaArgAsnSerVal 220
Db 689 TTTAATACTGTTTCCAAACTGGACACTGGAGATATCTCTGTGAAGCCCGCAATCTGTT 748

Qy 221 GlyTyRArgArgCysProGlyLysArgMetGlnValAspLeuAsnIleSerGlyIle 240
Db 749 GGATATCGCAGGTGCTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATC 808

Qy 241 IleAlaAlaValValValValAlaLeuValIleSerValCysGlyLeuGlyValCysTyR 260
Db 809 ATAGCAGCGGTAGTAGTTGTGGCCTTAGTGATTTCGGTTTGGCTTGGTGTATGCTAT 868

Qy 261 AlaGlnArgLysGlyTyRPheserLysGluThrSerPheGlnLysSerAsnSerSer 280
Db 869 GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCTCTCCAGAGAGTAAATCTTCATCT 928

Qy 281 LysAlaThrThrMetSerGluAsnValGlnTrpLeuThrProValIleProAlaLeuTrp 300
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Qy 301 LysAlaAlaAlaGlyLysSerArgGlyGlnGluPhe 312
Db 989 AAGGCGCGCGCGCGGATCACAGGTCAGGAGTTC 1024

RESULT 8
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; Sequence 63, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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; PRIOR FILING DATE: 1999-09-15
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; PRIOR FILING DATE: 1999-09-15
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-905-381A-63

Alignment Scores:
Pred. No.: 1 6e-183 Length: 1295
Score: 1605.00 Matches: 312
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-785-221-9 (1-312) x US-09-905-381A-63 (1-1295)

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Db 89 ATGGCGAGGAGGAGCGCCACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 148
Qy 21 LeuGlyTyHisLysAlaTyGlyPheSerAlaProLysAspGlnGlnValThAla 40
Db 149 CTGGGCTATCATAGGCTATGGGTTTTCTGCCCAAAAGACCAACAAGTAGTCACAGCA 208
Qy 41 ValGluTyGlnGluAlaLeuAlaCysLysThrProLysLysThrValSerSerArg 60
Db 209 GTAGAGTACCAAGAGGCTATTTTAGGCTGCAAAACCCCAAGAAAGACTGTTTCTCCAG 268
Qy 61 LeuGluTrpLysLysLeuGlyArgSerValSerPheValTyTyGlnGlnThrLeuGln 80
Db 269 TTAGAGTGGGAAGAACTGGGTCGGAGTGCTCTCTTTGTCTACTATCAACAGACTCTTCAA 328
Qy 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
Db 329 GGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCATATCCGATCAAAAATGTGACA 388
Qy 101 ArgSerAspAlaGlyLysTyArgCysGluValSerAlaProSerGluGlnGlnAen 120
Db 389 AGAAGTGATCGGGGAAATATCGTTGTGAAGTTAGTGCCCTCTGAGCAAGGCCAAAC 448
Qy 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
Db 449 CTGGAAGAGGATACAGTCACTCTGGAAGATTAGTGGCTCCAGCACTTCCATCATGTGAA 508
Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
Db 509 GTACCCCTCTCTGCTCTGAGTGAACTGTGTGTAGAGTACGATGTCAAGACAAAGAGGG 568
Qy 161 AsnProAlaProGluTyThrTrpPheLysAspGlyIleArgLeuLeuGluAsnProArg 180
Db 569 AATCCAGCTCCTGAATACATCGTTTAAAGATGGCATCCGTTTGTCTGAAATATCCAGA 628
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Qy 201 PheAsnThrValSerLysLeuAspThrGlyGluTySerCysGluAlaArgAenSerVal 220
Db 689 TTTAATACTGTTTCCAACTGGACACTGGAGAAATATCTCTGTGAAGCCCGCAATCTGTT 748
Qy 221 GlyTyArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
Db 749 GGATATCGCAGGTGCTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATC 808
Qy 241 IleAlaAlaValValValAlaLeuValIleSerValCysGlyLeuGlyValCysTy 260
Db 809 ATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTGTGGCCTTGTGTATGCTAT 868
Qy 261 AlaGlnArgLysGlyTyPheSerLysGluThrSerPheGlnLysSerAsnSerSer 280
Db 869 GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCTTCCAGAGAGTAATTTCTTCATCT 928
Qy 281 LysAlaThrThrMetSerGluAsnValGlnTrpLeuThrProValIleProAlaLeuTrp 300
Db 929 AAAGCCACGACAATGAGTGAAATGTCAGTGGCTCACGCTGTAAATCCAGCAGCTTTGG 988
Qy 301 LysAlaAlaAlaGlySerArgGlyGlnGluPhe 312
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RESULT 10
US-09-906-618-63
; Sequence 63, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-462-63

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Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-785-221-9 (1-312) x US-09-904-462-63 (1-1295)

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QY 21 LeuGlyTyrHisIysAlaTyrGlyPheSerAlaProIysAspGlnGlnValThrAla 40
DB 149 CTGGGCTATCATAGGCGCTATGTTCTGCCCAAAAGACCAACAGTAGTCACAGCA 208
QY 41 ValGluTyrGlnGluAlaIleLeuAlaCysLysThrProIysLysThrValSerSerArg 60
DB 209 GTAGAGTACCAAGAGGCTATTTAGCTGCGCAAAACCCCAAGAGACTGTTCTCCAGA 268
QY 61 LeuGluTrpLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
DB 269 TTAGAGTGGGAAGAACTGGGTCGGAGTGCTCTCTGTTGTCTACTATCAACAGACTCTTCAA 328
QY 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
DB 329 GGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCGGATCAAAAATGTGACA 388
QY 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlyGlnAsn 120
DB 389 AGAAGTGATGCGGGGAANAATCGTTGTGAAGTTAGTGCCCATCTGAGCAGGCCAAAC 448
QY 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
DB 449 CTGGAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCATCATGTGAA 508
QY 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
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QY 181 LeuGlySerGlnSerThrAsnSerSerTyrThrMetAsnThrLysThrGlyThrLeuGln 200
DB 629 CTTGGCTCCCAAGACCAACAGCTCATACACAATGAATACAAAACCTGGAACTCTGCAA 688
QY 201 PheAsnThrValSerLysLeuAspThrGlyGluTyrSerCysGluAlaArgAsnSerVal 220
DB 689 TTTAAATACTGTTTCCAAACTGGACACTGGAGAAATATTCCTGTGAAGCCCGCAATCTGT 748
QY 221 GlyTyrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
DB 749 GGATATCGCAGGCTCTCTGGGAACCAANTGCAAGTAGATGATCTCAACATAGTGCATC 808
QY 241 IleAlaAlaValValValAlaLeuValIleSerValCysGlyLeuGlyValCysTyr 260
DB 809 ATAGCAGCGGTAGTAGTTGGGCTTTAGTGAATTTTCGTTTGTGGCTTGTGTATGCTAT 868
QY 261 AlaGlnArgLysGlyTyrPheSerLysGluThrSerPheGlnLysSerAsnSerSerSer 280
DB 869 GCTCAGAGGAAGGCTACTTTTCAAAAGAAACCTCTCTCCAGAAGAGTAGTAATTTCTCAT 928
QY 281 LysAlaThrThrMetSerGluAsnValGlnTrpLeuThrProValIleProAlaLeuTrp 300
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; Sequence 63, Application US/09902736A
; Patent No. 6894148
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,736A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
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[illegible]

GenCore version 5.1.8
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Run on: May 17, 2006, 16:49:09 ; Search time 1354 Seconds
(without alignments)
4247.129 Million cell updates/sec

Title: US-10-785-221-9

Perfect score: 1605

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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 63, Appl					

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342	1605	100.0	1295	7	US-10-265-542-8	Sequence 8, Appl
357	1605	100.0	1295	7	US-10-299-976-63	Sequence 63, Appl
372	1605	100.0	1295	7	US-10-299-937-63	Sequence 63, Appl
499	1605	100.0	1295	7	US-10-298-993-63	Sequence 63, Appl
501	1605	100.0	1295	7	US-10-448-923-63	Sequence 63, Appl
502	1605	100.0	1295	7	US-10-449-656-63	Sequence 63, Appl
503	1605	100.0	1295	7	US-10-448-713-63	Sequence 63, Appl
506	1605	100.0	1295	8	US-10-425-447-63	Sequence 63, Appl
516	1605	100.0	1295	8	US-10-633-008-8	Sequence 8, Appl
518	1605	100.0	1295	8	US-10-215-371-63	Sequence 63, Appl
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520	1605	100.0	1295	8	US-10-785-221-8	Sequence 8, Appl
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1161	456.5	28.4	933	10	US-10-481-090A-6	Sequence 6, Appli
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1164	408	25.4	1894	3	US-09-764-853-94	Sequence 94, Appl
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1166	405	25.2	1421	6	US-10-152-661-70	Sequence 70, Appl
1167	404	25.2	900	10	US-10-481-090A-4	Sequence 4, Appli
1168	404	25.2	1421	3	US-09-866-050A-254	Sequence 254, App
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OM protein - nucleic search, using frame_plus_p2n model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	166.5	10.4	1329	7	US-11-246-999-137
4	157.5	9.8	1520	7	US-11-246-999-21
5	155.5	9.7	1508	7	US-11-246-999-28
6	146	9.1	3464	6	US-10-505-928-161
8	142	8.8	534	7	US-11-301-554-1325
9	142	8.8	2008	7	US-11-246-999-26
10	139	8.7	1386	7	US-11-246-999-118
11	139	8.7	1833	7	US-11-246-999-117
					Sequence 137, App
					Sequence 149, App
					Sequence 137, App
					Sequence 21, App
					Sequence 28, App
					Sequence 161, App
					Sequence 1325, App
					Sequence 26, App
					Sequence 118, App
					Sequence 117, App

Sequence 83, Appl
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Sequence 19, Appl
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Sequence 3, Appl
Sequence 665, App
Sequence 5, Appl
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Sequence 103, App
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Sequence 343, App
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Sequence 354, App
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95	97	6.0	3042	7	US-11-217-529-82534	Sequence 82534, A	177	83	5.2	720	7	US-11-211-917-55	Sequence 55, Appl
96	97	6.0	4987	6	US-10-505-928-433	Sequence 433, App	178	83	5.2	1237	6	US-10-511-937-430	Sequence 430, App
97	97	6.0	4987	7	US-11-251-465-4	Sequence 4, Appli	179	83	5.2	1362	6	US-10-981-300-15	Sequence 15, Appl
98	97	6.0	5014	7	US-11-251-465-5	Sequence 5, Appli	180	83	5.2	1398	7	US-11-211-917-37	Sequence 37, Appl
99	97	6.0	5522	7	US-11-181-115-15	Sequence 15, Appl	181	83	5.2	1410	7	US-11-211-917-53	Sequence 53, Appl
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102	96	6.0	1401	7	US-11-211-917-29	Sequence 29, Appl	183	83	5.2	1413	7	US-11-211-917-66	Sequence 5, Appli
103	96	6.0	1401	7	US-11-211-917-69	Sequence 69, Appl	184	83	5.2	1416	7	US-11-211-917-45	Sequence 45, Appl
104	96	6.0	1401	7	US-11-211-917-85	Sequence 85, Appl	185	83	5.2	1416	7	US-11-211-917-13	Sequence 13, Appl
C 106	96	6.0	3624	6	US-10-370-959-79	Sequence 79, Appl	186	83	5.2	1425	7	US-11-211-917-13	Sequence 368, App
C 107	96	6.0	3646	6	US-10-511-937-358	Sequence 358, App	187	83	5.2	1776	6	US-10-505-928-368	Sequence 750, App
C 108	96	6.0	4291	6	US-10-509-131-42	Sequence 42, Appl	C 188	83	5.2	6450	6	US-10-505-928-750	Sequence 572, App
C 109	96	6.0	15314	6	US-10-501-834-218	Sequence 218, App	190	82	5.1	1575	6	US-10-511-937-572	Sequence 52, Appl
C 110	95.5	6.0	347	6	US-10-505-928-440	Sequence 440, App	191	82	5.1	2234	1	US-09-949-925-52	Sequence 52, Appl
111	95.5	6.0	3189	6	US-10-511-937-352	Sequence 352, App	192	82	5.1	5515	6	US-10-524-021-1	Sequence 1, Appli
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113	94.5	5.9	1192	1	US-09-949-925-66	Sequence 66, Appl	C 193	82	5.1	6528	6	US-10-505-928-781	Sequence 781, App
C 114	94.5	5.9	3845	6	US-10-505-928-76	Sequence 76, Appl	C 194	82	5.1	9209	7	US-11-183-218-58	Sequence 58, Appl
C 115	94	5.9	6163	6	US-10-524-021-9	Sequence 9, Appli	195	82	5.1	591	7	US-11-305-447-10	Sequence 10, Appl
116	93	5.8	1395	7	US-11-211-917-21	Sequence 21, Appl	C 197	81	5.0	260	7	US-11-301-554-1208	Sequence 1208, Ap
117	93	5.8	5994	6	US-10-505-928-701	Sequence 701, App	198	81	5.0	516	7	US-11-305-447-12	Sequence 12, Appl
118	92.5	5.8	1330	6	US-10-981-300-19	Sequence 19, Appl	199	81	5.0	720	7	US-11-211-917-7	Sequence 7, Appli
119	92	5.7	2838	6	US-10-505-928-697	Sequence 697, App	200	81	5.0	720	7	US-11-211-917-39	Sequence 39, Appl
120	91	5.7	1076	1	US-09-949-925-25	Sequence 25, Appl	201	81	5.0	2271	6	US-10-505-928-792	Sequence 792, App
C 121	91	5.7	5047	6	US-10-505-928-575	Sequence 575, App	202	81	5.0	3475	6	US-10-511-937-399	Sequence 399, App
C 122	91	5.7	7758	6	US-10-505-928-236	Sequence 236, App	203	80.5	5.0	1120	7	US-11-326-148-3	Sequence 3, Appli
C 123	90.5	5.6	4086	7	US-11-301-554-1801	Sequence 1801, Ap	204	80.5	5.0	1632	7	US-11-257-581-16	Sequence 16, Appl
124	90	5.6	545	6	US-10-473-173-146	Sequence 146, App	205	80.5	5.0	232	7	US-11-217-529-81083	Sequence 81083, A
C 125	90	5.6	561	7	US-11-301-554-72	Sequence 72, Appl	206	80.5	5.0	2781	6	US-10-511-937-470	Sequence 470, App
C 126	90	5.6	10905	6	US-10-505-928-568	Sequence 568, App	C 207	80	5.0	403	6	US-10-488-619-441	Sequence 441, App
127	89.5	5.6	3223	7	US-11-312-797-3	Sequence 3, Appli	208	80	5.0	558	7	US-11-301-554-554	Sequence 554, App
128	89.5	5.6	3786	6	US-10-473-173-28	Sequence 28, Appl	209	80	5.0	720	7	US-11-211-917-31	Sequence 31, Appl
129	89	5.5	386	7	US-11-301-554-1620	Sequence 1620, Ap	210	80	5.0	720	7	US-11-211-917-63	Sequence 63, Appl
130	89	5.5	396	6	US-10-511-937-533	Sequence 533, App	211	80	5.0	887	6	US-10-511-937-350	Sequence 101, App
131	88.5	5.5	4500	7	US-11-283-522-8	Sequence 8, Appli	212	80	5.0	1593	7	US-11-257-581-18	Sequence 18, Appl
132	88.5	5.5	1944	7	US-11-217-529-81725	Sequence 81725, A	213	80	5.0	2798	7	US-11-145-307A-179	Sequence 179, App
133	88.5	5.5	3912	6	US-10-518-039-3	Sequence 3, Appli	214	80	5.0	3165	7	US-11-217-529-75763	Sequence 75763, A
134	88.5	5.5	4173	6	US-10-518-039-4	Sequence 4, Appli	215	80	5.0	3178	6	US-10-505-928-277	Sequence 277, App
135	88.5	5.5	6243	6	US-10-518-039-2	Sequence 2, Appli	C 216	80	5.0	3985	7	US-11-255-147-7	Sequence 7, Appli
136	88.5	5.5	6843	6	US-10-518-039-1	Sequence 1, Appli	217	80	5.0	15456	7	US-11-324-284-23	Sequence 23, Appl
C 137	88	5.5	1198	7	US-11-305-447-1	Sequence 1, Appli	219	80	5.0	1285	6	US-10-511-937-455	Sequence 455, App
C 141	88	5.5	1198	7	US-11-305-447-3	Sequence 3, Appli	220	79.5	5.0	1632	7	US-11-257-581-15	Sequence 15, Appl
142	88	5.5	42939	7	US-11-284-877-17	Sequence 17, Appl	221	79.5	5.0	2530	6	US-10-505-928-256	Sequence 256, App
143	87	5.4	461	7	US-11-301-554-884	Sequence 884, App	222	79.5	5.0	720	7	US-11-211-917-79	Sequence 79, Appl
C 144	87	5.4	7391	6	US-10-511-937-629	Sequence 629, App	223	79	4.9	1182	6	US-10-511-937-375	Sequence 375, App
C 145	87	5.4	70655	6	US-10-505-928-596	Sequence 596, App	224	79	4.9	1182	6	US-10-511-937-446	Sequence 446, App
C 146	86.5	5.4	1701	7	US-11-106-762-10	Sequence 10, Appl	225	79	4.9	1182	6	US-10-511-937-2877	Sequence 2877, Ap
147	86	5.4	1629	6	US-10-511-937-444	Sequence 444, App	226	79	4.9	1594	6	US-10-505-928-252	Sequence 252, App
C 148	86	5.4	2401	7	US-11-145-307A-258	Sequence 258, App	227	79	4.9	1723	6	US-10-511-937-606	Sequence 606, App
C 149	86	5.4	10905	6	US-10-505-928-568	Sequence 568, App	228	79	4.9	2649	7	US-11-242-505A-46	Sequence 46, Appl
150	85.5	5.3	1632	7	US-11-257-581-17	Sequence 17, Appl	229	79	4.9	2649	7	US-11-242-505A-47	Sequence 47, Appl
C 152	85.5	5.3	1768	7	US-11-101-316-113	Sequence 113, App	230	79	4.9	4204	6	US-10-505-928-760	Sequence 760, App
C 153	85	5.3	1143	6	US-10-511-937-377	Sequence 377, App	231	79	4.9	4896	7	US-11-258-767-61	Sequence 61, Appl
154	85	5.3	1279	1	US-09-949-925-59	Sequence 59, Appl	C 232	79	4.9	5220	6	US-10-511-937-2856	Sequence 2856, Ap
C 155	85	5.3	1593	7	US-11-257-581-19	Sequence 19, Appl	233	79	4.9	6243	6	US-10-518-039-2	Sequence 2, Appli
C 157	85	5.3	6065	6	US-10-528-659-3	Sequence 3, Appli	C 234	79	4.9	6843	6	US-10-518-039-1	Sequence 1, Appli
C 158	84.5	5.3	774	7	US-11-305-447-4	Sequence 4, Appli	C 235	79	4.9	6843	6	US-10-981-300-17	Sequence 17, Appl
C 159	84.5	5.3	774	7	US-11-305-447-5	Sequence 5, Appli	236	78.5	4.9	642	6	US-10-488-619-2890	Sequence 2890, Ap
C 160	84.5	5.3	2986	6	US-10-505-928-500	Sequence 500, App	237	78.5	4.9	695	6	US-10-511-937-486	Sequence 486, App
C 161	84	5.2	412	6	US-10-473-173-202	Sequence 202, App	238	78.5	4.9	1098	6	US-10-511-937-486	Sequence 6, Appli
C 162	84	5.2	444	7	US-11-301-554-1607	Sequence 1607, Ap	239	78.5	4.9	1213	7	US-11-244-678-6	Sequence 15, Appl
C 163	84	5.2	481	7	US-11-301-554-583	Sequence 583, App	241	78.5	4.9	2295	7	US-11-246-999-15	Sequence 148, App
C 164	84	5.2	513	7	US-11-301-554-909	Sequence 909, App	242	78.5	4.9	2338	7	US-11-246-999-148	Sequence 153, App
C 165	84	5.2	659	7	US-11-305-447-7	Sequence 7, Appli	243	78	4.9	1857	7	US-11-217-529-153	Sequence 612, App
166	84	5.2	720	7	US-11-211-917-15	Sequence 15, Appl	244	78	4.9	2010	6	US-10-511-937-612	Sequence 184, App
C 167	84	5.2	1261	7	US-11-263-326-110	Sequence 110, App	245	78	4.9	3408	6	US-10-505-928-184	Sequence 337, App
C 168	84	5.2	3084	6	US-10-511-937-448	Sequence 448, App	246	78	4.9	4365	7	US-11-223-738-1	Sequence 1, Appli
171	83.5	5.2	1076	7	US-11-101-316-45	Sequence 45, Appl	C 247	78	4.9	4631	7	US-11-246-999-25	Sequence 25, Appl
C 172	83.5	5.2	1484	6	US-10-511-937-339	Sequence 339, App	C 248	78	4.9	4995	7	US-11-246-999-17	Sequence 17, Appl
C 173	83.5	5.2	1748	7	US-11-246-999-16	Sequence 16, Appl	C 250	78	4.9	542	6	US-10-981-300-13	Sequence 13, Appl
C 174	83.5	5.2	2341	6	US-10-511-937-349	Sequence 349, App	251	77.5	4.8				

252	77.5	4.8	678	7	US-11-183-218-41	Sequence 41, Appl	c 331	72	4.5	468	6	US-10-511-937-592	Sequence 592, App
c 253	77.5	4.8	4534	6	US-10-473-691B-1	Sequence 1, Appl	c 332	72	4.5	777	7	US-11-217-529-7556	Sequence 7556, A
254	77.5	4.8	11185	6	US-10-505-928-450	Sequence 450, Appl	c 333	72	4.5	1131	6	US-10-511-937-592	Sequence 548, App
255	77	4.8	469	6	US-10-473-173-361	Sequence 361, App	334	72	4.5	1248	7	US-11-217-529-79827	Sequence 79827, A
c 256	77	4.8	520	7	US-11-301-554-927	Sequence 927, App	335	72	4.5	1410	7	US-11-217-529-1710	Sequence 1710, Ap
257	77	4.8	649	7	US-11-169-140-112	Sequence 112, App	338	72	4.5	1665	7	US-11-101-316-85	Sequence 85, Appl
258	77	4.8	1699	1	US-09-949-925-34	Sequence 34, Appl	339	72	4.5	1815	7	US-11-217-529-444	Sequence 444, App
259	77	4.8	1731	7	US-11-244-678-5	Sequence 5, Appl	341	72	4.5	3687	7	US-11-217-529-2694	Sequence 2694, Ap
260	77	4.8	3624	7	US-11-217-529-3816	Sequence 3816, Ap	c 342	71.5	4.5	540	7	US-11-301-554-14	Sequence 14, Appl
261	77	4.8	5133	6	US-10-511-917-2799	Sequence 2799, Ap	343	71.5	4.5	818	7	US-11-145-307A-157	Sequence 157, App
c 262	77	4.8	17569	7	US-11-301-554-1804	Sequence 1804, Ap	344	71.5	4.5	1650	7	US-11-217-529-2286	Sequence 2286, Ap
c 263	76.5	4.8	1053	7	US-11-217-529-80265	Sequence 80265, A	345	71.5	4.5	3301	6	US-10-370-359-10	Sequence 10, Appl
c 264	76	4.7	347	7	US-11-301-554-749	Sequence 749, App	c 346	71	4.4	400	7	US-11-301-554-241	Sequence 241, App
c 265	76	4.7	1434	7	US-11-217-529-75865	Sequence 75865, A	347	71	4.4	533	7	US-11-301-554-170	Sequence 170, App
267	76	4.7	1593	7	US-11-257-581-20	Sequence 20, Appl	348	71	4.4	1230	7	US-11-217-529-76131	Sequence 76131, A
268	76	4.7	1991	6	US-10-511-917-351	Sequence 351, App	349	71	4.4	1452	7	US-11-217-529-78450	Sequence 78450, A
269	76	4.7	4560	7	US-11-170-482-11	Sequence 11, Appl	351	71	4.4	2631	7	US-11-217-529-560	Sequence 560, App
270	76	4.7	4508	6	US-10-505-928-226	Sequence 226, App	352	71	4.4	8687	7	US-11-297-317-15	Sequence 15, Appl
c 271	75.5	4.7	347	7	US-11-222-810-3	Sequence 1, Appl	353	71	4.4	8687	7	US-11-297-317-16	Sequence 16, Appl
c 272	75.5	4.7	1290	1	US-09-949-925-48	Sequence 48, Appl	354	70.5	4.4	705	7	US-11-211-917-87	Sequence 87, Appl
c 273	75.5	4.7	1408	7	US-11-222-810-11	Sequence 11, Appl	355	70.5	4.4	862	7	US-11-219-563-129	Sequence 129, App
c 274	75.5	4.7	1554	7	US-11-222-810-13	Sequence 13, Appl	356	70.5	4.4	1569	7	US-11-217-529-78790	Sequence 78790, A
c 275	75.5	4.7	1554	7	US-11-217-529-2041	Sequence 2041, Ap	357	70.5	4.4	1822	6	US-10-505-928-16	Sequence 16, Appl
c 276	75.5	4.7	2542	6	US-10-505-928-598	Sequence 598, App	358	70.5	4.4	2184	7	US-11-217-529-80031	Sequence 80031, A
c 277	75.5	4.7	3135	7	US-11-217-529-3260	Sequence 3260, Ap	359	70.5	4.4	3474	7	US-11-217-529-80003	Sequence 114, App
c 278	75	4.7	399	6	US-10-473-173-485	Sequence 485, App	360	70	4.4	736	7	US-11-169-140-114	Sequence 3594, Ap
c 279	75	4.7	416	7	US-11-301-554-469	Sequence 469, App	361	70	4.4	1137	7	US-11-217-529-3594	Sequence 3594, Ap
c 280	75	4.7	963	7	US-11-211-917-71	Sequence 71, Appl	362	70	4.4	1473	7	US-11-217-529-3571	Sequence 3571, Ap
c 281	75	4.7	1089	1	US-09-949-925-57	Sequence 57, Appl	363	70	4.4	1545	7	US-11-217-529-838	Sequence 838, App
c 282	75	4.7	2661	6	US-10-505-928-848	Sequence 848, App	364	70	4.4	2416	6	US-10-501-834-5	Sequence 5, Appl
c 283	75	4.7	4156	6	US-10-511-917-453	Sequence 453, App	365	70	4.4	2760	7	US-11-302-678-61	Sequence 61, Appl
c 284	75	4.7	5198	6	US-10-505-928-342	Sequence 342, App	366	70	4.4	4044	7	US-11-217-529-81638	Sequence 81638, A
c 285	74.5	4.6	379	7	US-11-301-554-996	Sequence 996, App	367	70	4.4	4658	6	US-10-511-937-2809	Sequence 2809, Ap
c 286	74.5	4.6	963	7	US-11-183-218-49	Sequence 49, Appl	368	70	4.4	5658	7	US-11-217-529-6026	Sequence 6026, Ap
c 287	74.5	4.6	1026	6	US-11-219-563-135	Sequence 135, App	369	70	4.4	705	7	US-11-211-917-23	Sequence 23, Appl
c 288	74.5	4.6	1158	6	US-10-511-937-2857	Sequence 2857, Ap	370	69.5	4.3	1185	7	US-11-217-529-166612	Sequence 166612, A
c 289	74.5	4.6	1419	6	US-10-546-594-129	Sequence 129, App	371	69.5	4.3	1956	7	US-11-217-529-2243	Sequence 2243, Ap
c 290	74.5	4.6	1578	6	US-11-219-563-131	Sequence 131, App	372	69.5	4.3	2372	7	US-11-101-316-5	Sequence 5, Appl
c 291	74.5	4.6	5515	6	US-10-524-021-1	Sequence 1, Appl	373	69.5	4.3	2931	7	US-11-217-529-3493	Sequence 3493, Ap
c 292	74.5	4.6	6826	6	US-10-505-928-330	Sequence 330, App	374	69.5	4.3	3149	7	US-11-302-678-1	Sequence 1, Appl
c 293	74	4.6	420	6	US-10-488-619-713	Sequence 713, App	375	69.5	4.3	12225	6	US-10-501-834-1	Sequence 1, Appl
c 294	74	4.6	705	6	US-09-949-925-1	Sequence 1, Appl	376	69.5	4.3	238	7	US-11-301-554-995	Sequence 995, App
c 295	74	4.6	733	1	US-09-949-925-1	Sequence 1, Appl	377	69.5	4.3	531	7	US-11-217-529-1736	Sequence 1736, Ap
c 296	74	4.6	964	7	US-11-246-999-1	Sequence 91, Appl	378	69.5	4.3	1828	7	US-11-244-678-1	Sequence 1, Appl
c 297	74	4.6	1341	7	US-11-217-529-1100	Sequence 1100, Ap	379	69.5	4.3	2090	6	US-10-370-959-95	Sequence 95, Appl
c 298	74	4.6	1473	7	US-10-511-937-500	Sequence 500, App	380	69.5	4.3	2188	6	US-10-505-928-816	Sequence 816, App
c 299	74	4.6	2243	6	US-10-505-928-732	Sequence 732, App	381	69.5	4.3	2250	7	US-11-217-529-78606	Sequence 78606, A
c 300	74	4.6	3851	6	US-10-505-928-730	Sequence 730, App	382	69	4.3	5734	6	US-10-505-928-28	Sequence 28, Appl
c 301	73.5	4.6	1363	1	US-09-949-925-50	Sequence 50, Appl	383	69	4.3	6948	7	US-11-217-529-856	Sequence 856, App
c 302	73.5	4.6	1425	6	US-10-511-937-416	Sequence 416, App	384	69	4.3	846	7	US-11-217-529-77089	Sequence 77089, A
c 303	73.5	4.6	2106	7	US-11-217-529-1286	Sequence 1286, Ap	385	68.5	4.3	1837	1	US-09-949-925-72	Sequence 72, Appl
c 304	74	4.6	2358	7	US-11-217-529-2040	Sequence 2040, Ap	386	68.5	4.3	2197	6	US-10-505-928-384	Sequence 384, App
c 305	74	4.6	3345	7	US-11-217-529-82220	Sequence 82220, A	387	68.5	4.3	3444	7	US-10-505-928-1079	Sequence 1079, Ap
c 306	74	4.6	438	7	US-11-301-554-1549	Sequence 1549, Ap	388	68.5	4.3	3444	7	US-11-217-529-3542	Sequence 3542, Ap
c 307	73	4.5	2186	7	US-11-238-282-32	Sequence 32, Appl	389	68.5	4.3	8953	7	US-11-185-301-10	Sequence 10, Appl
c 308	73	4.5	3201	7	US-11-217-529-7539	Sequence 7539, A	390	68.5	4.3	8953	7	US-11-264-784-113	Sequence 113, App
c 309	73	4.5	3701	6	US-11-145-307A-170	Sequence 170, App	391	68.5	4.3	12690	7	US-11-024-544A-124	Sequence 124, App
c 310	73	4.5	4314	6	US-10-511-937-553	Sequence 553, App	392	68.5	4.3	12690	7	US-11-024-545-52	Sequence 52, Appl
c 311	73	4.5	4314	6	US-10-505-928-452	Sequence 452, App	393	68.5	4.3	12690	7	US-11-190-750-107	Sequence 107, App
c 312	73	4.5	4314	6	US-10-505-928-326	Sequence 326, App	394	68.5	4.3	12690	7	US-11-251-466-26	Sequence 26, Appl
c 313	72.5	4.5	361	7	US-11-301-554-446	Sequence 446, App	395	68.5	4.3	12690	7	US-11-251-466-26	Sequence 42, Appl
c 314	72.5	4.5	1815	7	US-11-217-529-4645	Sequence 4645, App	396	68.5	4.3	12690	7	US-11-264-784-128	Sequence 128, App
c 315	72.5	4.5	2430	7	US-11-217-529-76362	Sequence 76362, A	397	68.5	4.3	16325	6	US-11-264-784-127	Sequence 127, App
c 316	72.5	4.5	4157	7	US-11-145-307A-176	Sequence 176, App	398	68	4.2	462	6	US-10-473-173-180	Sequence 180, App
c 317	72.5	4.5	8540	7	US-11-183-218-57	Sequence 57, Appl	399	68	4.2	558	6	US-10-488-619-2378	Sequence 2378, Ap
c 318	72	4.5	370	7	US-11-301-554-1117	Sequence 1117, Ap	400	68	4.2	1341	7	US-11-217-529-4132	Sequence 4132, Ap

411	68	4.2	1380	7	US-11-217-529-201	Sequence 201, App	485	66	4.1	1761	7	US-11-217-529-75803	Sequence 75803, A
412	68	4.2	1446	7	US-11-217-529-1981	Sequence 1981, App	486	66	4.1	1908	7	US-11-217-529-80973	Sequence 80973, A
413	68	4.2	2043	7	US-11-217-529-77353	Sequence 77353, A	487	66	4.1	2892	7	US-11-217-529-2117	Sequence 2117, App
C 414	68	4.2	2101	6	US-10-505-528-756	Sequence 756, App	488	66	4.1	2901	7	US-11-303-935-4	Sequence 4, Appli
415	68	4.2	2190	7	US-11-217-529-727	Sequence 727, App	489	66	4.1	3114	7	US-11-217-529-174119	Sequence 174119, A
416	68	4.2	3246	7	US-11-217-529-78477	Sequence 78477, A	490	66	4.1	3125	7	US-11-217-529-3779	Sequence 3779, App
417	68	4.2	3485	7	US-11-145-307A-192	Sequence 192, App	491	66	4.1	3120	7	US-11-217-529-4779	Sequence 4779, App
C 418	68	4.2	3726	7	US-11-145-307A-170	Sequence 170, App	492	66	4.1	3408	7	US-11-217-529-2270	Sequence 2270, App
C 419	68	4.2	4987	6	US-10-505-928-433	Sequence 433, App	493	66	4.1	5084	6	US-10-511-937-357	Sequence 357, App
C 420	68	4.2	4987	7	US-11-251-465-4	Sequence 4, Appli	494	66	4.1	6163	6	US-10-524-021-9	Sequence 9, Appli
C 421	68	4.2	5014	7	US-11-251-465-5	Sequence 5, Appli	C 495	66	4.1	12515	6	US-10-505-928-358	Sequence 358, App
C 422	68	4.2	5479	6	US-10-505-928-472	Sequence 472, App	497	65.5	4.1	732	6	US-10-503-433B-16	Sequence 16, Appl
C 423	68	4.2	16351	6	US-10-501-834-217	Sequence 217, App	498	65.5	4.1	796	6	US-10-503-433B-24	Sequence 24, Appl
C 424	67.5	4.2	454	6	US-10-488-619-608	Sequence 608, App	499	65.5	4.1	1683	7	US-11-217-529-75479	Sequence 75479, A
C 425	67.5	4.2	1113	7	US-11-217-529-2143	Sequence 2143, App	500	65.5	4.1	2349	7	US-11-217-529-78080	Sequence 78080, A
C 426	67.5	4.2	1185	7	US-11-217-529-81156	Sequence 81156, A	C 501	65.5	4.1	4628	6	US-10-511-937-2809	Sequence 2809, App
427	67.5	4.2	1269	7	US-11-217-529-2111	Sequence 2111, App	502	65.5	4.1	6300	6	US-10-473-173-94	Sequence 94, Appl
428	67.5	4.2	1310	6	US-10-511-937-630	Sequence 630, App	503	65.5	4.1	8372	7	US-11-301-554-1893	Sequence 1893, App
429	67.5	4.2	1566	7	US-11-217-529-76167	Sequence 76167, A	504	65	4.0	339	7	US-11-254-679-55	Sequence 55, Appl
430	67.5	4.2	1671	7	US-11-217-529-78801	Sequence 78801, A	505	65	4.0	368	7	US-11-301-554-1584	Sequence 1584, App
431	67.5	4.2	2106	6	US-10-511-937-384	Sequence 384, App	506	65	4.0	460	7	US-11-242-317-5	Sequence 5, Appli
432	67.5	4.2	2163	7	US-11-217-529-4933	Sequence 4933, App	507	65	4.0	573	6	US-10-488-619-2756	Sequence 2756, App
C 433	67	4.2	505	6	US-10-473-173-224	Sequence 224, App	C 508	65	4.0	783	7	US-11-217-529-81127	Sequence 81127, A
C 434	67	4.2	590	7	US-11-301-554-495	Sequence 495, App	509	65	4.0	1002	7	US-11-217-529-1626	Sequence 1626, App
C 435	67	4.2	945	7	US-11-217-529-76947	Sequence 76947, A	C 510	65	4.0	1131	7	US-11-217-529-886	Sequence 886, App
436	67	4.2	975	7	US-11-203-609-1	Sequence 1, Appli	511	65	4.0	1215	7	US-11-217-529-75605	Sequence 75605, A
437	67	4.2	1984	7	US-11-217-529-4900	Sequence 4900, App	512	65	4.0	1216	6	US-10-511-937-490	Sequence 490, App
438	67	4.2	1404	7	US-11-217-529-2002	Sequence 2002, App	513	65	4.0	1341	7	US-11-217-529-33157	Sequence 3157, App
439	67	4.2	1620	7	US-11-217-529-75373	Sequence 75373, A	514	65	4.0	1838	7	US-11-301-554-1897	Sequence 1897, App
440	67	4.2	1647	7	US-11-217-529-78704	Sequence 78704, A	516	65	4.0	1849	7	US-11-101-316-21	Sequence 21, Appl
441	67	4.2	1650	7	US-11-312-958-39	Sequence 39, Appl	517	65	4.0	1923	7	US-11-217-529-905	Sequence 905, App
442	67	4.2	1923	7	US-11-217-529-77286	Sequence 77286, A	518	65	4.0	2241	7	US-11-217-529-3529	Sequence 3529, App
443	67	4.2	2394	7	US-11-217-529-6126	Sequence 6126, App	519	65	4.0	2335	7	US-11-217-529-1209	Sequence 1209, App
C 444	67	4.2	2476	6	US-10-501-834-211	Sequence 211, App	C 521	65	4.0	2571	7	US-11-217-529-5831	Sequence 5831, App
C 446	67	4.2	3102	7	US-11-217-529-82302	Sequence 82302, A	C 522	65	4.0	3309	7	US-11-217-529-1900	Sequence 1900, App
447	67	4.2	3438	7	US-11-217-529-1862	Sequence 1862, App	523	65	4.0	3486	7	US-11-217-529-191019	Sequence 191019, A
448	67	4.2	3687	7	US-11-217-529-841	Sequence 841, App	524	65	4.0	4027	7	US-11-169-140-1	Sequence 1, Appli
C 449	67	4.2	3859	6	US-10-511-937-2853	Sequence 2853, App	525	65	4.0	4631	7	US-11-246-999-25	Sequence 25, Appl
C 450	67	4.2	14468	7	US-11-481-115-7	Sequence 7, Appli	526	65	4.0	5411	6	US-10-504-120-5	Sequence 5, Appli
451	67	4.2	16351	6	US-10-501-834-217	Sequence 217, App	C 527	65	4.0	5487	6	US-10-473-173-27	Sequence 27, Appl
452	66.5	4.1	337	7	US-11-239-308-5	Sequence 5, Appli	C 528	65	4.0	5487	6	US-10-505-928-120	Sequence 120, App
453	66.5	4.1	340	7	US-11-239-308-3	Sequence 3, Appli	529	65	4.0	5543	6	US-10-504-120-6	Sequence 6, Appli
454	66.5	4.1	340	7	US-11-239-308-13	Sequence 13, Appl	530	65	4.0	7884	7	US-11-217-529-3160	Sequence 3160, App
455	66.5	4.1	813	7	US-11-217-529-81040	Sequence 81040, A	531	64.5	4.0	336	7	US-11-211-917-11	Sequence 11, Appl
C 456	66.5	4.1	957	7	US-11-217-529-78825	Sequence 78825, A	532	64.5	4.0	336	7	US-11-211-917-93	Sequence 93, Appl
457	66.5	4.1	1074	7	US-11-217-529-633	Sequence 633, App	533	64.5	4.0	539	6	US-10-473-173-26	Sequence 26, Appl
458	66.5	4.1	1344	7	US-11-246-999-24	Sequence 24, App	534	64.5	4.0	541	6	US-10-981-300-3	Sequence 3, Appli
459	66.5	4.1	1434	7	US-11-217-529-80879	Sequence 80879, A	535	64.5	4.0	672	6	US-10-488-619-1470	Sequence 1470, App
460	66.5	4.1	1545	7	US-11-217-529-372	Sequence 372, App	536	64.5	4.0	705	7	US-11-211-917-47	Sequence 47, Appl
461	66.5	4.1	1578	7	US-11-217-529-77864	Sequence 77864, A	C 537	64.5	4.0	711	7	US-11-217-529-76273	Sequence 76273, A
462	66.5	4.1	1638	7	US-11-217-529-3460	Sequence 3460, App	538	64.5	4.0	786	7	US-11-217-529-79673	Sequence 79673, A
463	66.5	4.1	2085	6	US-10-511-937-395	Sequence 395, App	539	64.5	4.0	1368	7	US-11-217-529-75571	Sequence 75571, A
464	66.5	4.1	2277	7	US-11-217-529-78053	Sequence 78053, A	540	64.5	4.0	1404	7	US-11-217-529-190888	Sequence 190888, A
465	66.5	4.1	2283	7	US-11-217-529-645	Sequence 645, App	541	64.5	4.0	1887	7	US-11-217-529-4937	Sequence 4927, App
466	66.5	4.1	2323	7	US-11-303-935-6	Sequence 6, Appli	542	64.5	4.0	1805	7	US-11-217-529-80161	Sequence 80161, A
467	66.5	4.1	2846	6	US-10-505-928-444	Sequence 444, App	C 543	64.5	4.0	1989	7	US-11-217-529-76484	Sequence 76484, A
468	66.5	4.1	2940	7	US-11-217-529-77568	Sequence 77568, A	544	64.5	4.0	2268	7	US-11-217-529-6178	Sequence 6178, App
469	66.5	4.1	5252	6	US-10-511-937-3101	Sequence 3101, App	545	64.5	4.0	2379	7	US-11-217-529-3141	Sequence 3141, App
470	66.5	4.1	5252	6	US-10-511-937-3102	Sequence 3102, App	546	64.5	4.0	2383	6	US-10-505-928-97	Sequence 97, Appl
C 471	66	4.1	363	7	US-11-301-554-878	Sequence 878, App	547	64.5	4.0	2427	7	US-11-217-529-4994	Sequence 4984, App
C 472	66	4.1	364	7	US-11-301-554-867	Sequence 867, App	548	64.5	4.0	2583	7	US-11-217-529-1533	Sequence 1533, App
473	66	4.1	367	7	US-11-301-554-1143	Sequence 1143, App	549	64.5	4.0	2631	7	US-11-217-529-78397	Sequence 78397, A
474	66	4.1	367	7	US-11-301-554-1626	Sequence 1626, App	550	64.5	4.0	2802	7	US-11-217-529-2662	Sequence 2662, App
475	66	4.1	368	7	US-11-301-554-1038	Sequence 1038, App	551	64.5	4.0	2802	7	US-11-217-529-78966	Sequence 78966, A
C 476	66	4.1	368	7	US-11-301-554-1044	Sequence 1044, App	552	64.5	4.0	2808	7	US-11-217-529-3229	Sequence 3229, App
C 477	66	4.1	368	7	US-11-301-554-1092	Sequence 1092, App	553	64.5	4.0	3312	6	US-10-523-014-1	Sequence 1, Appli
478	66	4.1	368	7	US-11-301-554-1164	Sequence 1164, App	554	64.5	4.0	4542	7	US-11-217-529-3362	Sequence 3362, App
479	66	4.1	447	7	US-11-301-554-646	Sequence 646, App	555	64.5	4.0	6400	6	US-10-505-928-396	Sequence 396, App
480	66	4.1	603	6	US-10-488-619-1286	Sequence 1286, App	556	64	4.0	327	7	US-11-254-679-10	Sequence 10, Appl
481	66	4.1	735	7	US-11-217-529-76358	Sequence 76358, A	557	64	4.0	391	6	US-10-511-937-583	Sequence 583, App
482	66	4.1	996	7	US-11-217-529-166795	Sequence 166795, A	558	64	4.0	491	7	US-11-301-554-1155	Sequence 1155, App
483	66	4.1	1188	6	US-10-511-937-456	Sequence 456, App	559	64	4.0	494	6	US-10-488-619-630	Sequence 630, App
484	66	4.1	1482	7	US-11-217-529-3676	Sequence 3676, App							

c 560	64	4.0	525	7	US-11-217-529-79833	Sequence 79833, A	635	63	3.9	1374	7	US-11-024-544A-114	Sequence 114, App
c 561	64	4.0	558	7	US-11-217-529-4115	Sequence 4115, App	636	63	3.9	1374	7	US-11-024-545-42	Sequence 42, App1
c 562	64	4.0	630	6	US-10-473-173-166	Sequence 166, App	637	63	3.9	1374	7	US-11-185-301-30	Sequence 30, App1
c 563	64	4.0	690	7	US-11-217-529-5668	Sequence 5668, App	638	63	3.9	1374	7	US-11-190-750-97	Sequence 97, App1
c 564	64	4.0	894	7	US-11-217-529-76304	Sequence 76304, A	639	63	3.9	1374	7	US-11-251-466-16	Sequence 16, App1
c 565	64	4.0	1131	7	US-11-217-529-82367	Sequence 82367, A	640	63	3.9	1374	7	US-11-254-173-30	Sequence 30, App1
c 566	64	4.0	1215	7	US-11-217-529-1512	Sequence 1512, App	641	63	3.9	1374	7	US-11-264-784-33	Sequence 33, App1
c 567	64	4.0	1191	7	US-11-217-529-5076	Sequence 5076, App	642	63	3.9	1524	7	US-11-217-529-479	Sequence 479, App
c 568	64	4.0	1317	7	US-11-217-529-3586	Sequence 3586, App	c 643	63	3.9	1580	7	US-11-145-307A-16	Sequence 16, App1
c 569	64	4.0	1461	7	US-11-185-301-1	Sequence 1, App1	644	63	3.9	1866	7	US-11-217-529-79057	Sequence 79057, A
c 570	64	4.0	1498	6	US-10-511-937-362	Sequence 362, App	645	63	3.9	1929	7	US-11-217-529-1871	Sequence 1871, App
c 571	64	4.0	1614	7	US-11-217-529-77221	Sequence 77221, A	c 646	63	3.9	2154	7	US-11-245-628-5	Sequence 5, App1
c 572	64	4.0	1674	7	US-11-217-529-77626	Sequence 77626, A	647	63	3.9	2235	7	US-11-217-529-82151	Sequence 82151, A
c 573	64	4.0	1938	7	US-11-217-529-4635	Sequence 4635, App	648	63	3.9	2460	7	US-11-217-529-1211	Sequence 1211, App
c 574	64	4.0	2103	7	US-11-217-529-2968	Sequence 2968, App	649	63	3.9	2499	7	US-11-217-529-1211	Sequence 1211, App
c 575	64	4.0	2424	7	US-11-217-529-2453	Sequence 2453, App	650	63	3.9	2853	7	US-11-217-529-1777	Sequence 1777, App
c 576	64	4.0	2424	7	US-11-217-529-2453	Sequence 2453, App	651	63	3.9	2853	7	US-11-217-529-880	Sequence 880, App
c 577	64	4.0	2445	6	US-10-505-928-777	Sequence 777, App	652	63	3.9	3115	7	US-11-301-554-802	Sequence 802, App
c 578	64	4.0	2532	7	US-11-217-529-77060	Sequence 77060, A	653	63	3.9	3173	6	US-10-513-076-790	Sequence 790, App
c 579	64	4.0	2664	7	US-11-217-529-80159	Sequence 80159, A	c 654	63	3.9	3225	7	US-11-217-529-1140	Sequence 1140, App
c 580	64	4.0	2811	7	US-11-217-529-162	Sequence 162, App	655	63	3.9	3357	7	US-11-217-529-77053	Sequence 77053, A
c 581	64	4.0	2904	7	US-11-145-307A-161	Sequence 161, App	656	63	3.9	3697	7	US-11-145-307A-69	Sequence 69, App1
c 582	64	4.0	3024	7	US-11-217-529-3308	Sequence 3308, App	657	63	3.9	3791	6	US-10-505-928-214	Sequence 214, App
c 583	64	4.0	3115	6	US-10-505-928-645	Sequence 645, App	658	63	3.9	4637	7	US-11-301-554-804	Sequence 804, App
c 584	64	4.0	3115	6	US-10-511-937-626	Sequence 626, App	659	63	3.9	4764	7	US-11-217-529-3236	Sequence 3236, App
c 585	64	4.0	3327	7	US-11-217-529-4590	Sequence 4590, App	660	63	3.9	6974	6	US-10-511-937-2858	Sequence 2858, App
c 586	64	4.0	3567	7	US-11-311-778-19	Sequence 19, App1	661	63	3.9	6974	6	US-10-505-928-673	Sequence 673, App
c 587	64	4.0	3771	7	US-11-217-529-3232	Sequence 3232, App	662	63	3.9	8462	7	US-11-264-784-145	Sequence 145, App
c 588	64	4.0	5650	6	US-10-505-928-212	Sequence 212, App	663	63	3.9	10195	7	US-11-264-784-149	Sequence 149, App
c 589	64	4.0	5698	6	US-10-505-928-218	Sequence 218, App	664	63	3.9	10809	7	US-11-264-784-151	Sequence 151, App
c 590	63.5	4.0	330	7	US-11-254-679-35	Sequence 35, App1	665	63	3.9	11046	7	US-11-264-784-146	Sequence 146, App
c 591	63.5	4.0	337	7	US-11-239-308-15	Sequence 15, App1	666	63	3.9	12649	7	US-11-024-544A-110	Sequence 110, App
c 592	63.5	4.0	337	7	US-11-211-917-35	Sequence 35, App1	667	63	3.9	12649	7	US-11-024-545-38	Sequence 38, App1
c 593	63.5	4.0	337	7	US-11-211-917-51	Sequence 51, App1	668	63	3.9	12649	7	US-11-185-301-27	Sequence 27, App1
c 594	63.5	4.0	350	6	US-10-488-619-434	Sequence 434, App	669	63	3.9	12649	7	US-11-190-750-93	Sequence 93, App1
c 595	63.5	4.0	378	7	US-11-217-529-1445	Sequence 1445, App	670	63	3.9	12649	7	US-11-251-466-12	Sequence 12, App1
c 596	63.5	4.0	714	7	US-11-217-529-77372	Sequence 77372, A	671	63	3.9	12649	7	US-11-254-173-26	Sequence 26, App1
c 597	63.5	4.0	825	7	US-11-217-529-877	Sequence 877, App	672	63	3.9	14864	7	US-11-264-784-114	Sequence 114, App
c 598	63.5	4.0	825	7	US-11-217-529-877	Sequence 877, App	673	63	3.9	14864	7	US-11-254-173-58	Sequence 58, App1
c 599	63.5	4.0	825	7	US-11-217-529-81241	Sequence 81241, App	674	63	3.9	14864	7	US-11-264-784-134	Sequence 134, App
c 600	63.5	4.0	1179	7	US-11-217-529-78853	Sequence 78853, A	675	62.5	3.9	455	6	US-10-981-300-1	Sequence 1, App1
c 601	63.5	4.0	1282	1	US-09-949-925-68	Sequence 68, App1	676	62.5	3.9	516	7	US-11-217-529-619	Sequence 619, App
c 602	63.5	4.0	1388	6	US-10-505-928-606	Sequence 606, App	677	62.5	3.9	543	7	US-11-217-529-81867	Sequence 81867, A
c 603	63.5	4.0	1414	7	US-11-263-326-100	Sequence 100, App	c 678	62.5	3.9	636	6	US-10-488-619-2903	Sequence 2903, App
c 604	63.5	4.0	1414	7	US-11-263-326-145	Sequence 145, App	679	62.5	3.9	764	6	US-10-503-433B-11	Sequence 11, App1
c 605	63.5	4.0	1485	7	US-11-217-529-166558	Sequence 166558, App	680	62.5	3.9	1008	7	US-11-217-529-174182	Sequence 174182, A
c 606	63.5	4.0	1674	7	US-11-217-529-1672	Sequence 1672, App	681	62.5	3.9	1131	7	US-11-217-529-80637	Sequence 80637, A
c 607	63.5	4.0	1827	1	US-09-949-925-13	Sequence 13, App1	682	62.5	3.9	1191	7	US-11-217-529-78508	Sequence 78508, A
c 608	63.5	4.0	1884	7	US-11-217-529-76882	Sequence 76882, A	683	62.5	3.9	1377	7	US-11-217-529-81289	Sequence 81289, A
c 609	63.5	4.0	1993	6	US-10-511-937-2894	Sequence 2894, App	684	62.5	3.9	1377	7	US-11-217-529-5539	Sequence 5539, App
c 610	63.5	4.0	1995	7	US-11-217-529-3311	Sequence 3311, App	685	62.5	3.9	1414	7	US-11-263-326-99	Sequence 99, App1
c 611	63.5	4.0	2163	7	US-11-217-529-4479	Sequence 4479, App	686	62.5	3.9	1506	7	US-11-217-529-78500	Sequence 78500, A
c 612	63.5	4.0	2253	7	US-11-217-529-77443	Sequence 77443, A	687	62.5	3.9	1509	7	US-11-217-529-1727	Sequence 1727, App
c 613	63.5	4.0	2511	7	US-11-217-529-522	Sequence 522, App	688	62.5	3.9	1679	7	US-11-217-529-80411	Sequence 80411, A
c 614	63.5	4.0	2511	7	US-11-248-122-3	Sequence 3, App1	689	62.5	3.9	1699	7	US-11-217-529-1446	Sequence 1446, App
c 615	63.5	4.0	2601	7	US-11-217-529-79161	Sequence 79161, A	690	62.5	3.9	1719	7	US-11-217-529-80736	Sequence 80736, A
c 616	63.5	4.0	3780	6	US-10-509-131-24	Sequence 24, App1	691	62.5	3.9	1758	7	US-11-217-529-76979	Sequence 76979, A
c 617	63.5	4.0	4304	7	US-11-303-935-1	Sequence 1, App1	692	62.5	3.9	1809	7	US-11-217-529-174100	Sequence 174100, A
c 618	63.5	4.0	4304	7	US-11-303-935-1	Sequence 1, App1	693	62.5	3.9	1929	7	US-11-217-529-518	Sequence 518, App
c 619	63.5	4.0	10173	6	US-10-488-015-9	Sequence 9, App1	694	62.5	3.9	1932	7	US-11-246-999-12	Sequence 12, App1
c 620	63	3.9	322	7	US-11-239-308-23	Sequence 23, App1	695	62.5	3.9	2511	7	US-11-217-529-77149	Sequence 77149, A
c 621	63	3.9	322	7	US-11-239-308-25	Sequence 25, App1	696	62.5	3.9	2522	7	US-11-246-999-23	Sequence 23, App1
c 622	63	3.9	350	7	US-11-222-810-18	Sequence 18, App1	697	62.5	3.9	2522	7	US-11-217-529-833	Sequence 833, App
c 623	63	3.9	416	7	US-11-301-554-971	Sequence 971, App	698	62.5	3.9	2589	7	US-10-511-937-562	Sequence 562, App
c 624	63	3.9	543	7	US-11-217-529-81857	Sequence 81857, App	699	62.5	3.9	2661	6	US-11-217-529-1838	Sequence 1838, App
c 625	63	3.9	557	7	US-11-301-554-196	Sequence 196, App	700	62.5	3.9	2673	7	US-10-982-908-27	Sequence 27, App1
c 626	63	3.9	795	7	US-11-167-773-44	Sequence 44, App1	701	62.5	3.9	2726	6	US-11-217-529-79792	Sequence 79792, A
c 627	63	3.9	807	7	US-11-219-563-23	Sequence 23, App1	702	62.5	3.9	2754	7	US-11-217-529-3592	Sequence 3592, App
c 628	63	3.9	807	7	US-11-219-563-24	Sequence 24, App1	703	62.5	3.9	3102	7	US-11-217-529-796	Sequence 796, App
c 629	63	3.9	821	6	US-10-488-619-654	Sequence 654, App	704	62.5	3.9	3494	6	US-10-505-928-344	Sequence 344, App
c 630	63	3.9	876	6	US-10-473-173-48	Sequence 48, App1	705	62.5	3.9	4045	6	US-10-511-937-571	Sequence 571, App
c 631	63	3.9	930	7	US-11-217-529-174496	Sequence 174496, A	706	62.5	3.9	4153	6	US-10-505-928-344	Sequence 344, App
c 632	63	3.9	957	7	US-11-217-529-80173	Sequence 80173, A	707	62.5	3.9	4153	6	US-10-524-021-2	Sequence 2, App1
c 633	63	3.9	1145	1	US-09-949-925-79	Sequence 79, App1	708	62.5	3.9	5373	6	US-10-528-659-1	Sequence 1, App1
c 634	63	3.9	1302	6	US-10-513-076-786	Sequence 786, App	709	62.5	3.9	5373	6	US-10-528-659-1	Sequence 1, App1
							710	62	3.9	322	7	US-11-239-308-19	Sequence 19, App1

c 711	62	3.9	368	7	US-11-301-554-1003	Sequence 1003, Ap	789	61	3.8	2031	7	US-11-217-529-78529	Sequence 78529, A
712	62	3.9	427	7	US-11-301-554-854	Sequence 854, App	790	61	3.8	2106	7	US-11-217-529-1594	Sequence 1594, Ap
713	62	3.9	621	7	US-11-217-529-536	Sequence 536, App	791	61	3.8	2274	7	US-11-217-529-2356	Sequence 2356, Ap
c 715	62	3.9	1177	7	US-11-301-516-129	Sequence 129, App	792	61	3.8	2298	6	US-10-505-928-354	Sequence 354, App
716	62	3.9	1281	6	US-10-511-937-632	Sequence 632, App	793	61	3.8	2298	6	US-10-511-937-434	Sequence 434, App
717	62	3.9	1581	7	US-11-217-529-79384	Sequence 79384, A	794	61	3.8	2304	7	US-11-251-465-1	Sequence 1, Appl
718	62	3.9	1679	6	US-10-473-173-65	Sequence 65, Appl	795	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
719	62	3.9	1679	6	US-10-505-928-746	Sequence 746, App	796	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
720	62	3.9	1679	6	US-10-511-937-428	Sequence 428, App	797	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
721	62	3.9	1679	6	US-10-511-937-2896	Sequence 2896, Ap	798	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
722	62	3.9	1679	6	US-10-511-937-2918	Sequence 2918, Ap	799	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
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724	62	3.9	1746	7	US-11-217-529-79085	Sequence 79085, A	c 801	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
726	62	3.9	2043	6	US-10-946-650-65	Sequence 65, Appl	802	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
727	62	3.9	2520	7	US-11-217-529-4495	Sequence 4495, Ap	803	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
728	62	3.9	2559	7	US-11-217-529-77496	Sequence 77496, A	804	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 729	62	3.9	2684	6	US-10-509-131-52	Sequence 52, Appl	805	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
730	62	3.9	2835	7	US-11-217-529-5468	Sequence 5468, Ap	806	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
731	62	3.9	2889	6	US-10-511-937-627	Sequence 627, App	c 807	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
732	62	3.9	3074	6	US-10-524-021-7	Sequence 7, Appl	808	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 733	62	3.9	3151	6	US-10-511-937-2860	Sequence 2860, Ap	809	61	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
735	62	3.9	3588	6	US-10-505-928-84	Sequence 84, Appl	810	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
736	62	3.9	4221	7	US-11-217-529-2728	Sequence 2728, Ap	811	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
737	62	3.9	4413	7	US-11-217-529-3933	Sequence 3933, Ap	812	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
738	62	3.9	4995	7	US-11-246-999-17	Sequence 17, Appl	813	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
739	62	3.9	6816	6	US-10-473-173-54	Sequence 54, Appl	814	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 740	62	3.9	12918	6	US-10-501-834-4	Sequence 4, Appl	815	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
741	61.5	3.8	336	7	US-11-211-917-3	Sequence 3, Appl	c 816	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
742	61.5	3.8	337	7	US-11-211-917-59	Sequence 59, Appl	817	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
743	61.5	3.8	366	7	US-11-254-679-73	Sequence 73, Appl	818	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
744	61.5	3.8	473	6	US-10-488-619-2659	Sequence 2659, Ap	819	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
745	61.5	3.8	573	7	US-11-217-529-1185	Sequence 1185, Ap	820	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 746	61.5	3.8	625	6	US-10-488-619-1484	Sequence 1484, Ap	821	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
747	61.5	3.8	729	7	US-11-169-140-113	Sequence 113, App	822	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
748	61.5	3.8	801	6	US-10-503-433B-14	Sequence 14, Appl	823	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 749	61.5	3.8	801	6	US-10-503-433B-14	Sequence 14, Appl	824	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
750	61.5	3.8	1101	7	US-11-217-529-75617	Sequence 75617, A	825	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
751	61.5	3.8	1221	7	US-11-217-529-78275	Sequence 78275, A	c 826	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
752	61.5	3.8	1282	6	US-10-511-937-413	Sequence 413, App	827	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 753	61.5	3.8	1410	7	US-11-217-529-3259	Sequence 3259, Ap	828	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
754	61.5	3.8	1434	7	US-11-217-529-75865	Sequence 75865, A	829	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
755	61.5	3.8	1434	7	US-11-217-529-80572	Sequence 80572, A	830	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
756	61.5	3.8	1434	7	US-11-217-529-4434	Sequence 4434, Ap	831	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
757	61.5	3.8	1473	7	US-11-217-529-81075	Sequence 81075, A	832	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
758	61.5	3.8	1689	7	US-11-217-529-696	Sequence 696, App	833	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
759	61.5	3.8	1734	7	US-11-217-529-81360	Sequence 81360, A	834	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 760	61.5	3.8	1758	7	US-11-217-529-76904	Sequence 76904, A	835	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
761	61.5	3.8	1759	7	US-11-311-754-3	Sequence 3, Appl	836	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 762	61.5	3.8	2052	7	US-11-217-529-634	Sequence 634, App	837	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
763	61.5	3.8	2307	7	US-11-217-529-2738	Sequence 2738, Ap	838	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
764	61.5	3.8	2328	7	US-11-217-529-1943	Sequence 1943, Ap	839	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
765	61.5	3.8	2424	7	US-11-217-529-3461	Sequence 3461, A	840	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
766	61.5	3.8	2466	7	US-11-217-529-78674	Sequence 78674, A	841	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 767	61.5	3.8	2467	6	US-10-505-928-313	Sequence 313, App	842	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
768	61.5	3.8	2577	7	US-11-217-529-601	Sequence 601, App	843	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
769	61.5	3.8	2796	7	US-11-217-529-81089	Sequence 81089, A	844	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
770	61.5	3.8	2868	7	US-11-217-529-81168	Sequence 81168, A	845	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
771	61.5	3.8	2987	7	US-11-264-784-280	Sequence 280, App	846	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
772	61.5	3.8	3054	6	US-10-505-928-492	Sequence 492, App	847	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
773	61.5	3.8	3087	7	US-11-217-529-79584	Sequence 79584, A	848	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 774	61.5	3.8	15543	7	US-11-264-784-124	Sequence 124, App	849	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
775	61	3.8	279	6	US-10-488-619-1847	Sequence 1847, Ap	850	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 776	61	3.8	616	6	US-10-488-619-1848	Sequence 1848, Ap	851	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
777	61	3.8	701	6	US-10-488-619-1848	Sequence 1848, Ap	852	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
c 778	61	3.8	777	7	US-11-217-529-79454	Sequence 79454, A	853	60.5	3.8	2370	7	US-11-217-529-77236	Sequence 77236, A
779	61	3.8	802	7	US-11-217-529-78484	Sequence 78484, A	854	60	3.7	2370	7	US-11-217-529-77236	Sequence 77236, A
c 780	61	3.8	1074	6	US-11-217-529-317	Sequence 317, App	855	60	3.7	2370	7	US-11-217-529-77236	Sequence 77236, A
781	61	3.8	1107	6	US-10-524-433-2	Sequence 2, Appl	856	60	3.7	2370	7	US-11-217-529-77236	Sequence 77236, A
782	61	3.8	1266	6	US-10-509-131-57	Sequence 57, Appl	857	60	3.7	2370	7	US-11-217-529-77236	Sequence 77236, A
783	61	3.8	1434	7	US-11-217-529-5339	Sequence 5339, Ap	858	60	3.7	2370	7	US-11-217-529-77236	Sequence 77236, A
784	61	3.8	1578	6	US-10-473-173-20	Sequence 20, Appl	c 859	60	3.7	2370	7	US-11-217-529-77236	Sequence 77236, A
c 786	61	3.8	1785	7	US-11-217-529-81561	Sequence 81561, A	860	60	3.7	2370	7	US-11-217-529-77236	Sequence 77236, A
787	61	3.8	1848	7	US-11-217-529-190849	Sequence 190849, A	861	60	3.7	2370	7	US-11-217-529-77236	Sequence 77236, A
c 788	61	3.8	1923	7	US-11-217-529-76610	Sequence 76610, A	862	60	3.7	2370	7	US-11-217-529-77236	Sequence 77236, A

862	60	3.7	690	7	US-11-217-529-82027	Sequence 82027, A	939	59.5	3.7	2265	7	US-11-217-529-5825	Sequence 5825, Ap
863	60	3.7	696	7	US-11-217-529-80241	Sequence 80241, A	941	59.5	3.7	2430	7	US-11-217-529-782	Sequence 782, App
864	60	3.7	780	7	US-11-217-529-4754	Sequence 4754, Ap	942	59.5	3.7	2448	7	US-11-217-529-1195	Sequence 1195, Ap
c 865	60	3.7	798	7	US-11-217-529-76596	Sequence 76596, A	943	59.5	3.7	2460	7	US-11-217-529-77247	Sequence 77247, A
c 866	60	3.7	824	6	US-10-488-619-1933	Sequence 1933, Ap	944	59.5	3.7	2797	7	US-11-181-115-17	Sequence 17, Appl
c 868	60	3.7	849	7	US-11-217-529-76262	Sequence 76262, A	945	59.5	3.7	3261	7	US-11-217-529-1461	Sequence 1461, Ap
c 869	60	3.7	918	7	US-11-217-529-77581	Sequence 77581, A	946	59.5	3.7	3516	7	US-11-217-529-82517	Sequence 82517, A
c 870	60	3.7	1008	7	US-11-217-529-80378	Sequence 80378, A	948	59.5	3.7	3877	7	US-11-101-316-71	Sequence 71, Appl
872	60	3.7	1041	7	US-11-217-529-6155	Sequence 6155, Ap	949	59.5	3.7	3930	7	US-11-217-529-76026	Sequence 76026, A
873	60	3.7	1074	7	US-11-217-529-76925	Sequence 76925, A	950	59.5	3.7	4224	7	US-11-217-529-191185	Sequence 191185,
874	60	3.7	1192	6	US-10-496-758-1	Sequence 1, Appli	951	59.5	3.7	5712	7	US-11-217-529-4691	Sequence 4691, Ap
875	60	3.7	1215	7	US-11-217-529-77416	Sequence 77416, A	952	59	3.7	311	6	US-10-488-619-514	Sequence 514, App
876	60	3.7	1224	7	US-11-217-529-81238	Sequence 81238, A	953	59	3.7	322	7	US-11-239-308-21	Sequence 21, Appl
877	60	3.7	1241	7	US-11-136-524-55	Sequence 55, Appl	954	59	3.7	567	6	US-11-217-529-5424	Sequence 5424, Ap
878	60	3.7	1290	7	US-11-217-529-3320	Sequence 3320, Ap	955	59	3.7	575	6	US-10-488-619-1578	Sequence 1578, Ap
c 879	60	3.7	1302	7	US-11-217-529-287	Sequence 287, App	957	59	3.7	918	7	US-11-217-529-79626	Sequence 79626, A
c 880	60	3.7	1494	7	US-11-217-529-119	Sequence 119, App	958	59	3.7	954	7	US-11-217-529-80214	Sequence 80214, A
c 881	60	3.7	1500	7	US-11-217-529-1568	Sequence 1568, Ap	c 959	59	3.7	984	7	US-11-217-529-4900	Sequence 4900, Ap
882	60	3.7	1602	7	US-11-217-529-5803	Sequence 5803, Ap	960	59	3.7	1002	7	US-11-217-529-82290	Sequence 82290, A
883	60	3.7	1704	7	US-11-217-529-2636	Sequence 2636, Ap	961	59	3.7	1185	7	US-11-217-529-4130	Sequence 4130, Ap
884	60	3.7	1755	7	US-11-217-529-173638	Sequence 173638, A	962	59	3.7	1500	7	US-11-217-529-639	Sequence 639, App
885	60	3.7	1761	7	US-11-217-529-78536	Sequence 78536, A	963	59	3.7	1545	7	US-11-217-529-2264	Sequence 2264, Ap
886	60	3.7	1806	7	US-11-217-529-80315	Sequence 80315, A	c 964	59	3.7	1650	7	US-11-217-529-5609	Sequence 5609, Ap
887	60	3.7	1820	7	US-11-244-678-3	Sequence 3, Appli	965	59	3.7	1680	7	US-11-217-529-225	Sequence 225, App
888	60	3.7	1968	7	US-11-217-529-81250	Sequence 81250, A	966	59	3.7	1716	7	US-11-217-529-6029	Sequence 6029, Ap
889	60	3.7	2013	7	US-11-217-529-77807	Sequence 77807, A	968	59	3.7	1743	6	US-10-511-937-405	Sequence 405, App
c 890	60	3.7	2025	7	US-11-217-529-507	Sequence 507, App	969	59	3.7	1782	7	US-11-217-529-3112	Sequence 3112, Ap
c 891	60	3.7	2412	7	US-11-217-529-6042	Sequence 6042, Ap	970	59	3.7	1812	7	US-11-217-529-78799	Sequence 78799, A
c 892	60	3.7	2433	7	US-11-217-529-77106	Sequence 77106, A	c 971	59	3.7	1824	6	US-10-473-173-81	Sequence 81, Appl
893	60	3.7	2526	7	US-11-217-529-3132	Sequence 3132, Ap	972	59	3.7	2144	7	US-11-217-529-80406	Sequence 80406, A
894	60	3.7	2949	7	US-11-170-482-13	Sequence 13, Appl	973	59	3.7	2154	7	US-11-217-529-82224	Sequence 82224, A
895	60	3.7	3075	7	US-11-226-605-51	Sequence 51, Appl	975	59	3.7	2025	7	US-11-217-529-80287	Sequence 80287, A
896	60	3.7	3157	6	US-10-468-193-29	Sequence 29, Appl	976	59	3.7	2073	7	US-11-217-529-78147	Sequence 78147, A
897	60	3.7	3162	7	US-11-217-529-300	Sequence 300, App	977	59	3.7	2082	7	US-11-217-529-79443	Sequence 79443, A
898	60	3.7	3303	7	US-11-217-529-261	Sequence 261, App	978	59	3.7	2127	7	US-11-217-529-77806	Sequence 77806, A
899	60	3.7	3327	7	US-11-217-529-78276	Sequence 78276, A	979	59	3.7	2144	7	US-11-245-628-11	Sequence 11, Appl
900	60	3.7	3662	6	US-10-505-928-844	Sequence 844, App	c 979	59	3.7	2154	7	US-11-217-529-1651	Sequence 1651, Ap
903	60	3.7	3891	7	US-11-217-529-1874	Sequence 1874, Ap	981	59	3.7	2202	7	US-11-217-529-76464	Sequence 76464, A
904	60	3.7	4767	6	US-10-505-928-360	Sequence 360, App	982	59	3.7	2280	7	US-11-217-529-405	Sequence 405, App
905	60	3.7	4767	7	US-11-145-307A-150	Sequence 150, App	983	59	3.7	2298	6	US-10-511-937-633	Sequence 633, App
906	60	3.7	5493	7	US-11-217-529-81749	Sequence 81749, A	984	59	3.7	2298	7	US-11-217-529-3750	Sequence 3750, Ap
907	60	3.7	5925	6	US-10-511-937-591	Sequence 591, App	985	59	3.7	2394	7	US-11-217-529-81691	Sequence 81691, A
908	59.5	3.7	337	7	US-11-239-308-11	Sequence 11, Appl	986	59	3.7	2454	7	US-11-217-529-76817	Sequence 76817, A
909	59.5	3.7	340	7	US-11-239-308-11	Sequence 1, Appli	987	59	3.7	2457	7	US-11-217-529-78765	Sequence 78765, A
c 910	59.5	3.7	414	7	US-11-217-529-4286	Sequence 4286, Ap	988	59	3.7	2475	7	US-11-217-529-77675	Sequence 77675, A
c 911	59.5	3.7	478	6	US-10-488-619-2558	Sequence 2558, Ap	989	59	3.7	2592	7	US-11-217-529-79167	Sequence 79167, A
912	59.5	3.7	518	7	US-11-301-554-1314	Sequence 1314, Ap	990	59	3.7	2694	7	US-11-217-529-76557	Sequence 76557, A
913	59.5	3.7	522	6	US-10-488-619-2559	Sequence 2559, Ap	c 991	59	3.7	2703	7	US-11-217-529-1904	Sequence 1904, Ap
914	59.5	3.7	618	7	US-11-217-529-76031	Sequence 76031, A	992	59	3.7	2706	7	US-11-217-529-733	Sequence 733, App
915	59.5	3.7	706	6	US-10-503-433B-17	Sequence 17, Appl	993	59	3.7	2712	7	US-11-217-529-174038	Sequence 174038,
916	59.5	3.7	717	7	US-11-217-529-166503	Sequence 166503, A	c 994	59	3.7	2776	6	US-10-511-937-2822	Sequence 2822, Ap
917	59.5	3.7	753	7	US-11-217-529-4328	Sequence 4328, Ap	995	59	3.7	2886	7	US-11-217-529-1022	Sequence 1022, Ap
918	59.5	3.7	819	7	US-11-217-529-1255	Sequence 1255, Ap	996	59	3.7	3115	6	US-10-505-928-645	Sequence 645, App
c 919	59.5	3.7	852	7	US-11-217-529-77585	Sequence 77585, A	997	59	3.7	3115	6	US-10-511-937-626	Sequence 626, App
920	59.5	3.7	924	7	US-11-217-529-173251	Sequence 173251, A	998	59	3.7	3231	7	US-11-217-529-1645	Sequence 1645, Ap
921	59.5	3.7	999	7	US-11-217-529-81597	Sequence 81597, A	c 999	59	3.7	3248	6	US-10-505-928-222	Sequence 222, App
c 922	59.5	3.7	1080	6	US-10-511-937-472	Sequence 472, App	c1000	59	3.7	3300	6	US-10-505-928-120	Sequence 120, App
923	59.5	3.7	1146	7	US-11-217-529-1383	Sequence 1383, Ap	1001	59	3.7	3363	7	US-11-217-529-75630	Sequence 75630, A
924	59.5	3.7	1299	7	US-11-134-445-19	Sequence 19, Appl	1002	59	3.7	3417	7	US-11-217-529-814	Sequence 814, App
925	59.5	3.7	1309	7	US-11-134-445-29	Sequence 29, Appl	c1003	59	3.7	3674	6	US-10-473-173-2	Sequence 2, Appli
926	59.5	3.7	1470	7	US-11-217-529-76296	Sequence 76296, A	c1004	59	3.7	4239	6	US-10-511-937-543	Sequence 543, App
927	59.5	3.7	1470	7	US-11-217-529-78356	Sequence 78356, A	1005	59	3.7	4308	7	US-11-217-529-82409	Sequence 82409, A
928	59.5	3.7	1506	7	US-11-217-529-284	Sequence 284, App	1006	59	3.7	4553	6	US-10-505-928-95	Sequence 95, Appl
929	59.5	3.7	1533	7	US-11-217-529-78051	Sequence 78051, A	1007	59	3.7	5171	6	US-10-501-834-216	Sequence 216, App
930	59.5	3.7	1635	7	US-11-217-529-79132	Sequence 79132, A	1008	59	3.7	6108	7	US-11-217-529-79911	Sequence 79911, A
931	59.5	3.7	1731	7	US-11-217-529-191194	Sequence 191194, A	c1009	59	3.7	6218	6	US-10-505-928-460	Sequence 460, App
932	59.5	3.7	1860	7	US-11-217-529-78566	Sequence 78566, A	1010	59	3.7	7131	7	US-11-217-529-77074	Sequence 77074, A
933	59.5	3.7	1890	7	US-11-217-529-78412	Sequence 78412, A	1011	59	3.7	15456	7	US-11-324-284-22	Sequence 22, Appl
934	59.5	3.7	1995	7	US-11-217-529-5393	Sequence 5393, Ap	1012	58.5	3.6	336	6	US-11-211-917-27	Sequence 27, Appl
935	59.5	3.7	2130	7	US-11-217-529-2017	Sequence 2017, Ap	1013	58.5	3.6	616	6	US-10-488-619-1840	Sequence 1840, Ap
936	59.5	3.7	2142	7	US-11-217-529-81955	Sequence 81955, A	1014	58.5	3.6	636	7	US-11-302-678-24	Sequence 24, Appl
c 937	59.5	3.7	2199	7	US-11-217-529-79391	Sequence 79391, A	1015	58.5	3.6	639	7	US-11-217-529-81468	Sequence 81468, A
938	59.5	3.7	2261	6	US-10-511-937-415	Sequence 415, App	c1016	58.5	3.6	729	6	US-10-488-619-2264	Sequence 2264, Ap

c1017	58.5	3.6	916	6	US-10-511-937-2921	Sequence 2921, Ap	1092	58	3.6	1848	7	US-11-217-529-79326	Sequence 79326, A
1018	58.5	3.6	918	7	US-11-217-529-1084	Sequence 1084, Ap	1093	58	3.6	1860	7	US-11-217-529-1515	Sequence 1515, Ap
1019	58.5	3.6	1050	7	US-11-217-529-1431	Sequence 1431, Ap	1094	58	3.6	1899	7	US-11-217-529-613	Sequence 613, App
1020	58.5	3.6	1083	7	US-11-217-529-80396	Sequence 80396, A	c1095	58	3.6	1956	7	US-11-217-529-4011	Sequence 4011, App
1021	58.5	3.6	1131	7	US-11-217-529-191110	Sequence 191110, A	c1096	58	3.6	2136	7	US-11-217-529-1356	Sequence 1356, Ap
1022	58.5	3.6	1341	7	US-11-217-529-78898	Sequence 78898, A	1097	58	3.6	2187	7	US-11-217-529-4382	Sequence 4382, Ap
1023	58.5	3.6	1377	7	US-11-318-156-1	Sequence 1, Appli	c1098	58	3.6	2164	7	US-11-217-529-1048	Sequence 1048, Ap
1024	58.5	3.6	1380	7	US-11-217-529-76526	Sequence 76526, A	c1099	58	3.6	2395	7	US-11-101-316-139	Sequence 139, App
1025	58.5	3.6	1449	7	US-11-217-529-2200	Sequence 2200, Ap	c1099	58	3.6	2500	6	US-10-505-928-394	Sequence 394, App
1026	58.5	3.6	1461	7	US-11-217-529-2098	Sequence 2098, Ap	1100	58	3.6	2511	7	US-11-217-529-76023	Sequence 76023, A
1028	58.5	3.6	1593	7	US-11-217-529-4414	Sequence 4414, Ap	1101	58	3.6	2694	7	US-11-217-529-77312	Sequence 77312, A
1029	58.5	3.6	1647	7	US-11-217-529-2095	Sequence 2095, Ap	1102	58	3.6	2716	7	US-11-246-976-2	Sequence 2, Appli
1030	58.5	3.6	1677	7	US-11-217-529-76495	Sequence 76495, A	1103	58	3.6	2716	7	US-11-246-976-4	Sequence 4, Appli
c1032	58.5	3.6	1804	7	US-11-251-465-7	Sequence 7, Appli	c1104	58	3.6	2815	6	US-10-505-928-526	Sequence 526, App
1033	58.5	3.6	1841	6	US-10-516-478-5	Sequence 5, Appli	1105	58	3.6	2815	6	US-10-505-928-526	Sequence 526, App
1034	58.5	3.6	1851	7	US-11-217-529-76890	Sequence 76890, A	1106	58	3.6	2931	7	US-11-217-529-3611	Sequence 3611, Ap
c1035	58.5	3.6	1875	1	US-09-949-925-40	Sequence 40, Appl	1107	58	3.6	3012	7	US-11-217-529-3912	Sequence 3912, Ap
1036	58.5	3.6	1890	7	US-11-217-529-599	Sequence 599, App	1108	58	3.6	3141	6	US-10-511-937-467	Sequence 467, App
1037	58.5	3.6	1953	7	US-11-217-529-1409	Sequence 1409, Ap	1109	58	3.6	3219	7	US-11-217-529-79	Sequence 79, Appl
1038	58.5	3.6	1961	6	US-10-505-928-80	Sequence 80, Appl	1110	58	3.6	3228	7	US-11-217-529-190982	Sequence 190982
1039	58.5	3.6	2010	7	US-11-217-529-2941	Sequence 2941, Ap	1111	58	3.6	3448	6	US-10-505-928-222	Sequence 222, App
1040	58.5	3.6	2079	7	US-11-217-529-76446	Sequence 76446, A	1112	58	3.6	3396	6	US-10-505-928-346	Sequence 346, App
1041	58.5	3.6	2130	7	US-11-217-529-854	Sequence 854, App	1113	58	3.6	3534	7	US-11-217-529-940	Sequence 940, App
1042	58.5	3.6	2250	7	US-11-170-482-15	Sequence 15, Appl	1114	58	3.6	3558	6	US-10-505-928-814	Sequence 814, App
1043	58.5	3.6	2270	7	US-11-302-678-22	Sequence 22, Appl	1115	58	3.6	3663	7	US-11-217-529-1369	Sequence 1369, Ap
1044	58.5	3.6	2430	7	US-11-217-529-1233	Sequence 1233, Ap	1116	58	3.6	3780	7	US-11-217-529-3169	Sequence 3169, Ap
1045	58.5	3.6	2457	7	US-11-217-529-79549	Sequence 79549, A	1117	58	3.6	4052	7	US-11-312-958-5	Sequence 5, Appli
1046	58.5	3.6	2472	7	US-11-217-529-77064	Sequence 77064, A	c1118	58	3.6	4482	7	US-11-217-529-4753	Sequence 4753, Ap
1047	58.5	3.6	2484	7	US-11-145-307A-65	Sequence 65, Appl	1119	58	3.6	4654	6	US-10-505-928-20	Sequence 20, Appl
1048	58.5	3.6	2929	6	US-10-511-455-61	Sequence 61, Appl	1120	58	3.6	5314	7	US-11-217-529-191147	Sequence 191147
1049	58.5	3.6	3036	7	US-11-217-529-76857	Sequence 76857, A	c1121	58	3.6	5408	6	US-10-485-397-9	Sequence 9, Appli
c1050	58.5	3.6	3096	7	US-11-217-529-80400	Sequence 80400, A	1122	58	3.6	6432	7	US-11-217-529-82021	Sequence 82021, A
1051	58.5	3.6	3105	7	US-11-217-529-771	Sequence 771, App	1123	58	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1052	58.5	3.6	3342	7	US-11-217-529-76353	Sequence 76353, A	1124	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1053	58.5	3.6	3342	7	US-11-217-529-76353	Sequence 76353, A	c1125	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1054	58.5	3.6	3516	6	US-10-505-928-106	Sequence 106, App	1126	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1055	58.5	3.6	4010	6	US-10-511-937-359	Sequence 359, App	1127	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1056	58.5	3.6	4283	7	US-11-327-900-5	Sequence 5, Appli	1128	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1057	58.5	3.6	4419	7	US-11-251-465-8	Sequence 8, Appli	1129	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1058	58.5	3.6	6371	7	US-11-251-465-8	Sequence 8, Appli	1130	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1059	58.5	3.6	7280	6	US-10-505-928-842	Sequence 842, App	1131	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1060	58	3.6	737	6	US-10-983-104-13	Sequence 13, Appl	1132	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1061	58	3.6	350	7	US-11-254-679-69	Sequence 69, Appl	1133	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1062	58	3.6	375	6	US-10-546-594-120	Sequence 120, App	1134	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1063	58	3.6	391	6	US-10-488-619-963	Sequence 963, App	c1135	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1064	58	3.6	392	6	US-10-488-619-963	Sequence 963, App	c1136	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1065	58	3.6	401	6	US-10-488-619-307	Sequence 307, App	1137	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1066	58	3.6	422	7	US-11-170-482-3	Sequence 3, Appli	1138	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1067	58	3.6	423	6	US-10-488-619-54	Sequence 54, Appl	1139	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1068	58	3.6	612	7	US-11-217-529-82720	Sequence 82720, A	c1140	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1069	58	3.6	717	7	US-11-217-529-75883	Sequence 75883, A	1141	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1070	58	3.6	767	6	US-10-488-619-1124	Sequence 1124, Ap	1142	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1071	58	3.6	812	6	US-10-510-162-1	Sequence 1, Appli	1143	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1072	58	3.6	852	7	US-11-217-529-81970	Sequence 81970, A	1144	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1073	58	3.6	1005	7	US-11-217-529-1550	Sequence 1550, Ap	1145	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1074	58	3.6	1008	7	US-11-217-529-5897	Sequence 5897, Ap	1146	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1075	58	3.6	1098	7	US-11-217-529-77660	Sequence 77660, A	1147	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1076	58	3.6	1119	7	US-11-217-529-81068	Sequence 81068, A	1148	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1077	58	3.6	1311	7	US-11-217-529-1776	Sequence 1776, Ap	1149	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1078	58	3.6	1325	6	US-10-505-928-742	Sequence 742, App	1150	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1079	58	3.6	1335	7	US-11-217-529-75936	Sequence 75936, A	1151	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1080	58	3.6	1356	7	US-11-217-529-489	Sequence 489, App	1152	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1081	58	3.6	1467	7	US-11-217-529-5430	Sequence 5430, Ap	1153	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1082	58	3.6	1518	7	US-11-217-529-76312	Sequence 76312, A	1154	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1083	58	3.6	1563	7	US-11-217-529-82562	Sequence 82562, A	1155	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1084	58	3.6	1644	7	US-11-217-529-76716	Sequence 76716, A	1156	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1085	58	3.6	1656	7	US-11-217-529-318	Sequence 318, App	1157	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1086	58	3.6	1656	7	US-11-217-529-77297	Sequence 77297, A	1158	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1087	58	3.6	1665	7	US-11-217-529-78311	Sequence 78311, A	1159	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1088	58	3.6	1692	7	US-11-217-529-551	Sequence 551, App	1160	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1089	58	3.6	1776	7	US-11-217-529-3257	Sequence 3257, Ap	c1161	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
1090	58	3.6	1833	7	US-11-217-529-3564	Sequence 3564, Ap	1162	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
c1091	58	3.6	1848	7	US-11-145-307A-37	Sequence 37, Appl	1163	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
							1164	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App
							1165	57.5	3.6	7465	6	US-10-505-928-311	Sequence 311, App

1166	57.5	3.6	2202	7	US-11-217-529-77013	Sequence 77013, A	1240	57	3.6	1965	7	US-11-217-529-1789	Sequence 1789, Ap
1167	57.5	3.6	2202	7	US-11-217-529-81299	Sequence 81299, A	c1241	57	3.6	2098	7	US-11-242-111-10	Sequence 10, Appl
1168	57.5	3.6	2259	7	US-11-217-529-374	Sequence 274, App	c1242	57	3.6	2140	6	US-10-505-928-707	Sequence 707, App
1169	57.5	3.6	2259	7	US-11-217-529-5592	Sequence 5592, Ap	1243	57	3.6	2145	7	US-11-217-529-81000	Sequence 81000, A
1170	57.5	3.6	2262	7	US-11-217-529-173643	Sequence 173643, A	1244	57	3.6	2244	7	US-11-217-529-1676	Sequence 1676, Ap
1171	57.5	3.6	2310	7	US-11-217-529-2824	Sequence 2824, Ap	1245	57	3.6	2259	7	US-11-217-529-75982	Sequence 75982, A
c1172	57.5	3.6	2400	7	US-11-217-529-77227	Sequence 77227, A	1246	57	3.6	2265	7	US-11-217-529-78929	Sequence 78929, A
1173	57.5	3.6	2454	7	US-11-217-529-6038	Sequence 6038, Ap	1247	57	3.6	2376	6	US-10-511-937-2800	Sequence 2800, Ap
1174	57.5	3.6	2537	7	US-11-217-529-3979	Sequence 3979, Ap	c1248	57	3.6	2405	7	US-11-258-767-57	Sequence 57, Appl
c1175	57.5	3.6	2547	7	US-11-217-529-174300	Sequence 174300, A	1250	57	3.6	2436	7	US-11-101-316-99	Sequence 99, Appl
1176	57.5	3.6	2580	7	US-11-217-529-78462	Sequence 78462, A	1251	57	3.6	2439	7	US-11-252-276-3	Sequence 3, Appli
1177	57.5	3.6	2694	7	US-11-217-529-5531	Sequence 5531, Ap	1252	57	3.6	2439	7	US-11-252-276-5	Sequence 5, Appli
1178	57.5	3.6	2732	6	US-10-473-173-75	Sequence 75, Appl	1253	57	3.6	2439	7	US-11-217-529-78157	Sequence 78157, A
1179	57.5	3.6	2745	7	US-11-217-529-476	Sequence 476, App	c1254	57	3.6	2481	7	US-11-217-529-79177	Sequence 79177, A
c1180	57.5	3.6	2889	6	US-10-511-937-627	Sequence 627, App	1256	57	3.6	2628	7	US-11-217-529-82381	Sequence 82381, A
1181	57.5	3.6	2934	7	US-11-217-529-683	Sequence 683, App	1257	57	3.6	2694	7	US-11-217-529-78800	Sequence 78800, A
1182	57.5	3.6	2997	7	US-11-217-529-1582	Sequence 1582, App	1258	57	3.6	2781	6	US-10-370-959-12	Sequence 12, Appl
1183	57.5	3.6	3117	7	US-11-217-529-774	Sequence 774, App	1259	57	3.6	2871	6	US-10-511-455-40	Sequence 40, Appl
1184	57.5	3.6	3213	7	US-11-217-529-77302	Sequence 77302, A	1260	57	3.6	2916	7	US-11-217-529-81609	Sequence 81609, A
1185	57.5	3.6	3213	7	US-11-217-529-2671	Sequence 2671, Ap	1261	57	3.6	3048	6	US-10-511-455-49	Sequence 49, Appl
1186	57.5	3.6	3549	7	US-11-217-529-2180	Sequence 2180, Ap	1262	57	3.6	3171	7	US-11-252-276-31	Sequence 31, Appl
1187	57.5	3.6	3631	6	US-10-199-329-5	Sequence 5, Appli	1263	57	3.6	3178	7	US-11-252-276-151	Sequence 151, Appl
1188	57.5	3.6	3648	7	US-11-217-529-684	Sequence 684, App	1264	57	3.6	3393	7	US-11-217-529-78969	Sequence 78969, A
1189	57.5	3.6	3655	6	US-10-511-937-346	Sequence 346, App	1265	57	3.6	3597	6	US-10-505-928-651	Sequence 651, App
1190	57.5	3.6	3783	6	US-10-473-173-100	Sequence 100, App	1266	57	3.6	3597	6	US-10-511-937-2802	Sequence 2802, Ap
1191	57.5	3.6	4068	7	US-11-217-529-487	Sequence 487, Appl	1267	57	3.6	3669	7	US-11-181-115-36	Sequence 36, Appl
1192	57.5	3.6	4074	7	US-11-217-529-4467	Sequence 4467, Ap	1268	57	3.6	3813	7	US-11-217-529-77490	Sequence 77490, A
1193	57.5	3.6	4845	7	US-11-217-529-2846	Sequence 2846, Ap	1269	57	3.6	3903	7	US-11-217-529-2311	Sequence 2311, Ap
1194	57.5	3.6	6811	7	US-11-066-633-2	Sequence 2, Appli	c1270	57	3.6	3982	6	US-10-505-928-350	Sequence 350, App
1195	57.5	3.6	9588	6	US-10-505-928-101	Sequence 101, App	1271	57	3.6	4056	7	US-11-217-529-76436	Sequence 76436, A
1196	57.5	3.6	9890	6	US-10-473-173-5	Sequence 5, Appli	1272	57	3.6	4077	6	US-10-505-928-134	Sequence 134, App
c1197	57	3.6	375	7	US-11-217-529-82191	Sequence 82191, A	1273	57	3.6	4143	7	US-11-217-529-81170	Sequence 81170, A
1198	57	3.6	508	6	US-10-488-619-1426	Sequence 1426, Ap	c1274	57	3.6	4592	6	US-10-511-937-646	Sequence 646, App
1199	57	3.6	514	6	US-10-981-300-9	Sequence 9, Appli	c1275	57	3.6	4828	6	US-10-511-937-555	Sequence 555, App
c1200	57	3.6	540	6	US-10-488-619-2626	Sequence 2626, Ap	1276	57	3.6	4833	7	US-11-252-276-21	Sequence 21, Appl
1201	57	3.6	750	6	US-11-217-529-4205	Sequence 4205, Ap	c1277	57	3.6	4863	7	US-11-217-529-75783	Sequence 75783, A
1202	57	3.6	750	6	US-10-524-433-12	Sequence 12, Appl	1278	57	3.6	4911	7	US-11-217-529-75783	Sequence 75783, A
1203	57	3.6	828	7	US-11-217-529-76763	Sequence 76763, A	1279	57	3.6	5251	7	US-11-217-529-191127	Sequence 191127, A
1204	57	3.6	858	7	US-11-217-529-80270	Sequence 80270, A	1280	57	3.6	5262	7	US-11-217-529-2924	Sequence 2924, Ap
c1205	57	3.6	861	7	US-11-217-529-5731	Sequence 5731, Ap	c1281	57	3.6	6417	6	US-10-511-937-540	Sequence 540, App
1206	57	3.6	867	7	US-11-217-529-76840	Sequence 76840, A	1282	57	3.6	7701	6	US-10-520-210-25	Sequence 25, Appl
1207	57	3.6	921	7	US-11-217-529-80604	Sequence 80604, A	1283	57	3.6	7926	6	US-10-520-210-24	Sequence 24, Appl
c1208	57	3.6	945	7	US-11-217-529-82783	Sequence 82783, A	1284	57	3.6	12515	6	US-10-505-928-358	Sequence 358, App
1210	57	3.6	984	7	US-11-217-529-5301	Sequence 5301, Ap	1285	56.5	3.5	337	7	US-11-239-308-17	Sequence 17, Appl
c1211	57	3.6	1003	7	US-11-226-605-53	Sequence 53, Appl	1286	56.5	3.5	369	6	US-10-983-104-14	Sequence 14, Appl
1212	57	3.6	1071	7	US-11-217-529-3180	Sequence 3180, Ap	c1287	56.5	3.5	550	7	US-11-145-307A-178	Sequence 178, App
c1213	57	3.6	1079	1	US-09-949-925-11	Sequence 11, Appl	1288	56.5	3.5	573	7	US-11-217-529-77032	Sequence 77032, A
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-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMBOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_estl1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1434	89.3	1143	6	CR605305
2	1434	89.3	1329	6	CR618843
3	1434	89.3	1511	6	CR621227
4	1434	89.3	1598	6	CR610497

CR599894	full-leng
CR621411	full-leng
AL570767	AL570767
AV610145	Sus scrofa
BX375908	BX375908
DT815807	LB01628.C
DT809612	LB0164.CR
CR5984497	DOG_EST_P
AX463390	BX463390
BX463390	BX463390
AK013914	Mus muscu
AK010616	Mus muscu
AK078128	Mus muscu
AK028757	Mus muscu
BU750529	CH3#034.A
BU750529	CH3#019.G
CH3478394	CH3478394
AL576601	AL576601
BX345642	BX345642
AK153636	Mus muscu
CR984480	DOG_EST_P
AX920450	BX920450
CR347901	CR347901
CR994893	CR994893
AL522795	AL522795
CR089477	BX089477
BI739594	603361849
BY762264	BY762264
CB992775	AGENCOURT
BM704815	UI-E-C11-
BP144687	BP144687
BU730372	UI-E-C11-
BI916904	603177882
BX364561	BX364561
CR200154	MNS00784
CR864800	nacl2b02.
CR988602	DOG_EST_P
CK109386	AGENCOURT
CK004092	AGENCOURT
AL548850	AL548850
DV920425	LB02921.C
BX396187	BX396187
GL-CF-738	GL-CF-738
BM704455	UI-E-C11-
AL573256	AL573256
MXS32767	MXS32767
AL544740	AL544740
BX332035	BX332035
CF127652	UI-HF-ET0
DA215500	DA215500
DR769469	ILLUMIGEN
BY710030	BY710030
BU736621	UI-E-C11-
CN543699	UI-R-D21-
BY712952	BY712952
DB289885	DB289885
BO210314	UI-R-DV1-
CR747485	CR747485
AA406389	zv12a02.r
DA293800	AGENCOURT
CB994990	AGENCOURT
BP427892	BP427892
BX345643	BX345643
DB235140	DB235140
DA860407	DA860407
DA190737	DA190737
AA725566	a124d02.8
CR763155	AGENCOURT
DA224223	DA224223
CG482835	602502431
CV558990	UI-M-H20-
AM034135	AM034135
AM034782	AM034782
CO658359	DG34-2f23
DA313755	DA313755

[illegible]

224	456.5	28.4	424	12	CG500225	OST42979	297	433	27.0	1008	4	BX424991	BX424991
225	455.5	28.4	810	4	CG382308	662081 NC	298	432.5	26.9	773	9	CG470770	JGI_X2G45
226	455	28.3	722	5	C805128	UI-M-GW0-	299	432.5	26.9	783	3	BP706416	BP706416
227	454.5	28.3	330	12	CG495419	OST34804	300	432.5	26.9	876	3	BU912987	BU912987
228	454.5	28.3	377	12	CG493835	OST39661	301	432.5	26.9	1074	10	DM033067	DM033067
229	454.5	28.3	854	10	DT289652	JGI_CAAW2	302	432	26.9	617	1	AJ740389	AFW220-H1
230	453.5	28.3	922	3	BO894075	AGENCOURT	303	432	26.9	801	9	CX504625	JGI_X2G64
231	453	28.2	541	12	CG570152	OST198791	C 304	432	26.9	808	4	BX771524	BX771524
232	452.5	28.2	343	12	CG496542	OST36638	305	431.5	26.9	870	4	CA988238	AGENCOURT
233	452.5	28.2	445	12	CG551037	OST157738	306	431.5	26.9	1057	4	BX398530	BX398530
234	452.5	28.2	445	12	CG568316	OST195236	C 307	431	26.9	879	9	DN085105	JGI_CABE5
235	452.5	28.2	482	12	CG539560	OST130739	308	431	26.9	926	4	CA788073	AGENCOURT
236	452.5	28.2	513	10	CG625693	OST332417	309	431	26.9	972	3	BM804795	AGENCOURT
237	451.5	28.1	640	10	DR435443	DR435443 nsw18903.	310	430.5	26.8	454	12	CG507182	OST57042
238	451.5	28.1	803	10	DV834666	LB0196.CR	311	430.5	26.8	782	5	CK807818	AGENCOURT
239	450	28.0	435	12	CG506984	OST56760	C 312	430.5	26.8	811	4	BX761240	BX761240
240	450	28.0	933	14	AY417084	Homo sapi	313	430.5	26.8	935	4	CA787978	AGENCOURT
241	449	28.0	1237	9	DN660583	CEC47-F04	314	430	26.8	935	3	BU916163	AGENCOURT
242	448	27.9	534	9	DA125245	DA125245	315	430	26.8	941	3	BU912943	AGENCOURT
243	447.5	27.9	924	3	BQ933843	AGENCOURT	316	430	26.8	1146	10	DT982431	CLJ200-D1
244	446.5	27.8	339	12	CG534649	CG534649 OST68527	317	430	26.8	1200	9	DN698730	CLJ19-C11
245	446.5	27.8	380	12	CG535813	OST123088	318	429.5	26.8	1289	10	DT958182	DT958182
246	446.5	27.8	408	12	CG605104	OST281411	319	429	26.7	885	10	DT314434	JGI_CAA4X
247	446.5	27.8	454	12	CG523774	OST96556	320	428.5	26.7	437	12	CG541713	CG541713
248	445.5	27.8	468	12	CG635842	OST359320	321	428.5	26.7	827	8	CR445411	CR445411
249	444	27.7	403	1	AI332805	qp74b05.x	322	428	26.7	533	12	CG663203	CG663203
250	444	27.7	714	8	CN366080	170004243	323	427.5	26.6	806	9	CG336513	JGI_X2T119
251	444	27.7	765	4	BX453733	BX453733	324	427	26.6	347	12	CG514469	CG514469
252	443.5	27.6	445	12	CG616790	CG616790 OST309395	325	427	26.6	1088	10	DM621443	DM621443
253	443.5	27.6	840	9	CX456159	JGI_X2G53	326	427	26.6	1244	9	DN675756	DN675756
254	443	27.6	1051	10	DM027391	DM027391 FWT239-CO	327	426.5	26.6	944	4	CA982250	AGENCOURT
255	442	27.5	308	7	AW593293	AW593293 hg12e12.x	328	425.5	26.5	928	4	BX399333	BX399333
256	442	27.5	426	9	DN085106	JGI_CABE5	329	424.5	26.4	422	12	CG504458	CG504458
257	441.5	27.5	428	12	CG658984	OST436033	330	424.5	26.4	969	10	DM639665	DM639665
258	441.5	27.5	457	12	CG655131	CG655131 OST425078	331	424	26.4	1420	9	DN664864	DN664864
259	441.5	27.5	823	9	CX826569	JGI_CAAK5	332	423.5	26.4	332	12	CG6661287	CG6661287
260	441.5	27.5	882	4	BX728325	BX728325	C 333	423	26.4	356	1	AI017553	AI017553
261	441	27.5	706	1	AJ740392	AJ740392	334	423	26.4	1280	10	DT972551	DT972551
262	441	27.5	766	5	CF347228	CF347228 AGENCOURT	335	422.5	26.3	1123	10	DM032988	DM032988
263	440.5	27.4	790	10	DT402855	DT402855 JGI_CAB15	336	422	26.3	1040	10	DM659166	DM659166
264	440.5	27.4	848	9	CX494851	CX494851 JGI_X2G37	337	422	26.3	1131	10	DT972813	DT972813
265	440.5	27.4	853	10	DT410137	DT410137 JGI_CAB11	338	422	26.3	1290	9	DM675156	DM675156
266	439.5	27.4	846	9	CK470602	CK470602 JGI_X2G44	339	420.5	26.2	330	12	CG571674	CG571674
267	439.5	27.4	993	10	DM635833	DM635833 CLJ365-B0	340	420.5	26.2	356	12	CG599907	CG599907
268	439	27.3	833	8	CN837756	CN837756 AGENCOURT	341	420.5	26.2	496	12	CG643181	CG643181
269	438.5	27.3	403	12	CG572210	CG572210 OST202508	342	420	26.2	853	9	CX418954	CX418954
270	438.5	27.3	876	8	CV812074	CV812074 AGENCOURT	343	418	26.0	799	8	CR409324	CR409324
271	438.5	27.3	883	8	CX313706	CX313706 JGI_X2T93	344	417	26.0	1054	4	BX379087	BX379087
272	438	27.3	843	3	BU750528	BU750528 CH3#034_A	345	416.5	26.0	1300	10	DT957099	DT957099
273	438	27.3	914	4	CA973670	CA973670 AGENCOURT	346	416	25.9	892	4	BA789011	BA789011
274	437.5	27.3	1049	1	AL540733	AL540733 AGENCOURT	347	415.5	25.9	981	3	BQ694910	BQ694910
275	437.5	27.3	1144	9	DN699320	DN699320 CLJ22-H04	348	414	25.8	489	12	CG625930	CG625930
276	437	27.2	534	12	CG654462	CG654462 OST422612	C 349	413	25.7	732	9	DR107648	DR107648
277	437	27.2	833	9	CX510407	CX510407 JGI_X2G36	350	412.5	25.7	762	8	CA207969	CA207969
278	436.5	27.2	786	5	CF216645	CF216645 AGENCOURT	351	412.5	25.7	836	5	CF147692	CF147692
279	436.5	27.2	819	9	CX923799	CX923799 JGI_CAA99	352	412	25.7	451	12	CG650844	CG650844
280	436.5	27.2	889	4	BX406216	BX406216 BX406216	353	412	25.7	764	10	DR175152	DR175152
281	436	27.2	930	8	CN315936	CN315936 AGENCOURT	354	411.5	25.6	762	3	BP676567	BP676567
282	435.5	27.1	339	12	CG598159	CG598159 OST262313	355	411.5	25.6	866	3	BU908994	BU908994
283	435.5	27.1	408	12	CG648347	CG648347 DT401540	356	411	25.6	841	4	CA790268	CA790268
284	435.5	27.1	495	12	CG640726	CG640726 OST374100	357	411	25.6	923	1	AL550639	AL550639
285	435.5	27.1	502	4	BY477702	BY477702 JGI_X2G13	358	411	25.6	1462	9	DN664598	DN664598
286	435.5	27.1	774	9	CX426771	CX426771 JGI_X2G51	359	410.5	25.6	743	8	CA243586	CA243586
287	435	27.1	870	9	CX483181	CX483181 JGI_X2G51	360	410.5	25.6	1161	1	AL550180	AL550180
288	434	27.0	804	8	CF414090	CF414090 JGI_X2G51	361	408.5	25.5	817	4	CH558461	CH558461
289	434	27.0	825	9	CX443355	CX443355 JGI_X2G90	C 362	408	25.4	343	7	AW264246	AW264246
290	433.5	27.0	751	9	CX413556	CX413556 JGI_X2G58	C 363	408	25.4	345	7	AW474261	AW474261
291	433.5	27.0	816	5	CF220776	CF220776 AGENCOURT	C 364	408	25.4	346	1	A1366088	A1366088
292	433.5	27.0	819	10	DT400258	DT400258 JGI_CAB14	365	408	25.4	411	12	CG598103	CG598103
293	433.5	27.0	856	5	CF237672	CF237672 AGENCOURT	366	408	25.4	412	12	CG585601	CG585601
294	433.5	27.0	860	9	CX337259	CX337259 JGI_X2T19	367	408	25.4	470	7	BF189965	BF189965
295	433	27.0	557	8	C0592416	DG2-62c19	368	407	25.4	932	4	CA792692	CA792692
296	433	27.0	760	9	CX892430	JGI_CAAW4	369	407	25.4	1514	6	CR617300	full-long

370	407	25.4	1594	6	CR617107	CR617107 full-leng	381	23.7	355	1	AI052637	AI052637 oz18a04.x
371	406.5	25.3	902	3	BQ737472	AGENCOURT	381	23.7	644	5	CD372018	CD372018 UT-R-G00-
372	406	25.3	1359	6	CNS0EP53	CR635265 Tetraodon	381	23.7	738	8	CR564541	CR564541 CR564541
373	405.5	25.3	346	12	CG559115	CG559115 OST436465	380.5	23.7	311	12	CG513247	CG513247 OST66533
374	405.5	25.3	759	3	CV562830	UT-M-HL0-	379.5	23.6	735	3	CF521823	CF521823 AGENCOURT
375	405.5	25.3	939	3	BM921497	AGENCOURT	379.5	23.6	963	3	BU912290	BU912290 AGENCOURT
376	405	25.2	532	9	DB336126	DB336126 DB336126	379	23.6	803	9	CR788836	CR788836 HSC3 103
377	404.5	25.2	1000	10	DW629854	CLJ356-D1	378.5	23.6	666	4	CA334547	CA334547 NISC 1a10
378	404	25.2	492	8	CO594463	DG2-96d21	378.5	23.6	711	8	CR202776	CR202776 WNS04731
379	404	25.2	2014	6	HSM801619	AL136649 Homo sapi	378.5	23.6	959	8	CN024397	CN024397 AGENCOURT
380	403.5	25.1	700	9	CF760486	AGENCOURT	376.5	23.5	386	12	CG615648	CG615648 OST306561
381	403.5	25.1	763	3	BP677127	BP677127	376.5	23.5	761	5	CF521799	CF521799 AGENCOURT
382	403	25.1	423	12	CG595339	CG595339 OST254712	376.5	23.5	772	9	DN948507	DN948507 AGENCOURT
383	403	25.1	914	1	AL583534	AL583534 AL583534	376	23.4	376	1	AI849051	AI849051 UT-M-AHL-
384	403	25.1	1127	1	AL549623	AL549623 AL549623	376	23.4	810	8	CO799885	CO799885 AGENCOURT
385	402.5	25.1	442	12	CG668943	CG668943 OST465402	375.5	23.4	572	8	CN110984	CN110984 EC2CAA36B
386	402.5	25.1	1034	1	AL553289	AL553289	375.5	23.4	578	10	DT816959	DT816959 LB0165.CR
387	401.5	25.0	1488	6	CR608619	full-leng	375.5	23.4	355	12	CG564765	CG564765 OST189087
388	400.5	25.0	908	3	BU912219	AGENCOURT	375	23.4	501	12	CG587221	CG587221 OST236599
389	400	24.9	915	3	BU914386	AGENCOURT	375	23.4	501	12	CG587221	CG587221 OST236599
390	399.5	24.9	469	12	CG517537	CG517537 OST78071	373	23.2	534	9	DA231316	DA231316 DA231316
391	399.5	24.9	874	5	CF265792	CF265792 AGENCOURT	373	23.2	870	8	CO929900	CO929900 AGENCOURT
392	399	24.9	392	4	CB133611	K-EST0184	372.5	23.2	345	12	CG666529	CG666529 OST456665
393	399	24.9	651	5	CD806831	UT-M-GW0-	372.5	23.2	375	12	CG624086	CG624086 OST327063
394	398.5	24.8	1020	2	BM548873	BM548873 AGENCOURT	372.5	23.2	426	12	CG604841	CG604841 OST280915
395	398	24.8	1129	9	DN704258	CLJ52-D01	371.5	23.1	624	9	DA371467	DA371467 DA371467
396	397	24.7	894	10	DW642491	DW642491 CLJ374-P2	371.5	23.1	652	1	AL846235	AL846235 AGENCOURT
397	397	24.7	915	10	DW648652	CLJ384-D0	371.5	23.1	817	4	CA789692	CA789692 AGENCOURT
398	396.5	24.7	743	10	DY319046	DY319046 AGENCOURT	370.5	23.1	717	5	CF724990	CF724990 UT-M-G20-
399	396.5	24.7	859	10	DV933392	DV933392 LB03028.C	370.5	23.1	824	9	DB294480	DB294480 DB294480
400	396.5	24.7	947	3	BU912281	AGENCOURT	370	23.1	333	12	CG669324	CG669324 OST466157
401	396	24.7	886	3	BQ945091	AGENCOURT	370	23.1	957	2	BG435143	BG435143 602507157
402	396	24.7	900	14	DQ046257	DQ046257 Homo sapi	369.5	23.0	922	12	CG456904	CG456904 OST37225
403	395.5	24.6	879	5	CB250780	CB250780 AGENCOURT	369.5	23.0	940	8	CN015949	CN015949 AGENCOURT
404	395	24.6	740	4	CD208127	CD208127 AGENCOURT	368.5	22.9	327	12	CG497834	CG497834 OST38673
405	394.5	24.6	844	10	DV818104	DV818104 LB01724.C	368	22.9	622	2	BF916758	BF916758 IL3-UT011
406	394.5	24.6	857	10	DV918318	DV918318 LB02912.C	368	22.9	694	7	AW422931	AW422931 f166803.Y
407	394.5	24.6	876	5	CK948326	CK948326 4073246.B	368	22.9	820	10	DV883268	DV883268 LB02626.C
408	394	24.5	1033	4	BK458171	BK458171 BX458171	367.5	22.9	470	7	BE653351	BE653351 UT-M-AL1-
409	394	24.5	2453	6	AK033574	Mus muscu	367.5	22.9	601	8	CN078561	CN078561 EC2BBA15A
410	393	24.5	399	4	BY514942	BY514942	367.5	22.9	643	4	BX852232	BX852232 BX852232
411	393	24.5	683	10	DT173749	DT173749 JGI ANNO4	367.5	22.9	772	3	BP686752	BP686752 BP686752
412	393	24.5	772	9	DN332017	DN332017 LB3534.0	367	22.9	513	12	CG605974	CG605974 OST283410
413	393	24.5	988	10	DV047935	DV047935 DAY20.19	366.5	22.8	780	10	DT165416	DT165416 JGI ANNO3
414	392	24.4	519	1	AI418268	AI418268 tg36505.x	366.5	22.8	816	10	DV923219	DV923219 LB02930.C
415	392	24.4	900	14	DQ046258	DQ046258 Pan trogl	366	22.8	381	1	AI556456	AI556456 UT-R-C2p-
416	391.5	24.4	993	1	AL560725	AL560725 AL560725	366	22.8	422	12	CG580233	CG580233 OST219462
417	391	24.4	498	8	CO591452	CO591452 DG2-49n6	365.5	22.8	796	9	DR157466	DR157466 HSC2 78
418	389.5	24.3	767	2	EG970299	EG970299 602838903	365.5	22.8	921	3	BU520481	BU520481 AGENCOURT
419	389.5	24.3	824	5	CK470323	CK470323 AGENCOURT	365.5	22.8	957	3	BQ940516	BQ940516 AGENCOURT
420	389	24.2	930	4	BK414581	BK414581 BX414581	365	22.7	689	8	CN368088	CN368088 170005313
421	388	24.2	391	12	CG507979	CG507979 OST58238	365	22.7	819	10	DT680096	DT680096 AGENCOURT
422	388	24.2	767	7	AW175139	AW175139 f132f09.Y	364.5	22.7	560	9	DA399075	DA399075 DA399075
423	388	24.2	889	8	CR976629	CR976629 CR976629	364.5	22.7	855	10	DV852272	DV852272 LB0233.CR
424	387	24.1	941	3	BQ928243	BQ928243 AGENCOURT	363.5	22.6	559	8	CR434750	CR434750 CR434750
425	386	24.0	263	12	CG495820	CG495820 OST35449	363.5	22.6	587	9	DA441303	DA441303 DB441303
426	386	24.0	789	5	CK000533	CK000533 AGENCOURT	363.5	22.6	600	9	DB230115	DB230115 DB230115
427	386	24.0	874	8	CO733078	CO733078 S11T02c04	363.5	22.6	651	9	DA863107	DA863107 DA863107
428	385.5	24.0	630	1	AL859286	AL859286	363.5	22.6	819	9	DN897011	DN897011 nsp16e01.
429	385.5	24.0	721	10	DR722564	DR722564 AGENCOURT	363	22.6	731	8	CX165301	CX165301 HSC2 89
430	385.5	24.0	825	5	CF222141	CF222141 AGENCOURT	362.5	22.6	798	9	DR158357	DR158357 HSC2 79
431	385	24.0	896	4	BK379273	BK379273 BX379273	362.5	22.6	816	10	DV834662	DV834662 LB0196.CR
432	385	24.0	905	3	BU182251	BU182251 AGENCOURT	362	22.6	527	9	DB070238	DB070238 DB070238
433	385	24.0	1321	6	CN0582X3	CG538890 Tetraodon	361.5	22.5	571	1	AU310695	AU310695 AU310695
434	384	23.9	906	3	BU916159	BU916159 AGENCOURT	361.5	22.5	907	3	BQ928239	BQ928239 AGENCOURT
435	383.5	23.9	607	3	BQ133340	fz40c11.Y	361	22.5	595	9	DA112680	DA112680 DA112680
436	383.5	23.9	782	9	CK436075	JGI_XZGS8	360.5	22.5	700	9	CK455776	CK455776 JGI XZGS3
437	382.5	23.8	814	8	CO810649	CO810649 AGENCOURT	359.5	22.4	807	5	CK769977	CK769977 958092.MA
438	382.5	23.8	833	9	CK934062	JGI_CAA03	359	22.4	593	2	BF916759	BF916759 IL3-UT011
439	382	23.8	869	8	CN014069	CN014069 AGENCOURT	358.5	22.3	423	12	CG535702	CG535702 OST122877
440	382	23.8	898	5	CF223675	CF223675 AGENCOURT	358.5	22.3	847	8	CN014126	CN014126 AGENCOURT
441	381.5	23.8	916	5	CK407789	AUF 1fLvr	358.5	22.3	880	3	BU542115	BU542115 AGENCOURT
442	381.5	23.8	939	2	BM451147	BM451147 AGENCOURT	358.5	22.3	884	2	BI771277	BI771277 603054624

516	358	22.3	427	5	CJ188900	CJ188900	589	341.5	21.3	832	7	BE563419
517	357.5	22.3	723	5	CF288279	AGENCYCOURT	590	341.5	21.3	968	4	CA982290
518	357.5	22.3	812	5	CO426708	UI-M-HUO-	591	341	21.2	545	7	AW082343
519	357	22.2	707	8	CO433531	UI-M-HXO-	592	340.5	21.2	725	2	BG965243
520	356.5	22.2	709	2	BG862721	602796454	593	340.5	21.2	786	8	CN302526
521	356.5	22.2	730	8	CN366076	170005331	594	340.5	21.2	855	2	B1554904
522	356.5	22.2	847	7	BE549277	601077966	595	340	21.2	738	1	AL546926
523	356	22.2	383	12	CG624186	OST327284	596	340	21.2	790	9	DB166292
524	355	22.1	226	7	AW900593	CMI-NN100	597	339.5	21.2	671	1	AL859372
525	354.5	22.1	402	12	CG555414	OST170007	598	339	21.1	344	12	CG509012
526	354.5	22.1	583	8	CN366082	170005325	599	338.5	21.1	626	3	BU273030
527	354.5	22.1	630	3	BQ390372	NISC_mg12	600	338.5	21.1	753	8	CX205944
528	354.5	22.1	638	1	AL863639	AL863639	601	338.5	21.1	853	9	CX755127
529	354	22.1	537	9	DA857664	DA857664	602	338.5	21.1	938	8	CN021991
530	354	22.1	680	5	CF899461	A0303802-	603	338	21.1	855	10	DT127507
531	354	22.1	910	3	BQ895192	AGENCYCOURT	604	337.5	21.0	484	9	CX893673
532	352.5	22.0	539	1	AL918320	AL918320	605	337.5	21.0	537	9	DA871999
533	352.5	22.0	826	8	CO922861	AGENCYCOURT	606	337.5	21.0	692	8	CN302521
534	352	21.9	419	12	CG621100	OST318899	607	337.5	21.0	700	3	BP677680
535	351.5	21.9	546	7	AW652985	101460 MA	608	337.5	21.0	738	9	DN997061
536	351.5	21.9	696	10	DY315045	AGENCYCOURT	609	336.5	21.0	785	9	DA730791
537	351	21.9	802	9	DN997828	TC114147	610	336	20.9	340	2	BF932982
538	350.5	21.8	726	2	B1656384	603285705	611	335.5	20.9	510	2	BF916525
539	350.5	21.8	848	8	CN020324	AGENCYCOURT	612	335	20.9	592	7	BE681207
540	350.5	21.8	867	4	CA788252	AGENCYCOURT	613	335	20.9	711	10	DT078729
541	350.5	21.8	878	3	BQ887533	AGENCYCOURT	614	334.5	20.8	708	9	CX452574
542	350	21.8	792	2	B1772811	603054461	615	334.5	20.8	794	10	DT827817
543	350	21.8	1039	3	BQ057979	AGENCYCOURT	616	334.5	20.8	835	10	DR727214
544	349.5	21.8	570	9	DA039603	DA039603	617	334	20.8	637	5	CF924873
545	349.5	21.8	889	3	BQ730650	AGENCYCOURT	618	334	20.8	834	10	DV596148
546	349	21.7	479	7	AW652305	100208 MA	619	333.5	20.8	258	12	CG425392
547	349	21.7	757	4	CB953709	AGENCYCOURT	620	333.5	20.8	664	7	BB623335
548	348.5	21.7	548	9	DA725684	DA725684	621	333.5	20.8	797	5	CD642524
549	348.5	21.7	579	9	DA450847	DA450847	622	333	20.7	583	3	BP320097
550	348.5	21.7	761	2	BQ734603	BQ734603	623	333	20.7	695	5	CK949734
551	348.5	21.7	772	9	BQ639445	UMC-bem1v	624	333	20.7	727	5	CK961924
552	348.5	21.7	1009	3	BQ732954	AGENCYCOURT	625	333	20.7	769	10	DV835556
553	348	21.7	269	12	CG643424	OST382333	626	333	20.7	868	10	DT881549
554	348	21.7	520	9	DA757224	DA757224	627	333	20.7	897	4	CD050073
555	348	21.7	891	5	CD384890	AGENCYCOURT	628	332.5	20.7	533	3	BM751080
556	347.5	21.7	411	12	CG570174	OST198840	629	332.5	20.7	582	7	BE698576
557	347.5	21.7	560	9	DB163445	DB163445	630	332	20.7	857	4	BX342099
558	347	21.6	389	4	BY508025	BY508025	631	331.5	20.7	724	9	DA646403
559	347	21.6	860	8	CR791424	CR791424	632	331.5	20.7	895	7	BE907794
560	346.5	21.6	779	5	CK691256	CK691256	633	331	20.6	898	8	CN506689
561	346.5	21.6	891	2	B1261031	602972219	634	331	20.6	906	2	BG831312
562	346	21.6	916	3	BQ502623	AGENCYCOURT	635	330.5	20.6	649	2	BQ060110
563	345.5	21.5	798	5	CD656120	AGENCYCOURT	636	330.5	20.6	695	5	CF951399
564	345.5	21.5	886	8	CN014625	AGENCYCOURT	637	330.5	20.6	810	8	CR856526
565	345.5	21.5	888	8	CO248933	AGENCYCOURT	638	329.5	20.5	645	1	AL846277
566	344.5	21.5	484	10	W80145	me91501.r1	639	329.5	20.5	713	10	DR715064
567	344.5	21.5	673	8	CN366089	170005313	640	329	20.5	536	7	BE698574
568	344.5	21.5	821	10	DV597488	AGENCYCOURT	641	328.5	20.5	598	1	AL856990
569	344.5	21.5	850	8	CN320000	AGENCYCOURT	642	328.5	20.5	736	10	DR723216
570	344	21.4	582	3	BP229524	BP229524	643	328.5	20.5	848	5	CK699066
571	343.5	21.4	553	3	DA717102	DA717102	644	327.5	20.4	807	9	DA729943
572	343.5	21.4	629	1	AL657340	AL657340	645	327.5	20.4	845	9	DN640515
573	343.5	21.4	661	1	AL872179	AL872179	646	327	20.4	285	12	CG439366
574	343.5	21.4	900	5	CN022276	AGENCYCOURT	647	327	20.4	335	2	BF932991
575	343	21.4	1319	6	CN5089YJ	Tetraodon	648	326.5	20.3	876	9	CN171168
576	342.5	21.3	516	2	BQ029408	BQ029408	649	326.5	20.3	668	8	DA411205
577	342.5	21.3	551	9	DA433624	DA433624	650	326	20.3	586	2	B1706452
578	342.5	21.3	552	7	BF043334	BF043334	651	326	20.3	711	4	CA750190
579	342.5	21.3	766	1	AM140548	AM140548	652	325.5	20.3	677	8	CV027585
580	342.5	21.3	808	2	B1833165	603090890	653	325.5	20.3	782	4	BG639555
581	342	21.3	385	12	CG524839	OST992240	654	325	20.2	734	4	CB595085
582	341.5	21.3	726	8	CN302510	170005318	655	324.5	20.2	537	7	BE026113
583	341.5	21.3	732	9	DN601876	HESC3_73	656	324.5	20.2	624	1	AL968116
584	341.5	21.3	739	8	CN302524	170004710	657	324.5	20.2	635	1	AL878745
585	341.5	21.3	752	8	CN302505	170004245	658	324.5	20.2	641	1	AL892168
586	341.5	21.3	755	8	CN302501	170005322	659	324.5	20.2	695	5	CF286290
587	341.5	21.3	796	5	CD653854	AGENCYCOURT	660	324	20.2	525	9	DN354248
588	341.5	21.3	805	5	CF785901	AGENCYCOURT	661	323.5	20.2	528	8	CN302527

662	323.5	20.2	687	3	BP690580	BP690580 BP690580	735	307.5	19.2	600	5	CF907778	CF907778 A0514E12-
663	323.5	20.2	782	10	DT109155	DT109155 JGI_ANN01	736	307.5	19.2	617	1	AL879507	AL879507 AL879507
664	323.5	20.2	834	4	CA789049	CA789049 AGENCOURT	737	307.5	19.2	818	5	CD759332	CD759332 AGENCOURT
665	323.5	20.2	848	8	CN019851	CN019851 AGENCOURT	738	307.5	19.1	214	12	CG502403	CG502403 OST47345
666	323.5	20.1	498	7	BF614832	BF614832 dg17f12.y	739	306.5	19.1	613	1	DL957122	DL957122 AL957122
667	323.5	20.1	556	7	BE698578	BE698578 RCO-UT002	740	306	19.1	733	10	DV598350	DV598350 AGENCOURT
668	323.5	20.1	588	7	BE698579	BE698579 RCO-UT002	741	306	19.1	773	5	CK477501	CK477501 AGENCOURT
669	323.5	20.1	776	4	CB237206	CB237206 AGENCOURT	742	306	19.1	780	8	CV113731	CV113731 AGENCOURT
670	322.5	20.1	396	4	CB772835	CB772835 AMGNNUC:S	743	305.5	19.0	535	7	BE709697	BE709697 IL3-HT061
671	322.5	20.1	611	1	AL594502	AL594502 AL594502	744	305.5	19.0	581	7	BE698577	BE698577 RCO-UT002
672	322.5	20.1	761	10	DT075217	DT075217 AGENCOURT	745	305.5	19.0	763	2	BE921356	BE921356 602842417
673	322.5	20.1	677	8	CR546744	CR546744 DXF2p470N	746	305.5	19.0	962	10	DT343771	DT343771 JGI_CAAAX8
674	322.5	20.1	749	5	CK698709	CK698709 ZF101-P00	747	305.5	19.0	581	2	BF818581	BF818581 WB3-CI018
675	322.5	20.1	875	2	BI655543	BI655543 603285613	748	305	19.0	667	2	BI654678	BI654678 603285596
676	321.5	20.0	633	2	BJ057623	BJ057623 BJ057623	749	305	19.0	772	10	DT167418	DT167418 JGI_ANN04
677	321.5	20.0	682	4	BX851305	BX851305 BX851305	750	305	19.0	629	8	CN366077	CN366077 170005325
678	321.5	20.0	714	10	DR726507	DR726507 AGENCOURT	751	304.5	19.0	629	8	CN366077	CN366077 170005325
679	321.5	20.0	779	8	CV484820	CV484820 AGENCOURT	752	304	19.0	994	3	BU913991	BU913991 AGENCOURT
680	321.5	20.0	480	3	BM797742	BM797742 K-EST0081	753	303	18.9	603	1	AV602516	AV602516 AV602516
681	320.5	20.0	796	10	DT066083	DT066083 AGENCOURT	754	303	18.9	736	5	CK367468	CK367468 AGENCOURT
682	320.5	20.0	797	9	DN948340	DN948340 AGENCOURT	755	303	18.9	798	5	CK481268	CK481268 AGENCOURT
683	320	19.9	550	1	AI942636	AI942636 fc73h07.y	756	303	18.9	848	3	BU176471	BU176471 AGENCOURT
684	320	19.9	722	10	DT820755	DT820755 LB00216.C	757	302.5	18.8	765	2	BG721684	BG721684 602695833
685	319.5	19.9	721	2	BM046916	BM046916 603627134	758	302	18.8	468	4	CA988641	CA988641 AGENCOURT
686	319.5	19.9	844	8	CO803873	CO803873 AGENCOURT	759	302	18.8	772	10	DV597115	DV597115 AGENCOURT
687	319	19.9	735	2	BG468155	BG468155 602509740	760	302	18.8	784	5	CK710370	CK710370 ZF201-P00
688	318.5	19.8	612	7	BE783711	BE783711 601471108	761	301.5	18.8	627	5	CF734484	CF734484 UI-M-HA0-
689	318.5	19.8	687	9	DB294533	DB294533 DB294533	762	301.5	18.8	697	5	CJ044502	CJ044502 CJO44502
690	318	19.8	513	12	CG512160	CG512160 OST64940	763	301.5	18.8	1236	6	AK160648	AK160648 Mub muscu
691	318	19.8	699	8	CK977397	CK977397 4108735 B	764	301	18.8	336	12	CG637270	CG637270 OST363580
692	318	19.8	847	3	BU912742	BU912742 AGENCOURT	765	301	18.8	679	5	CF900715	CF900715 A0319A05-
693	317	19.8	771	8	CX244417	CX244417 NNA01671	766	301	18.8	778	5	CK238939	CK238939 AGENCOURT
694	316.5	19.7	645	4	BY795995	BY795995 BY795995	767	301	18.8	786	7	BE306404	BE306404 601103309
695	316.5	19.7	824	5	CF289551	CF289551 AGENCOURT	768	300.5	18.7	634	8	CA219635	CA219635 MNS34770
696	316	19.7	747	10	DT878311	DT878311 AGENCOURT	769	300.5	18.7	638	9	DA326428	DA326428 DA326428
697	315.5	19.7	627	5	CK730521	CK730521 oc0410.y	770	300.5	18.7	638	9	DA863059	DA863059 DA863059
698	315.5	19.7	641	5	CK624709	CK624709 m124c12.y	771	300.5	18.7	639	8	CO593712	CO593712 DG2-82B22
699	315	19.6	769	8	CV107264	CV107264 AGENCOURT	772	300.5	18.7	714	4	BY708143	BY708143 BY708143
700	314.5	19.6	620	1	AL876779	AL876779 AL876779	773	300.5	18.7	758	5	CF996930	CF996930 AGENCOURT
701	314.5	19.6	620	1	AL892876	AL892876 AL892876	774	300.5	18.7	991	7	BE563484	BE563484 601334965
702	314.5	19.6	750	5	CF595870	CF595870 AGENCOURT	775	300	18.7	578	9	DB173414	DB173414 DB173414
703	314.5	19.6	817	5	CV483562	CV483562 AGENCOURT	776	300	18.7	762	8	CN177139	CN177139 AGENCOURT
704	314	19.6	670	7	BE728270	BE728270 601562134	777	299.5	18.7	579	8	CN366085	CN366085 170005326
705	314	19.6	759	5	CK238273	CK238273 AGENCOURT	778	299.5	18.7	731	8	CK366075	CK366075 170005312
706	314	19.6	872	9	DN022854	DN022854 JGI_CAAK3	779	299	18.6	715	2	BF717855	BF717855 fd52802.y
707	312.5	19.5	661	9	DA863489	DA863489 DA863489	780	299	18.6	745	2	BI458028	BI458028 603199034
708	312.5	19.5	740	9	DA641718	DA641718 DA641718	781	298.5	18.6	897	4	BK355860	BK355860 BK355860
709	312	19.4	291	1	AA865038	AA865038 oh32b03.8	782	298	18.6	609	5	DA832633	DA832633 DA832633
710	312	19.4	473	7	BE709749	BE709749 IL3-HT061	783	297.5	18.5	781	5	CK624406	CK624406 m120q12.y
711	312	19.4	738	5	CF221589	CF221589 AGENCOURT	784	297	18.5	668	4	CB4411569	CB4411569 692057 NA
712	312	19.4	741	5	CF997897	CF997897 AGENCOURT	785	296.5	18.5	790	10	DT300724	DT300724 JGI_CAAW1
713	312	19.4	894	9	DN022853	DN022853 JGI_CAAK3	786	296	18.4	473	2	BG548970	BG548970 RUA2 c1on
714	311.5	19.4	726	4	BX116635	BX116635 BX116635	787	295.5	18.4	295	12	CG515752	CG515752 OST72660
715	311.5	19.4	758	4	CB987241	CB987241 AGENCOURT	788	295.5	18.4	485	4	CB727038	CB727038 AMGNNUC:N
716	311.5	19.4	775	10	DR882022	DR882022 AGENCOURT	789	295.5	18.4	559	9	DB082583	DB082583 DB082583
717	311	19.4	801	8	CV103872	CV103872 AGENCOURT	790	295.5	18.4	832	8	CO554162	CO554162 AGENCOURT
718	311	19.4	809	5	CK025774	CK025774 AGENCOURT	791	295.5	18.4	832	8	CO554162	CO554162 AGENCOURT
719	310.5	19.3	622	9	AL897939	AL897939 AL897939	792	295	18.4	788	10	DT182545	DT182545 JGI_ANN04
720	310.5	19.3	652	9	DA415551	DA415551 DA415551	793	295	18.4	862	9	CK465276	CK465276 JGI_XZG46
721	310.5	19.3	661	2	BG611699	BG611699 602613057	794	294.5	18.3	806	9	DB0895025	DB0895025 nao62a11.
722	310	19.3	780	10	DT178993	DT178993 JGI_ANN04	795	294.5	18.3	957	3	BO958397	BO958397 AGENCOURT
723	310	19.3	900	8	CN177719	CN177719 AGENCOURT	796	294	18.3	464	3	BM723158	BM723158 UI-E-E01-
724	309.5	19.3	553	2	BF723249	BF723249 mab29g02.	797	294	18.3	466	1	AI201753	AI201753 qb76d11.x
725	309.5	19.3	619	10	DR337704	DR337704 LB01117.C	798	294	18.3	564	9	DA810910	DA810910 DA810910
726	309.5	19.3	603	7	BE744931	BE744931 601576391	799	293.5	18.2	940	3	BQ944890	BQ944890 AGENCOURT
727	309	19.3	927	1	AL890116	AL890116 AL890116	800	292.5	18.2	722	5	CD683717	CD683717 EST237 hu
728	309	19.3	650	1	AL658021	AL658021 AL658021	801	292	18.2	333	12	CG650172	CG650172 OST406631
729	309	19.3	806	7	BE783472	BE783472 601471501	802	292	18.2	660	9	DA863360	DA863360 DA863360
730	308.5	19.2	741	9	DR004360	DR004360 TC124603	803	292	18.2	667	4	CB418724	CB418724 591542 MA
731	308	19.2	281	12	CG515360	CG515360 OST70439	804	292	18.2	745	2	BI080347	BI080347 602876784
732	308	19.2	617	1	AL873699	AL873699 AL873699	805	291.5	18.2	608	2	BG815656	BG815656 dad70c11.
733	308	19.2	723	2	BG974950	BG974950 602844949	806	291	18.1	459	3	BQ132546	BQ132546 f260f09.y
734	308	19.2	779	2	BM047466	BM047466 603628759	807	290.5	18.1	600	2	BI991715	BI991715 4104-46 M

808	230.5	18.1	770	10	DV598693	AGENCOURT	881	268	16.7	666	8	CN702372	E0461E05-
809	290	18.1	635	1	AL896070	AL896070	c 882	267.5	16.7	617	11	BH055189	BH055189 RPI-24-2
810	290	18.1	694	5	CK792923	AGENCOURT	883	267	16.6	761	10	DV600519	DV600519 AGENCOURT
811	289.5	18.0	748	2	DA731878	DA731878	884	266.5	16.6	565	2	BI901451	BI901451 idf0a12.Y
812	289	18.0	588	2	BJ058095	BJ058095	885	266.5	16.6	650	5	CK692178	CK692178 ZF101-P00
813	289	18.0	643	1	AL872898	AL872898	886	266.5	16.6	900	4	CB319992	CB319992 AGENCOURT
814	288.5	18.0	566	9	DB125538	DB125538	887	266	16.6	611	9	DN351295	DN351295 LI83579-0
815	288.5	18.0	566	9	DB233297	DB233297	888	265.5	16.5	563	2	BI901913	BI901913 idf5b10.Y
816	288.5	18.0	610	3	BQ392121	NISC ng22	889	265.5	16.5	567	9	DA966835	DA966835 DA966835
817	288	17.9	679	9	DN864801	nac12b02.	890	265.5	16.5	568	9	DB149308	DB149308 DB149308
818	287.5	17.9	598	1	AL968085	AL968085	891	265.5	16.5	596	9	DA243934	DA243934
819	287	17.9	759	5	CK865917	AGENCOURT	892	265.5	16.5	596	9	DA306094	DA306094
820	287	17.9	837	2	BI769525	60305080	893	265.5	16.5	596	9	DA389031	DA389031
821	286.5	17.9	646	9	DA227610	DA227610	894	265.5	16.5	597	9	DA331677	DA331677
822	286.5	17.9	907	7	BE743983	BE743983	895	265.5	16.5	612	1	AL778870	AL778870
823	286	17.8	552	7	AW871744	da93e07.Y	896	265.5	16.5	631	9	DA218924	DA218924
824	286	17.8	555	9	DB133113	DB133113	897	265.5	16.5	735	3	BU277958	BU277958 603611795
825	286	17.8	556	9	DB065689	DB065689	898	265	16.5	705	2	BG970928	BG970928 602839910
826	286	17.8	565	9	DA233331	DA233331	899	264.5	16.5	587	9	DB291660	DB291660 DB291660
827	286	17.8	895	3	BU165328	AGENCOURT	900	264.5	16.5	885	4	CA789691	CA789691 AGENCOURT
828	285.5	17.8	673	8	CN302518	CN302518	901	264	16.4	598	1	AL894010	AL894010
829	285	17.8	627	1	AL775021	AL775021	902	264	16.4	868	9	CK760937	CK760937 AGENCOURT
c 830	284	17.7	464	1	AL140139	q87e10.X	903	264	16.4	891	10	DT868565	DT868565 AGENCOURT
831	284	17.7	710	9	DB165867	DB165867	904	263.5	16.4	473	8	CR758630	CR758630
832	284	17.7	925	5	CK418372	AUF IPova	905	263.5	16.4	587	2	BI715824	BI715824 ic63f09.Y
833	283.5	17.7	454	1	AI416013	fb30h11.Y	906	263.5	16.4	681	7	BE974183	BE974183 601680540
834	283.5	17.7	635	3	BQ393937	NISC ng06	907	263.5	16.4	793	2	BI868231	BI868231 603392178
835	283.5	17.7	1273	9	DN670182	CFW55-B01	908	263	16.4	640	8	CN721071	CN721071 E0815E02-
836	283	17.6	734	5	CF348124	AGENCOURT	909	262.5	16.4	574	9	DA249708	DA249708
837	283	17.6	791	8	CV109767	AGENCOURT	910	262.5	16.4	585	2	BM004794	BM004794 da336h07.
838	282	17.6	553	9	DB220037	DB220037	911	262.5	16.4	607	1	AL632871	AL632871
839	282	17.6	663	10	DV877464	DV877464	912	262.5	16.4	674	5	CD693893	CD693893 EST10416
840	281.5	17.5	472	3	BQ745868	UI-M-EX0-	913	262.5	16.4	893	3	BU192286	BU192286 AGENCOURT
841	281	17.5	508	8	CN366078	CN366078	914	262	16.3	765	10	DV591946	DV591946 AGENCOURT
842	281	17.5	522	9	DA991815	DA991815	915	261.5	16.3	518	2	BG731189	BG731189 dae11f11.
843	281	17.5	844	10	DR721224	AGENCOURT	916	261.5	16.3	588	4	BY712182	BY712182
844	280.5	17.5	639	9	DA410655	DA410655	917	261.5	16.3	591	1	AL655957	AL655957
845	279.5	17.4	587	1	AL802054	AL802054	918	261.5	16.3	592	9	DA336494	DA336494
846	279	17.4	497	2	BI319823	ie44b05.Y	919	261.5	16.3	592	9	DB230069	DB230069
847	278.5	17.4	1055	4	BK378088	BK378088	920	261.5	16.3	593	9	DA125529	DA125529
848	278	17.3	607	1	AL642674	AL642674	921	261.5	16.3	593	9	DA334409	DA334409
849	278	17.3	693	10	DT722442	DT722442	922	261.5	16.3	594	9	DA245480	DA245480
850	278	17.3	769	10	DT111209	JGI ANNOI	923	261.5	16.3	595	9	DA331839	DA331839
851	278	17.3	778	10	DT862655	AGENCOURT	924	261.5	16.3	598	9	DA243832	DA243832
852	277.5	17.3	523	1	AL777628	AL777628	925	261	16.3	534	8	CV221551	CV221551 Le mx0.49
853	277.5	17.3	657	2	BI547643	BI547643	926	261	16.3	633	8	CV221551	CV221551 Le mx0.49
854	277.5	17.3	667	8	CK164837	CK164837	927	261	16.3	1170	2	BM551307	BM551307 AGENCOURT
855	277.5	17.3	673	9	DN997320	DN997320	928	260.5	16.2	553	2	BI439295	BI439295 ic62a05.Y
856	277	17.3	508	9	DB263521	DB263521	929	260.5	16.2	585	5	CK029800	CK029800 AGENCOURT
857	276	17.2	949	3	BU517996	BU517996	930	260.5	16.2	592	9	DA238808	DA238808
858	275	17.1	770	9	CK439077	JGI XZG70	931	260.5	16.2	600	2	BM192221	BM192221 da121a08.
859	275	17.1	811	7	BE746660	BE746660	932	260	16.2	728	10	DT847008	DT847008 LB00475.C
c 860	274	17.1	292	1	AJ940336	AJ940336	933	259.5	16.2	582	9	DB250685	DB250685
861	274	17.1	384	12	CG508260	CG508260	934	259.5	16.2	589	9	DB266183	DB266183
862	274	17.1	643	2	BI822014	BI822014	935	259.5	16.2	613	2	BI442231	BI442231 da137e12.
863	273.5	17.0	561	9	DB235646	DB235646	936	259.5	16.2	624	9	DR157877	DR157877 HESC2.83
864	273.5	17.0	569	2	BJ039261	BJ039261	937	259.5	16.2	673	3	BU129583	BU129583 603117196
865	273.5	17.0	600	9	DA116749	DA116749	938	259.5	16.2	693	3	BU130131	BU130131 603116985
866	272	16.9	830	9	CK495230	JGI XZG37	939	259	16.1	318	7	BB218442	BB218442
867	271	16.9	245	7	AW865421	PM4-SN002	940	259	16.1	718	2	BG243874	BG243874 602357913
868	271	16.9	766	10	DT090179	JGI ANNK2	941	258.5	16.1	979	9	DA812069	DA812069
869	270.5	16.9	388	4	CA873163	K923C07-	942	257.5	16.0	579	9	DA189617	DA189617
870	270.5	16.9	407	7	AW463902	AW463902	943	257.5	16.0	580	9	DA189340	DA189340
871	270.5	16.9	556	9	DA31868	DA31868	944	257.5	16.0	580	9	DB153130	DB153130
872	269.5	16.8	449	7	AW136481	ui-H-B11-	945	257.5	16.0	581	3	BP342398	BP342398
873	269.5	16.8	453	1	AI650503	AI650503	946	257.5	16.0	581	9	DA194190	DA194190
874	269	16.8	653	8	CO050703	Le mx0.17	947	257.5	16.0	581	9	DA279270	DA279270
c 875	268.5	16.7	473	8	CR759539	CR759539	948	257.5	16.0	581	9	DA332721	DA332721
876	268.5	16.7	595	9	DA240812	DA240812	949	257.5	16.0	581	9	DA391224	DA391224
877	268.5	16.7	599	9	DA864230	DA864230	950	257.5	16.0	581	9	DB225201	DB225201
878	268.5	16.7	602	9	DB163956	DB163956	951	257.5	16.0	582	9	DA354920	DA354920
879	268.5	16.7	609	8	CV573437	od36b12.Y	952	257.5	16.0	582	9	DB019753	DB019753
880	268.5	16.7	838	5	CK865360	AGENCOURT	953	257.5	16.0	583	9	DA189301	DA189301

954	257.5	16.0	583	9	DB095020	DB095020	DB095020	1027	254.5	15.9	547	9	DA413365	DA413365
955	257.5	16.0	584	9	DA332543	DA332543	DA332543	1028	254.5	15.9	551	9	DB277680	DB277680
956	257.5	16.0	584	9	DA395356	DA395356	DA395356	1029	254.5	15.9	553	9	DA183597	DA183597
957	257.5	16.0	584	9	DB233258	DB233258	DB233258	1030	254.5	15.9	553	9	DA192849	DA192849
958	257.5	16.0	585	9	DA290655	DA290655	DA290655	1031	254.5	15.9	553	9	DA326728	DA326728
959	257.5	16.0	586	9	DA236916	DA236916	DA236916	1032	254.5	15.9	553	9	DA389581	DA389581
960	257.5	16.0	586	9	DB087084	DB087084	DB087084	1033	254.5	15.9	553	9	DA401481	DA401481
961	257.5	16.0	586	9	DB230477	DB230477	DB230477	1034	254.5	15.9	553	9	DA405294	DA405294
962	257.5	16.0	587	9	DA111809	DA111809	DA111809	1035	254.5	15.9	553	9	DB286024	DB286024
963	257.5	16.0	589	9	DA244447	DA244447	DA244447	1036	254.5	15.9	554	9	DB286245	DB286245
964	257.5	16.0	589	9	DB232272	DB232272	DB232272	1037	254.5	15.9	555	9	DA861637	DA861637
965	257.5	16.0	590	9	DA241541	DA241541	DA241541	1038	254.5	15.9	555	9	DB278237	DB278237
966	257.5	16.0	590	9	DA387149	DA387149	DA387149	1039	254.5	15.9	556	9	DA097647	DA097647
967	257.5	16.0	592	9	DA193232	DA193232	DA193232	1040	254.5	15.9	556	9	DA288233	DA288233
968	257.5	16.0	593	9	DA241128	DA241128	DA241128	1041	254.5	15.9	556	9	DA299140	DA299140
969	257.5	16.0	849	7	BF339081	BF339081	BF339081	1042	254.5	15.9	556	9	DA402323	DA402323
970	256.5	16.0	581	3	BP374612	BP374612	BP374612	1043	254.5	15.9	556	9	DA404957	DA404957
971	256.5	16.0	582	3	BP251065	BP251065	BP251065	1044	254.5	15.9	556	9	DB063538	DB063538
972	256.5	16.0	595	9	DA248018	DA248018	DA248018	1045	254.5	15.9	557	9	DA220444	DA220444
973	256.5	16.0	598	8	CN302531	CN302531	CN302531	1046	254.5	15.9	558	9	DB148670	DB148670
974	256.5	16.0	601	2	B1447896	B1447896	B1447896	1047	254.5	15.9	559	1	AU280703	AU280703
975	256.5	16.0	657	3	BM786395	BM786395	BM786395	1048	254.5	15.9	559	9	DA186083	DA186083
976	256.5	16.0	873	10	DT880922	DT880922	DT880922	1049	254.5	15.9	559	9	DA323931	DA323931
977	256.5	16.0	908	8	CO803906	CO803906	CO803906	1050	254.5	15.9	559	9	DA406770	DA406770
978	256.5	16.0	1121	3	BU913480	BU913480	BU913480	1051	254.5	15.9	559	9	DA407257	DA407257
979	256.5	16.0	604	8	CX060193	CX060193	CX060193	1052	254.5	15.9	559	9	DA409990	DA409990
980	256.5	16.0	612	2	B1889677	B1889677	B1889677	1053	254.5	15.9	559	9	DA415942	DA415942
981	255.5	15.9	555	2	B1901831	B1901831	B1901831	1054	254.5	15.9	559	9	DA856574	DA856574
982	255.5	15.9	567	9	DA197445	DA197445	DA197445	1055	254.5	15.9	559	9	DB223548	DB223548
983	255.5	15.9	568	9	DA314205	DA314205	DA314205	1056	254.5	15.9	560	9	DA219249	DA219249
984	255.5	15.9	568	9	DA324013	DA324013	DA324013	1057	254.5	15.9	560	9	DA310843	DA310843
985	255.5	15.9	568	9	DA326492	DA326492	DA326492	1058	254.5	15.9	560	9	DA406834	DA406834
986	255.5	15.9	568	9	DA405757	DA405757	DA405757	1059	254.5	15.9	560	9	DA413040	DA413040
987	255.5	15.9	568	9	DA545136	DA545136	DA545136	1060	254.5	15.9	560	9	DB069903	DB069903
988	255.5	15.9	569	9	DA228891	DA228891	DA228891	1061	254.5	15.9	561	9	DA326594	DA326594
989	255.5	15.9	569	9	DA322463	DA322463	DA322463	1062	254.5	15.9	562	9	DA398057	DA398057
990	255.5	15.9	569	9	DA336133	DA336133	DA336133	1063	254.5	15.9	563	9	DA193181	DA193181
991	255.5	15.9	569	9	DA399321	DA399321	DA399321	1064	254.5	15.9	563	9	DA227727	DA227727
992	255.5	15.9	569	9	DA759454	DA759454	DA759454	1065	254.5	15.9	563	9	DA301150	DA301150
993	255.5	15.9	570	9	DA100752	DA100752	DA100752	1066	254.5	15.9	563	9	DA327445	DA327445
994	255.5	15.9	570	9	DA14759	DA14759	DA14759	1067	254.5	15.9	563	9	DA390969	DA390969
995	255.5	15.9	571	9	DA191241	DA191241	DA191241	1068	254.5	15.9	563	9	DA396242	DA396242
996	255.5	15.9	571	9	DA338467	DA338467	DA338467	1069	254.5	15.9	563	9	DA400350	DA400350
997	255.5	15.9	571	9	DB076572	DB076572	DB076572	1070	254.5	15.9	563	9	DA404306	DA404306
998	255.5	15.9	571	9	DB170516	DB170516	DB170516	1071	254.5	15.9	563	9	DA414435	DA414435
999	255.5	15.9	571	9	DB229121	DB229121	DB229121	1072	254.5	15.9	563	9	DA758822	DA758822
1000	255.5	15.9	572	9	DA333005	DA333005	DA333005	1073	254.5	15.9	563	9	DA861025	DA861025
1001	255.5	15.9	572	9	DA727038	DA727038	DA727038	1074	254.5	15.9	563	9	DB073820	DB073820
1002	255.5	15.9	573	9	DA236959	DA236959	DA236959	1075	254.5	15.9	563	9	DB086633	DB086633
1003	255.5	15.9	573	9	DB076420	DB076420	DB076420	1076	254.5	15.9	563	9	DB291621	DB291621
1004	255.5	15.9	574	9	DA236068	DA236068	DA236068	1077	254.5	15.9	564	9	DA095976	DA095976
1005	255.5	15.9	574	9	DA236326	DA236326	DA236326	1078	254.5	15.9	564	9	DA738622	DA738622
1006	255.5	15.9	574	9	DA247887	DA247887	DA247887	1079	254.5	15.9	565	9	DA211872	DA211872
1007	255.5	15.9	574	9	DA276326	DA276326	DA276326	1080	254.5	15.9	565	9	DA406262	DA406262
1008	255.5	15.9	574	9	DA856095	DA856095	DA856095	1081	254.5	15.9	566	9	DA213366	DA213366
1009	255.5	15.9	576	9	DB079170	DB079170	DB079170	1082	254.5	15.9	566	9	DA227179	DA227179
1010	255.5	15.9	576	9	DB290169	DB290169	DB290169	1083	254.5	15.9	566	9	DA330173	DA330173
1011	255.5	15.9	577	9	DA101356	DA101356	DA101356	1084	254.5	15.9	567	9	DA154310	DA154310
1012	255.5	15.9	577	9	DA247867	DA247867	DA247867	1085	254.5	15.9	567	9	DA232247	DA232247
1013	255.5	15.9	577	9	DA335078	DA335078	DA335078	1086	254.5	15.9	567	9	DA309754	DA309754
1014	255.5	15.9	577	9	DB078836	DB078836	DB078836	1087	254.5	15.9	567	9	DA314344	DA314344
1015	255.5	15.9	577	9	DB224164	DB224164	DB224164	1088	254.5	15.9	567	9	DA398147	DA398147
1016	255.5	15.9	578	9	DA333347	DA333347	DA333347	1089	254.5	15.9	567	9	DB233660	DB233660
1017	255.5	15.9	578	9	DA853577	DA853577	DA853577	1090	254.5	15.9	568	9	DA326059	DA326059
1018	255.5	15.9	579	9	DA093448	DA093448	DA093448	1091	254.5	15.9	582	9	DA394401	DA394401
1019	255.5	15.9	579	9	DA318565	DA318565	DA318565	1092	254.5	15.9	835	7	BE740414	BE740414
1020	255.5	15.9	579	9	DA336487	DA336487	DA336487	1093	254.5	15.9	1069	9	DN703510	DN703510
1021	255.5	15.9	580	9	DA333655	DA333655	DA333655	1094	254.5	15.8	956	8	CN016876	CN016876
1022	255.5	15.9	620	9	DA811961	DA811961	DA811961	1095	253.5	15.8	561	9	DA778273	DA778273
1023	255.5	15.9	693	5	CK710559	CK710559	CK710559	1096	253.5	15.8	563	9	DA409384	DA409384
1024	255.5	15.9	713	10	DV595105	DV595105	DV595105	1097	253.5	15.8	565	9	DA094216	DA094216
1025	254.5	15.9	571	1	AL898638	AL898638	AL898638	1098	253.5	15.8	568	9	DA304354	DA304354
1026	254.5	15.9	541	4	CB274688	CB274688	CB274688	1099	253.5	15.8	571	9	DA304354	DA304354

1100	253.5	15.8	658	3	BM837513	BM837513 K-EST0113	1173	249	15.5	913	7	BE912082	BE912082 601663261
1101	253	15.8	586	9	DA240720	DA240720	1174	248.5	15.5	551	9	DA758345	DA758345
1102	253	15.8	593	9	DA402971	DA402971	1175	248.5	15.5	520	1	AJ448243	AJ448243
1103	253	15.8	602	9	DA127769	DA127769	1176	248.5	15.5	665	5	CD685173	CD685173 EST1693 h
1104	253	15.8	767	8	CN024222	AGENCOURT	1177	248	15.5	278	12	CG566581	CG566581 OST192325
1105	252.5	15.7	541	9	DA329621	DA329621	1178	248	15.5	549	9	DA223995	DA223995
1106	252.5	15.7	547	9	DA315430	DA315430	1179	248	15.5	560	9	DA853745	DA853745
1107	252.5	15.7	549	9	DA212767	DA212767	1180	247.5	15.4	535	9	DA408207	DA408207
1108	252.5	15.7	549	9	DA317627	DA317627	1181	247.5	15.4	535	9	DB278390	DB278390
1109	252.5	15.7	549	9	DA402125	DA402125	1182	247.5	15.4	536	9	DB071064	DB071064
1110	252.5	15.7	549	9	DA798693	DA798693	1183	247.5	15.4	537	9	DA215510	DA215510
1111	252.5	15.7	549	9	DB285654	DB285654	1184	247.5	15.4	537	9	DA313849	DA313849
1112	252.5	15.7	550	9	DA402164	DA402164	1185	247.5	15.4	537	9	DA315472	DA315472
1113	252.5	15.7	551	9	DA748268	DA748268	1186	247.5	15.4	537	9	DB276611	DB276611
1114	252.5	15.7	551	9	DB281553	DB281553	1187	247.5	15.4	538	9	DA857657	DA857657
1115	252.5	15.7	552	9	DA095326	DA095326	1188	247.5	15.4	540	9	DA760017	DA760017
1116	252.5	15.7	552	9	DA319531	DA319531	1189	247.5	15.4	561	9	DA405431	DA405431
1117	252.5	15.7	552	9	DA399522	DA399522	1190	247.5	15.4	566	9	DB096233	DB096233
1118	252.5	15.7	552	9	DA409481	DA409481	1191	247.5	15.4	597	5	CK691560	CK691560 ZF101-P00
1119	252.5	15.7	553	9	DA330825	DA330825	1192	247.5	15.4	743	10	DT868924	DT868924 AGENCOURT
1120	252.5	15.7	560	9	DA225665	DA225665	1193	247	15.4	864	2	BG867213	BG867213 602786238
1121	252.5	15.7	561	9	DA346658	DA346658	1194	246.5	15.4	196	14	DU823819	DU823819 H002G08 G
1122	252.5	15.7	571	9	DA858835	DA858835	1195	246.5	15.4	536	9	DB081709	DB081709
1123	252.5	15.7	573	9	DA223792	DA223792	1196	246.5	15.4	549	9	DA406588	DA406588
1124	252.5	15.7	578	9	DA455494	DA455494	1197	246.5	15.4	565	9	DA247419	DA247419
1125	252.5	15.7	587	9	DA192232	DA192232	1198	246.5	15.4	567	9	DA407287	DA407287
1126	252.5	15.7	870	2	BG109047	602281420	1199	246.5	15.4	587	9	DA396428	DA396428
1127	252.5	15.7	900	2	BI453435	603170825	1200	246.5	15.4	598	9	DA809748	DA809748
1128	252	15.7	803	5	CF996271	AGENCOURT	1201	246.5	15.4	784	2	BI835838	BI835838 603087832
1129	251.5	15.7	550	9	DA862970	DA862970	1202	246.5	15.4	895	2	BG387412	BG387412 602456178
1130	251.5	15.7	574	9	DA862970	DA862970	c1203	246	15.3	548	4	BI8392306	BI8392306
1131	251.5	15.7	622	8	CX203536	MNS05855	1204	246	15.3	557	9	DA183995	DA183995
1132	251.5	15.7	748	2	BG747508	602704628	1205	246	15.3	579	9	DA474019	DA474019
1133	251	15.6	376	12	CG570237	OST198959	1206	246	15.3	633	8	CN302516	CN302516 170005326
1134	251	15.6	569	9	DA811193	DA811193	1207	245.5	15.3	557	9	DA401071	DA401071
1135	251	15.6	569	9	DA859268	DA859268	1208	245.5	15.3	564	9	DA384136	DA384136
1136	251	15.6	579	9	DA310705	DA310705	1209	245.5	15.3	579	3	BP289637	BP289637
1137	251	15.6	586	9	DA338845	DA338845	1210	245.5	15.3	583	3	BP229387	BP229387
1138	251	15.6	616	7	BF045629	BP2500068	1211	245.5	15.3	592	9	DA418781	DA418781
1139	251	15.6	756	4	CB180932	AGENCOURT	1212	245.5	15.3	840	4	CB587721	CB587721 AGENCOURT
1140	250.5	15.6	505	1	AI663309	uk27004.Y	1213	245	15.3	580	1	AI723119	AI723119 f25911.Y
1141	250.5	15.6	541	9	DA313533	DA313533	1214	245	15.3	586	4	CB840696	CB840696 M15E-1066
1142	250.5	15.6	541	9	DA857727	DA857727	c1215	245	15.3	891	10	DM020398	DM020398 PMAD-aap7
1143	250.5	15.6	543	9	DA417918	DA417918	1216	245	15.3	1009	10	DM635514	DM635514 CLJ364-J1
1144	250.5	15.6	543	9	DA864930	DA864930	1217	244.5	15.2	477	7	BE927878	BE927878 MR3-CT046
1145	250.5	15.6	544	9	DA211476	DA211476	1218	244.5	15.2	532	9	DA797866	DA797866
1146	250.5	15.6	545	9	DA312024	DA312024	1219	244.5	15.2	533	3	BU058986	BU058986 UI-M-PRO-
1147	250.5	15.6	546	9	DA414270	DA414270	1220	244.5	15.2	533	9	DA217554	DA217554
1148	250.5	15.6	546	9	DA755589	DA755589	1221	244.5	15.2	533	9	DA314600	DA314600
1149	250.5	15.6	546	9	DB224300	DB224300	1222	244.5	15.2	533	9	DB067874	DB067874
1150	250.5	15.6	549	9	DB071512	DB071512	1223	244.5	15.2	534	9	DA315838	DA315838
1151	250.5	15.6	550	9	DA143771	DA143771	1224	244.5	15.2	537	9	DA315236	DA315236
1152	250.5	15.6	553	9	DA279150	DA279150	1225	244.5	15.2	563	9	DA738642	DA738642
1153	250.5	15.6	569	9	DB235855	DB235855	1226	244.5	15.2	584	9	DB239262	DB239262
1154	250.5	15.6	579	9	DA237065	DA237065	1227	244.5	15.2	708	5	CK694007	CK694007 ZF101-P00
1155	250.5	15.6	585	9	DA235213	DA235213	1228	244.5	15.2	979	10	DM653748	DM653748 CLJ391-M1
1156	250.5	15.6	751	7	BF159813	BF159813 601767067	1229	244	15.2	547	1	AI588817	AI588817 f599901.Y
1157	250	15.6	532	9	DA240274	DA240274	1230	244	15.2	599	5	CK688471	CK688471 ZF101-P00
1158	250	15.6	536	1	AL899766	AL899766	1231	244	15.2	876	8	CN323083	CN323083 AGENCOURT
1159	250	15.6	565	9	DA326785	DA326785	1232	244	15.2	1279	10	DT958550	DT958550 CFW157-G1
1160	250	15.6	658	8	CN347866	CN347866 170006000	1233	243.5	15.2	523	3	BJ035828	BJ035828
1161	250	15.6	735	9	DN766711	AGENCOURT	1234	243.5	15.2	536	7	AW765376	AW765376 da90d03.Y
1162	250	15.6	752	10	DV592631	AGENCOURT	1235	243.5	15.2	542	9	DB064860	DB064860
1163	250	15.6	1002	10	DM633314	CLJ361-F0	1236	243.5	15.2	555	2	BG354650	BG354650 77A11 Har
c1164	249.5	15.5	516	2	BF816476	BF816476 MR1-CT018	1237	243.5	15.2	555	9	DA232784	DA232784
1165	249.5	15.5	538	9	DB137044	DB137044	1238	243.5	15.2	565	9	DA311474	DA311474
1166	249.5	15.5	539	9	DB278636	DB278636	1239	243.5	15.2	575	9	DA858459	DA858459
1167	249.5	15.5	556	9	DA759303	DA759303	1240	243.5	15.2	576	9	DA158008	DA158008
1168	249.5	15.5	569	9	DB238960	DB238960	1241	243.5	15.2	611	7	BE272401	BE272401 601126115
c1169	249.5	15.5	611	4	CB441915	CB441915 692441 MA	1242	243	15.1	311	4	CB137090	CB137090 K-EST0189
1170	249.5	15.5	861	2	BG334972	602403404	1243	243	15.1	544	4	CB360423	CB360423 ZF001-P00
1171	249	15.5	197	12	CG539407	OST130413	1244	243	15.1	563	9	DB225366	DB225366
1172	249	15.5	582	9	DA293612	DA293612	1245	242.5	15.1	543	9	DA123810	DA123810

1246	242.5	15.1	565	9	DA948695	DA948695	1319	233.5	14.5	537	9	DB062575	DB062575
1247	242.5	15.1	565	9	DB224170	DB224170	1320	233.5	14.5	564	9	DA223497	DA223497
1248	242.5	15.1	569	9	DA860432	DA860432	1321	233.5	14.5	576	9	DB079946	DB079946
C1249	242	15.1	434	2	BG013078	PM1-GN018	1322	233.5	14.5	591	9	DB237376	DB237376
1250	242	15.1	538	9	DA187075	DA187075	1323	233.5	14.5	628	2	BG970268	BG970268
1251	242	15.1	551	9	DA098010	DA098010	1324	233	14.5	285	12	CG541092	CG541092
1252	242	15.1	710	10	DT121224	JGI_ANN07	1325	233	14.5	287	12	CG646149	CG646149
1253	242	15.1	719	10	AM138448	AM138448	1326	233	14.5	466	1	AA711322	AA711322
1254	242	15.1	807	9	CA498191	JGI_XZG43	1327	233	14.5	494	12	CG650240	CG650240
1255	242	15.1	853	10	DV597342	AGENCOURT	1328	233	14.5	555	9	DB281775	DB281775
1256	242	15.1	928	3	BU504526	AGENCOURT	1329	233	14.5	827	9	CA453779	JGI_XZG55
1257	242	15.1	1367	3	BM922387	AGENCOURT	1330	232.5	14.5	530	9	DB074103	DB074103
C1258	241.5	15.0	428	4	CB794084	AMGNNUC.N	1331	232.5	14.5	552	9	DB065031	DB065031
1259	241.5	15.0	535	9	DB070406	DB070406	1332	232.5	14.5	558	9	DA885886	DA885886
1260	241.5	15.0	548	9	DB219176	DB219176	1333	232.5	14.5	561	9	DA413535	DA413535
1261	241.5	15.0	558	9	DA216590	DA216590	1334	232.5	14.5	577	2	BG830192	BG830192
1262	241.5	15.0	559	9	DA411538	DA411538	1335	232.5	14.5	602	5	CD703043	DA674426
1263	241.5	15.0	567	9	DA097777	DA097777	1336	232.5	14.5	622	5	CD703043	EST19312
1264	241.5	15.0	591	9	DA807791	DA807791	1337	232.5	14.5	734	4	CD053252	LITH2F000
1265	241.5	15.0	1399	9	DN703328	CLJ46-H03	1338	232	14.5	322	12	CG597062	OST7360039
1266	241.5	15.0	715	2	B1112618	602900575	1339	232	14.5	322	3	BU393351	603807260
1267	240.5	15.0	389	9	CX767952	UT-M-HU0-	1340	232	14.5	633	2	BJ074329	BU074329
1268	240.5	15.0	538	9	DB282268	DB282268	1341	232	14.5	799	9	CA468672	JGI_XZG33
1269	240.5	15.0	539	9	DB281978	DB281978	1342	231.5	14.4	326	8	CN302511	170060005
1270	240.5	15.0	561	9	DA504190	DA504190	1343	231.5	14.4	357	4	CB812950	CB812950
1271	240.5	15.0	566	8	CN347865	170059999	1344	231.5	14.4	600	9	DB230375	DB230375
1272	240	15.0	235	8	CV827146	EST001444	1345	231.5	14.4	893	8	CO803380	AGENCOURT
1273	240	15.0	343	4	CB357447	ZF001-P00	C1346	231	14.4	427	1	AA410345	2v12802.8
1274	240	15.0	845	10	DV584978	AGENCOURT	1347	231	14.4	591	5	CK965229	4080066.B
1275	239.5	14.9	561	4	CA535206	C0215C11-	1348	230	14.3	533	7	BB763748	BB763748
1276	239.5	14.9	571	8	CB671782	A0910G05-	1349	230	14.3	553	9	DA322380	DA322380
1277	239.5	14.9	572	5	CF902544	A0342D02-	1350	230	14.3	581	2	B1560894	B1560894
1278	239.5	14.9	574	2	BG088306	BH315D05-	1351	230	14.3	810	3	BU910296	BU910296
1279	239.5	14.9	580	8	CM669994	AO887A09-	1352	230	14.3	862	10	DM022073	PMAD-asp7
1280	239.5	14.9	689	7	BF537995	602049441	1353	229.5	14.3	546	4	BX311380	BX311380
C1281	239	14.9	252	1	AA987434	OQ93G04.8	1354	229.5	14.3	563	9	DA476353	DA476353
1282	239	14.9	543	9	DA807555	DA807555	1355	229	14.3	535	9	DA327497	DA327497
1283	239	14.9	698	3	BU366425	603567913	1356	229	14.3	590	9	DA331480	DA331480
1284	238.5	14.9	583	9	DN401885	LI84004-0	1357	229	14.3	724	10	DV585753	DV585753
1285	238.5	14.9	603	9	DA672824	DA672824	1358	229	14.3	804	8	CV480535	AGENCOURT
1286	238.5	14.9	616	2	BG541803	602569688	1359	229	14.3	808	4	BX730019	BX730019
1287	238.5	14.9	850	10	DT825297	LB00237.C	1360	228.5	14.2	678	5	CD695315	EST11838
1288	238.5	14.9	851	10	DT808155	LB0173.CR	1361	228.5	14.2	788	8	CV480305	AGENCOURT
1289	238.5	14.9	859	10	DT826308	LB00242.C	1362	228.5	14.2	642	10	DT818383	DT818383
1290	238	14.8	800	5	CA548996	CU458996	1363	228	14.2	694	2	BJ705774	BJ705774
1291	237.5	14.8	500	2	BG553501	dab85b12.	1364	228	14.2	744	10	DV593317	DV593317
1292	237.5	14.8	531	7	BE134590	ug16G04.Y	1365	228	14.2	819	4	BM978966	BM978966
1293	237.5	14.8	532	4	BX517553	BX517553	1366	228	14.2	832	10	DV599562	DV599562
1294	237.5	14.8	629	4	CB068169	in90e08.Y	1367	227.5	14.2	439	4	CB750603	CB750603
1295	237	14.8	792	10	DV591934	AGENCOURT	1368	227.5	14.2	564	9	DB087773	DB087773
1296	236.5	14.7	788	3	BU334135	BU334135	1369	227.5	14.2	573	3	BP251084	BP251084
1297	236	14.7	435	10	T87045	y488G03.r1	1370	227.5	14.2	595	9	DA452294	DA452294
1298	236	14.7	540	1	AJ679277	AJ679277	1371	227	14.1	832	10	DV599562	DV599562
1299	236	14.7	747	14	CT255560	Sub.scrof	1372	227	14.1	866	8	CO914488	CO914488
1300	236	14.7	784	2	BM047943	603619019	1373	227	14.1	903	10	DM035274	DM035274
1301	235.5	14.7	537	9	DB086130	DB086130	1374	226.5	14.1	590	9	DA244326	DA244326
1302	235.5	14.7	553	9	DA418041	DA418041	1375	226.5	14.1	762	4	BY703587	BY703587
1303	234.5	14.6	538	9	DA225905	DA225905	1376	226.5	14.1	1035	7	BF158932	BF158932
1304	234.5	14.6	559	9	DA745807	DA745807	1377	226	14.1	498	1	AI641322	fc13604.Y
1305	234.5	14.6	584	9	DA846725	DA846725	1378	226	14.1	643	3	BM957830	BM957830
1306	234.5	14.6	585	9	DB191326	DB191326	1379	226	14.1	677	8	CN015282	AGENCOURT
1307	234.5	14.6	603	9	DB233119	DB233119	1380	226	14.1	802	8	CV490496	CV490496
C1308	234.5	14.6	772	10	DT315345	JGI_CAAX4	1381	226	14.1	818	8	CN178642	CN178642
1309	234.5	14.6	1066	3	BU517890	AGENCOURT	1382	226	14.1	868	8	CO929661	CO929661
1310	234	14.6	390	12	CG598273	OST262624	1383	226	14.1	885	8	CV488863	AGENCOURT
1311	234	14.6	418	4	CA967685	CcLL03a10	1384	226	14.1	1226	9	DN662469	DN662469
1312	234	14.6	539	7	BE373894	601227914	1385	225.5	14.0	524	9	DB073117	DB073117
1313	234	14.6	782	8	CO318371	AGENCOURT	1386	225.5	14.0	551	9	DB175747	DB175747
C1314	234	14.6	1408	9	DN698729	CLJ19-C11	1387	225.5	14.0	554	9	DA455736	DA455736
1315	233.5	14.5	512	2	BG731383	dael14d01.	1388	225.5	14.0	556	9	DB220622	DB220622
1316	233.5	14.5	530	9	DB062247	DB062247	1389	225.5	14.0	560	9	DA294694	DA294694
1317	233.5	14.5	530	9	DB279376	DB279376	1390	225.5	14.0	570	9	DB081146	DB081146
1318	233.5	14.5	531	9	DB061061	DB061061	1391	225.5	14.0	572	9	DA461346	DA461346

1392	225.5	14.0	577	9	DA432027	DA432027	DA432027	1465	220.5	13.7	635	5	CD770479	CD770479	AGENCOURT
1393	225.5	14.0	579	9	DB238184	DB238184	DB238184	1466	220	13.7	403	12	CG662492	CG662492	OST446275
1394	225.5	14.0	593	9	DB239758	DB239758	DB239758	1467	220	13.7	537	2	BI903247	BI903247	IG24403.Y
1395	225.5	14.0	595	5	DA675459	DA675459	DA675459	1468	219.5	13.7	517	9	DA185293	DA185293	DA185293
1396	225.5	14.0	775	5	CF959719	AGENCOURT	CF959719	1469	219.5	13.7	550	9	DA188349	DA188349	DA188349
1397	225	14.0	628	4	CA334445	NISC.L809	CA334445	1470	219.5	13.7	560	9	DA398581	DA398581	DA398581
1398	225	14.0	734	2	BI889434	CF637-2-0	BI889434	1471	219.5	13.7	728	2	EG431301	EG431301	60249877
1399	225	14.0	798	9	CK342853	JGI_X2T46	CK342853	1472	219.5	13.7	870	8	CO921756	CO921756	AGENCOURT
1400	224.5	14.0	520	1	AL865145	AL865145	AL865145	1473	219	13.6	668	8	CNI79598	CNI79598	AGENCOURT
1401	224.5	14.0	553	9	DA921374	DA921374	DA921374	1474	219	13.6	734	10	DT066064	DT066064	AGENCOURT
1402	224.5	14.0	558	8	CN302507	170005325	CN302507	1475	219	13.6	882	8	CO922623	CO922623	AGENCOURT
1403	224.5	14.0	569	9	DA592592	DA592592	DA592592	1476	218.5	13.6	590	3	BM941662	BM941662	UI-M-CG0P
1404	224.5	14.0	572	9	DA455843	DA455843	DA455843	1477	218.5	13.6	594	3	DA242961	DA242961	DA242961
1405	224.5	14.0	573	9	DA457482	DA457482	DA457482	1478	218.5	13.6	721	5	CK837004	CK837004	4062021.B
1406	224.5	14.0	574	9	DB013726	DB013726	DB013726	1479	218.5	13.6	788	10	DT821474	DT821474	LB00219.C
1407	224.5	14.0	576	9	DA462180	DA462180	DA462180	1480	218.5	13.6	792	10	DT822934	DT822934	LB00226.C
1408	224.5	14.0	576	9	DA822254	DA822254	DA822254	1481	218.5	13.6	799	10	DT819903	DT819903	LB00212.C
1409	224.5	14.0	577	9	DB055520	DB055520	DB055520	1482	218.5	13.6	805	10	DT827310	DT827310	LB00251.C
1410	224.5	14.0	578	9	DA458001	DA458001	DA458001	1483	218.5	13.6	897	4	BK699002	BK699002	BK699002
1411	224.5	14.0	582	9	DA636015	DA636015	DA636015	1484	218.5	13.6	916	10	DW600582	DW600582	CGX149-CO
1412	224.5	14.0	583	9	DA441543	DA441543	DA441543	1485	218	13.6	648	2	BM157163	BM157163	fv45a03.Y
1413	224.5	14.0	583	9	DA671106	DA671106	DA671106	1486	218	13.6	888	5	CK424119	CK424119	AUF_IPSto
1414	224.5	14.0	583	9	DB239109	DB239109	DB239109	1487	217.5	13.6	579	9	DA749528	DA749528	DA749528
1415	224.5	14.0	585	9	DA443571	DA443571	DA443571	1488	217.5	13.6	756	10	DT117059	DT117059	JGI_ANN04
1416	224.5	14.0	585	9	DA591720	DA591720	DA591720	1489	217	13.5	628	2	BF717835	BF717835	fgs2e02.Y
1417	224.5	14.0	585	9	DA458194	DA458194	DA458194	1490	216.5	13.5	774	9	CO933403	CO933403	AGENCOURT
1418	224.5	14.0	589	9	DB237928	DB237928	DB237928	1491	216.5	13.5	811	8	CO399110	CO399110	AGENCOURT
1419	224.5	14.0	591	9	DA439030	DA439030	DA439030	1492	216	13.5	257	4	BK633581	BK633581	BK633581
1420	224.5	14.0	591	9	DB238593	DB238593	DB238593	1493	216	13.5	873	5	CF251316	CF251316	esg023.e1
1421	224.5	14.0	591	9	DB239709	DB239709	DB239709	1494	215.5	13.4	412	4	CB801434	CB801434	AMGNNUC:N
1422	224.5	14.0	595	9	DB239612	DB239612	DB239612	1495	215.5	13.4	634	4	CB178189	CB178189	in94f04.Y
1423	224.5	14.0	601	9	DA854298	DA854298	DA854298	1496	215	13.4	283	1	AV161763	AV161763	AV161763
1424	224.5	14.0	661	7	BB625093	BB625093	BB625093	1497	215	13.4	380	2	BF846977	BF846977	CMO-EN004
1425	224.5	14.0	785	8	CJ463784	CJ463784	CJ463784	1498	215	13.4	390	2	BF846980	BF846980	CMO-EN004
1426	224.5	14.0	785	8	CN020078	AGENCOURT	CN020078	1499	215	13.4	664	5	CK957517	CK957517	4057965.B
1427	224	14.0	625	4	CB578224	AMGNNUC:M	CB578224	1500	215	13.4	668	9	DA812296	DA812296	DA812296
1428	224	14.0	728	5	CF996552	AGENCOURT	CF996552								
1429	224	14.0	1021	10	DM035842	CFW262-FO	DM035842								
1430	223.5	13.9	560	7	BE374988	BE374988	BE374988								
1431	223.5	13.9	564	1	AL796589	AL796589	AL796589								
1432	223.5	13.9	596	9	DN767805	AGENCOURT	DN767805								
1433	223	13.9	542	1	AL644694	AL644694	AL644694								
1434	223	13.9	875	7	BE570490	601328602	BE570490								
1435	223	13.9	417	4	CB766737	AMGNNUC:N	CB766737								
1436	222.5	13.9	419	4	CB765314	AMGNNUC:N	CB765314								
1437	222.5	13.9	595	9	DB230032	DB230032	DB230032								
1438	222.5	13.9	599	9	DB230982	DB230982	DB230982								
1439	222	13.8	315	12	CG619644	CG619644	CG619644								
1440	222	13.8	535	9	DA410723	DA410723	DA410723								
1441	221.5	13.8	403	4	CB768474	AMGNNUC:C	CB768474								
1442	221.5	13.8	453	3	BQ300494	PMO-K7000	BQ300494								
1443	221.5	13.8	543	9	DB065255	DB065255	DB065255								
1444	221.5	13.8	569	9	DB018166	DB018166	DB018166								
1445	221.5	13.8	571	9	DA943837	DA943837	DA943837								
1446	221.5	13.8	574	9	DA457954	DA457954	DA457954								
1447	221.5	13.8	585	9	DA584670	DA584670	DA584670								
1448	221.5	13.8	591	9	DA876548	DA876548	DA876548								
1449	221.5	13.8	595	9	DA674105	DA674105	DA674105								
1450	221.5	13.8	624	5	CD684421	EST941.hu	CD684421								
1451	221.5	13.8	792	10	DR857665	JGI_CABG3	DR857665								
1452	221.5	13.8	821	10	DT826980	LB00249.C	DT826980								
1453	221.5	13.8	893	9	DN932775	AGENCOURT	DN932775								
1454	221.5	13.8	926	4	CB204084	AGENCOURT	CB204084								
1455	221	13.8	537	2	BG724020	602697181	BG724020								
1456	221	13.8	780	10	DV584863	AGENCOURT	DV584863								
1457	220.5	13.7	440	8	CO353133	DR_ATE_FL	CO353133								
1458	220.5	13.7	570	9	DA442264	DA442264	DA442264								
1459	220.5	13.7	577	9	DA439582	DA439582	DA439582								
1460	220.5	13.7	577	9	DA461262	DA461262	DA461262								
1461	220.5	13.7	578	9	DA879128	DA879128	DA879128								
1462	220.5	13.7	580	9	DA461572	DA461572	DA461572								
1463	220.5	13.7	581	9	DA461613	DA461613	DA461613								
1464	220.5	13.7	592	9	DA455131	DA455131	DA455131								

ALIGNMENTS

RESULT 1

CR605305

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CR605305 1143 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CSID01022YK04 of Placentia Cot 25-normalized
of Homo sapiens (human).

CR605305.1 GI:50486112

HTC; CNSLT cDNA.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1143)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue

2 (bases 1 to 1143)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)

- Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

Location/Qualifiers

1. .1143

US-10-785-221-9 (1-312) x CR621411

Qy	209	ThrGlyGlutyrSerCysGluAlaAraAsnSerValGlyTyrArgArgCysProGlyLys	228
Dd	306	ACTGGAGAATATTCTGTGAAGCCSCAAATTCGTGTGATATCGACGTGTCTGGGAAA	247
Qy	229	ArgMetGlnValAcgApLeuAnIlleSerGlyllellaalaValvalValala	248
Dd	246	CGAATSCAAAGTAGATGATCTCAATATTAGTGGCATCATMGACGCCGTAGTTGTGGCC	187
Qy	249	LeuVallIeSerValCysGlyLeuGlyValCystYrAlaGlnArGLysGlyTyPheSer	268
Dd	186	TTAGTGATTTCCGTTTTGTGGCTTGGTGATGCTATGCTCNAGAGAAAGGCTACTTTTCA	127
Qy	269	LysGluThrSerPheGlnLysSerAsnSerSerLySalaThrThrMetSerGluAn	288
Dd	126	AAGAAACCCTCTCCAGAGAGTAATCTTTCATCTTAAAGCACGACAATGAGTGAAAAAT	67
RESULT 8			
AY610145 1184 bp mRNA linear HTC 31-JAN-2005			
Sus scrofa clone Clu_80125.scr.msk.p1.Contigl, mRNA sequence.			
DEFINITION			
AY610145			
VERSION			
AY610145.1 GI:52351715			
KEYWORDS			
HTC.			
SOURCE			
Sus scrofa (pig)			
ORGANISM			
Sus scrofa			
REFERENCE			
AUTHORS			
Jorgensen,F.G., Hobolth,A., Hornshoj,H., Bendixen,C., Fredholm,M. and Schierup,M.H.			
TITLE			
Comparative analysis of protein coding sequences from human, mouse and the domesticated pig			
JOURNAL			
PUBMED			
15679890			
REFERENCE			
2 (bases 1 to 1184)			
Hornshøj H., Bendixen C. and Panitz F. Direct Submission Submitted (28-APR-2004) Animal Breeding and Genetics, Danish Institute of Agricultural Sciences, Research Centre Foulum, Postbox 50, Tjele DK-8830, Denmark			
FEATURES			
source			
1..1184			
/organism="Sus scrofa"			
/mol_type="mRNA"			
/db_xref="taxon:9823"			
/clones="Clu_80125.scr.msk.p1.Contigl"			
misc_feature			
1..1184			
/note="similar to AF255910.1 Homo sapiens vascular endothelial junction-associated molecule"			
ORIGIN			
Alignment Scores:			
Pred. No.: 1.27e-129 Length: 1184			
Score: 1313.00 Matches: 253			
Percent Similarity: 93.4% Conservative: 16			
Best Local Similarity: 87.8% Mismatches: 19			
Query Match: 81.8% Indels: 0			
DB: Gaps: 0			
 US-10-785-221-9 (1-312) x AY610145 (1-1184)			
Qy	1	MetalArgSerArgHisArgLeuleuleuleuleuleuArgTyrLeuValValala	20
Dd	182	ATGGCGAGGAGGAGCGCGCACCGCTCTCTCTGTCTGTCTGTGGCTACCTGGTGGCC	241
Qy	21	LeuGlyTyrHisLysAlaTyrGlyPheSerAlaProLysaspGlnValValThrala	40
Dd	242	CTGACTATCATAGAGGCTGTGGATTTCTTGACCCAAGATCATCAGTAGTCACAGCA	301
Qy	41	ValGluTyrGlnGluAlalleLeuAlaCysLysThrProLysLysThrValSerSerArg	60
:	:	:	:

302	ATAGATGATCAAGAGGTTATTTTACCTGCTGTAATATCCAAAGAGAACCGTGCTCTCCAGA	361
61	LeuGluTrpLysLysLeuGlyArgSerValSerPheValTyrGlnGlnThrLeuGln	80
362	TTAGAATGGAAGAAACCTGGGCGGGTATCTCCTTTGTCTACTATCAACAGGCTCTTCAA	421
81	GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr	100
422	GGTGCTTTTAAAGATCAGCTGAGCTGATAGATTTTCAGCATACGGATCAAAAATGTATACA	481
101	ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlyGlnAsn	120
482	AGAAATGATGCCGGAAGTATCGTTGTGAATATAGTGCTCATCCGAAACAAAGGTCAAAC	541
121	LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu	140
542	CTGCGACAGGATACGGTCACCTCGGAAGTATTAGTGGCTCCAGCAGTTCATCATGTGAA	601
141	ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly	160
602	GTACCCAGTCTGTCTCTGAGCGGCACCTACCGTAGAGCTGGCATGTCAAGACAAAGAGGC	661
161	AsnProAlaProGluTyrThrTropPheLysAspGlyIleArgLeuLeuGluAsnProArg	180
662	AAATCCAGCTCCCGAATACACATGGTTTAAAGATGGCATCCGTTGTTCAGGGAAATCCAAGA	721
181	LeuGlySerGlnSerThrAsnSerSerTyrThrMetAsnThrLysThrGlyThrLeuGln	200
722	CTGGATGCCCAAGCACCAAGCTCATATACATGATGTAATCTGGAAGTCTGCATA	781
201	PheAsnThrValSerLysLeuAspThrGlyGluTyrSerCysGluAlaLysAsnSerVal	220
782	TTTAAATGCTGTTTCAAACTGGACAGTGGAGATATTTCTGTGAAGCCCGTAATCTGTCT	841
221	GlyTyrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle	240
842	GGACATCCGAAGTGTCTCGGGAACGAATGCAAGTAGACCATCTCAACATAAGTGGCATC	901
241	IleAlaAlaValValValAlaLeuValIleSerValCysGlyLeuGlyValCysTyr	260
902	ATAGCGCGGTAGTCTGCTGGCCATAGTGTCTCTCTGTGGCCTTGGCGTGTGCTAT	961
261	AlaGlnArgLysGlyTyrPheSerLysGluThrSerPheGlnLysSerAsnSerSer	280
962	GCTCAGAGGAAAGCGTACTTTTCAAAAGAAACCTCTCTCCAGAAGAGTGGTCTGTGCATCT	1021
281	LysAlaThrThrMetSerGluAsn	288
1022	AAAGCCCTTACAATGAGTGAAAAAT	1045
RESULT 9		
BX375908/c		
LOCUS	BX375908	864 bp mRNA linear EST 26-APR-2004
DEFINITION	BX375908 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens	
	cDNA clone CS0BC019YD23 3-PRIME, mRNA sequence.	
ACCESSION	BX375908	
VERSION	BX375908.2	GI:46573233
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
REFERENCE	1 (bases 1 to 864)	
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished (2001)	
COMMENT	On May 8, 2003 this sequence version replaced gi:30448456.	
	Contact: Genoscope	
	Genoscope - Centre National de Sequencage	
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE	
	Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr	
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime	

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10286.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DC019CB12NP1&c=10286.f.

FEATURES

source

Location/Qualifiers

1..864

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DC019YD23"

/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 3,57e-126 Length: 864
Score: 1279.00 Matches: 253
Percent Similarity: 96.9% Conservative: 0
Best Local Similarity: 96.9% Mismatches: 7
Query Match: 79.7% Indels: 1
DB: 4 Gaps: 0

US-10-785-221-9 (1-312) x BX375908 (1-864)

Qy 29 PheSerAlaProLysAspGlnValThrAlaValGluTyrGlnGluAlaIleLeu 48
Db 849 TTTTTCGCCCDAAAGACCCYACCAAGTAGTCACAGCAGTAGTACCTAGAGCGCTATTTTA 790
Qy 49 AlaCysLysThrProLysLysThrValSerArgLeuGluTyrLysLysLeuGlyArg 68
Db 789 GCCTGCANAAACCCCAAGAGACTGTTTCTCCAGATTAGATGGGAAGAACTGGGTCCG 730
Qy 69 SerValSerPheValTyrTyrGlnGlnThrLeuGlnGlyAspPheLysAsnArgAlaGlu 88
Db 729 AGTGTCTCCTTTGCTACTATCAACAGACTTTCAAGGTGATTTTAAAAATCGAGCTGAG 670
Qy 89 MetIleAspPheAsnIleArgIleLysAsnValThrArgSerAspAla-GlyLysTyrArg 108
Db 669 ATGATAGATTTCATATCCGGATCAAAAATGTAAACAGNAGTAGTCGCGGGAATATCG 610
Qy 108 GCysGluValSerAlaProSerGluGlnGlnAsnLeuGluAspThrValThrLe 128
Db 609 TTGTGAAGTTAGTCCCATCTGAGCAGGCCAANAACCTGGGAAGGATACAGTCACTCT 550
Qy 128 uGluValLeuValAlaProAlaValProSerCysGluValProSerSerAlaLeuSerG 148
Db 549 GGAAGTATTAGTGGCTCCAGCAGTCCATCATGTGAAGTACCCCTCTCTGCTCTGAGTG 490
Qy 148 yThrValValGluLeuArgCysGlnAspLysGluGlyAsnProAlaProGluTyrThrTr 168
Db 489 AACTGTGGTAGAGCTACGATGTCAAGACAAAGAGGGAATCCAGCTCCTCGGATACACAT 430
Qy 168 pPheLysAspGlyIleArgLeuLeuGluAsnProArgLeuGlySerGlnSerThrAsnSe 188
Db 429 GTTTAAGGATGGCATCCGTTTGTAGAAATCCAGACTTGGCTCCCAAGACCAACAG 370
Qy 188 rSerTyrThrMetAsnThrLysThrGlyThrLeuGlnPheAsnThrValSerLysLeuAs 208
Db 369 CTCATACAAATGAATACAAAACCTGGAATCTGCAATTTAATCTGTTTCCAACTGGA 310
Qy 208 pThrGlyGluTyrSerCysGluAlaArgAsnSerValGlyTyrArgArgCysProGlyLy 228
Db 309 CACTGGAGAATATTCTCTGTGAAGCCCGCAATTCCTGTTGGATATCGCAGGTCTCTGGGA 250
Qy 228 sArgMetGlnValAspAspLeuAsnIleSerGlyIleIleAlaAlaValValValAl 248

Db 249 ACCAATGCAAGTAGATGATCTTCACATNAGTGGCATATAGCAGCCGTAGTAGTTGTGGC 190
Qy 248 aleuValIleSerValCysGlyLeuGlyValCysTyrAlaGlnArgLysGlyTyrPheSe 268
Db 189 CTTAGTAGATTTCGGTTTGTGGCTTGTGGTATGTCTAGAGGAAAGGCTACTTTTC 130
Qy 268 rLysGluThrSerPheGlnLysSerAsnSerSerLysAlaThrThrMetSerGluAs 288
Db 129 AAAAGAAACCTCTCTCCAGNAGTAGTAATCTTCMTCTAAAGCCMGCAACATGAGTGAAA 70
Qy 288 n 288
Db 69 T 69
RESULT 10
DT815807 898 bp mRNA linear EST 12-OCT-2005
LOCUS LB01628.CR F07 GC_BGC-16 Bos taurus cDNA clone IMAGE:8088297 5',
DEFINITION mRNA sequence.
ACCESSION DT815807.1 GI:75747683
VERSION DT815807
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 898)
AUTHORS Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y.,
Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C.,
Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakaliff, R.,
Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R.,
Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R. R., Stott, J.,
Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S. J. and Marra, M. A.
Bovine Genome Sequencing Program: Full-length cDNA Sequencing
Unpublished (2005)
JOURNAL Contact: Robert Kirkpatrick
COMMENT Canada's Michael Smith Genome Sciences Centre
BC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
Canada, V5Z 4S6
Tel: 1-604-707-5900 x5406
Fax: 1-604-876-3561
Email: robertk@bcgsc.ca
Plate: LB01628 row: F column: 7
High quality sequence stop: 898.
FEATURES
source
1..898
/organism="Bos taurus"
/mol_type="mRNA"
/strain="LI Hereford"
/db_xref="taxon:9913"
/clone="IMAGE:8088297"
/sex="female"
/tissue type="Uterus"
/dev_stage="8.5 months old"
/lab_host="E. coli DH10B T1 Phage Resistant"
/clone_lib="GC_BGC-16"
/note="Organ: Uterus; Vector: pExpress 1; Site 1: Blunt
(5' end of cDNA); Site_2: NotI (3' end of cDNA)"
ORIGIN
Alignment Scores:
Pred. No.: 2,74e-122 Length: 898
Score: 1243.00 Matches: 238
Percent Similarity: 96.2% Conservative: 15
Best Local Similarity: 90.5% Mismatches: 10
Query Match: 77.4% Indels: 0
DB: 10 Gaps: 0
US-10-785-221-9 (1-312) x DT815807 (1-898)
Qy 26 AlaTyrGlyPheSerAlaProLysAspGlnGlnValThrAlaValGluTyrGlnGlu 45

division of Invitrogen.

This sequence belongs to sequence cluster 10286.f

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?e=CS0DN001DB12NP1&c=10286.f>.

FEATURES

Location/Qualifiers
1..984
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN001YD24"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_libs="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 2,79e-116 Length: 984
Score: 1187.50 Matches: 235
Percent Similarity: 97.5% Conservatives: 0
Best Local Similarity: 97.5% Mismatches: 5
Query Match: 74.0% Indels: 2
DB: 4 Gaps: 1

US-10-785-221-9 (1-312) x BX463390 (1-984)

Qy 48 LeuAlaCysLysThrProLysLysThrValSerSerArgLeuGluTrpLysLysLeuGly 67
Db 970 TTAGCCTGCAAAACCCCAAGAGACTGTTCCCTCCAGATTAGAGTGGAGAACTCGGT 911
Qy 68 ArgSerValSerPheValTyrGlnGlnThrLeuGlnGlyAspPheLysAsnArgAla 87
Db 910 CGGAGTGCTCTCTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCT 851
Qy 88 GluMetIleAspPheAsnIleArgIleLysAsnValThrArgSerAspAlaGlyLysTyr 107
Db 850 GAGATGATAGATTTCATATCCGGATCAAAATGTGACAGAGTGTATGCGGGAAATAT 791
Qy 108 ArgCysGluValSerAlaProSerGluGlnGlnAsnLeuGluGluAspThrValThr 127
Db 790 CGCTGTGAAGTTAGTGCCTCATCTGAGCAAGGCCCAAAACCTGGAAGAGGATACAGTCACT 731
Qy 128 LeuGluValLeuValAlaProAlaValProSerCysGluValProSerSerAlaLeuSer 147
Db 730 CTGGAAGTATTAGTGGCTCCAGCAGATTCCATCATGTGAACTACCTCTCTGCTCTGAGT 671
Qy 148 GlyThrValValGluLeuArgCysGlnAspLysGluGlyValAsnProAlaProGluTyrThr 167
Db 670 GGAACGTGTGTAGCTTACGATGTCAAGACAAGAGGGAATCCAGCTCTCTGAATACACA 611
Qy 168 TrpPheLysAspGlyIleArgLeuLeuGluAsnProArgLeuGlySerGlnSerThrAsn 187
Db 610 TGGTTAAAGATGGCATCCCTTTGCTAGAAAATCCACAGACTTGGCTCCCAAGCACCAC 551
Qy 188 SerSerTyrThrMetAsnThrLysThrGlyThrLeuGlnPheAsnThrValSerLeu 207
Db 550 AGCTCATACAAATGATACAAAACCTGGAACCTGCAATTTAATACTGTTTCCAAACTG 491
Qy 208 AspThrGlyLysSerCysGluAlaArgAsnSerValGlyTyrArgArgCysProGly 227
Db 490 GACACTGGAGAAATTCCTGTGAAGCCCGCAATTCGTGTGGATATCGAGGTCTCTGGG 431
Qy 228 LysArgMetGlnValAspAspLeuAsnIleSerGlyIleIleAlaAlaValValVal 247
Db 430 AAMGATGCAAT----GATCTCAACATAGTGGCATCATAGACCGGTAGTGTGTG 375
Qy 248 AlaLeuValIleSerValCysGlyLeuGlyValCysTyrAlaGlnArgLysGlyTyrPhe 267
Db 374 GCCTTAGTATWTCGGTTTGTGGCTTGGTGTATGCTATGCTCATGAGGAAAGGCTACTTT 315

Qy 268 SerLysGluThrSerPheGlnLysSerAsnSerSerLysAlaThrThrMetSerGlu 287
Db 314 TCRAAGAAACCCCTTCCAGAGAGTAAATCTTCATCTAAAGCCACGACATGAGTAA 255

Qy 288 Asn 288
Db 254 AAT 252

RESULT 14

AK013914

LOCUS

DEFINITION

Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched

library, clone:310002C20 product:junction cell adhesion molecule

2, full insert sequence.

ACCESSION

AK013914

VERSION

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KEYWORDS

HTC; CAP trapper.

SOURCE

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ORGANISM

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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

10349636

REFERENCE

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

11042159

REFERENCE

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,

Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishie, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

REFERENCE

4

The RIKEN Genome Exploration Research Group Phase II Team and the

PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

REFERENCE

5

The PANTOM Consortium, the RIKEN Genome Exploration Research Group

Phase I and II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

REFERENCE

6

RIKEN Genome Exploration Research Group, Genome Science Group

(Genome Network Core Team) and the PANTOM Consortium.

Antisense transcription in the Mammalian Transcriptome

Science 309, 1564-1566 (2005)

REFERENCE

7

The PANTOM Consortium, Riken Genome Exploration Research Group and

Genome Science Group (Genome Network Project Core Group).

The Transcriptional Landscape of the Mammalian Genome

Science 309, 1559-1563 (2005)

8 (bases 1 to 1167)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,

Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

Furuno, M., Hanagaki, T., Harai, A., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,

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 Direct Submission
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
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 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kikunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohtsuka, S., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE
RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multipillar sequencer

JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)

PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)

REFERENCE	5
AUTHORS	The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420. 563-573 (2002)

6	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium. Antisense Transcription in the Mammalian Transcriptome
REFERENCE	Science 309, 1564-1566 (2005)
AUTHORS	
TITLE	
JOURNAL	

7 The FANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome
Science 309, 1559-1563 (2005)
8 (bases 1 to 1312)

AUTHORS
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
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Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshino, M., Yuramatsu, M. and Hayashizaki, Y.

TITLE Direct submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-resgsc@riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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SUMMARIES

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C 87	14	4.5	55135	3	US-09-949-016-15687	Sequence 16587, A	160	13	4.2	601	3	US-09-949-016-160597	Sequence 160597,
C 88	14	4.5	55298	3	US-09-431-356C-1	Sequence 1, Appli	161	13	4.2	601	3	US-09-949-016-177531	Sequence 177531,
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C 90	14	4.5	62327	3	US-09-949-016-16809	Sequence 16809, A	163	13	4.2	601	3	US-09-949-016-177533	Sequence 177533,
C 91	14	4.5	64034	3	US-09-949-016-17593	Sequence 17593, A	164	13	4.2	601	3	US-09-949-016-186525	Sequence 186525,
C 92	14	4.5	70323	3	US-09-949-016-17594	Sequence 17594, A	165	13	4.2	601	3	US-09-949-016-205521	Sequence 205521,
C 93	14	4.5	72602	3	US-09-949-016-14385	Sequence 14385, A	166	13	4.2	601	3	US-09-949-016-205522	Sequence 205522,
C 94	14	4.5	77586	3	US-09-949-016-13320	Sequence 13320, A	167	13	4.2	601	3	US-09-949-001-446	Sequence 446, App
C 95	14	4.5	77586	3	US-09-949-016-13321	Sequence 13321, A	168	13	4.2	601	3	US-09-949-002-6894	Sequence 6894, App
C 96	14	4.5	80269	3	US-09-949-016-16318	Sequence 16318, A	169	13	4.2	601	3	US-09-949-002-6933	Sequence 6933, App
C 97	14	4.5	80269	3	US-09-949-016-15681	Sequence 15681, A	170	13	4.2	775	4	US-09-297-648-3721	Sequence 3721, App
C 98	14	4.5	85369	3	US-09-949-016-12171	Sequence 12171, A	171	13	4.2	2613	3	US-10-104-047-1308	Sequence 1308, App
C 99	14	4.5	87629	3	US-09-949-016-15262	Sequence 15262, A	172	13	4.2	3115	3	US-10-104-047-1154	Sequence 1154, App
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C 105	14	4.5	96202	3	US-09-949-016-16433	Sequence 16433, A	178	13	4.2	15358	3	US-09-949-016-13382	Sequence 13382, A
C 106	14	4.5	112874	3	US-09-949-016-13180	Sequence 13180, A	179	13	4.2	16869	3	US-09-719-554-64	Sequence 64, Appli
C 107	14	4.5	113028	3	US-09-949-016-16664	Sequence 16664, A	180	13	4.2	19813	3	US-09-949-016-15087	Sequence 15087, A
C 108	14	4.5	133278	3	US-09-949-016-12254	Sequence 1254, A	181	13	4.2	22010	3	US-09-949-016-13960	Sequence 13960, A
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C 111	14	4.5	134242	3	US-09-949-016-15813	Sequence 15813, A	184	13	4.2	23257	3	US-09-949-016-12894	Sequence 12894, A
C 112	14	4.5	134242	3	US-09-949-016-15814	Sequence 15814, A	185	13	4.2	23260	3	US-09-949-016-14300	Sequence 14300, A
C 113	14	4.5	134242	3	US-09-949-016-15815	Sequence 15815, A	186	13	4.2	23533	3	US-09-949-016-15377	Sequence 15377, A
C 114	14	4.5	134890	3	US-09-949-016-15602	Sequence 15602, A	187	13	4.2	23501	3	US-09-949-016-16773	Sequence 16773, A
C 115	14	4.5	150032	3	US-09-949-016-14321	Sequence 14321, A	188	13	4.2	25966	3	US-09-949-003-632	Sequence 632, App
C 116	14	4.5	162450	3	US-09-345-882-1	Sequence 1, Appli	189	13	4.2	25966	3	US-09-949-002-813	Sequence 813, App
C 117	14	4.5	162450	3	US-10-071-179-1	Sequence 1, Appli	190	13	4.2	25969	3	US-09-949-016-13397	Sequence 13397, A
C 118	14	4.5	179904	3	US-09-949-002-577	Sequence 577, App	191	13	4.2	26134	3	US-09-949-016-15285	Sequence 15285, A
C 119	14	4.5	179905	3	US-09-949-002-705	Sequence 705, App	192	13	4.2	27794	3	US-09-949-016-15133	Sequence 15133, A
C 120	14	4.5	187595	3	US-09-949-016-15346	Sequence 15346, A	193	13	4.2	28253	3	US-09-949-003-761	Sequence 761, App
C 121	14	4.5	194714	3	US-09-949-016-11869	Sequence 11869, A	194	13	4.2	28253	3	US-09-949-003-762	Sequence 762, App
C 122	14	4.5	196714	3	US-09-949-016-15474	Sequence 15474, A	195	13	4.2	28316	3	US-09-949-003-766	Sequence 766, App
C 123	14	4.5	218940	3	US-09-949-016-17539	Sequence 17539, A	196	13	4.2	28316	3	US-09-949-003-767	Sequence 767, App
C 124	14	4.5	304533	3	US-09-949-016-15371	Sequence 15371, A	197	13	4.2	32351	5	US-09-543-679A-2874	Sequence 2874, App
C 125	14	4.5	304533	3	US-09-949-016-15372	Sequence 15372, A	198	13	4.2	33578	3	US-09-949-016-15670	Sequence 15670, A
C 126	13	4.2	300	4	US-09-237-648-1551	Sequence 1551, App	199	13	4.2	36023	3	US-09-949-016-15577	Sequence 15577, A
C 127	13	4.2	554	4	US-09-880-107-3176	Sequence 3176, App	200	13	4.2	36651	3	US-09-738-894A-3	Sequence 3, Appli
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C 129	13	4.2	601	3	US-09-949-016-18798	Sequence 18798, A	202	13	4.2	36651	5	US-10-425-962-3	Sequence 3, Appli
C 130	13	4.2	601	3	US-09-949-016-18799	Sequence 18799, A	203	13	4.2	36677	3	US-09-949-002-832	Sequence 832, App
C 131	13	4.2	601	3	US-09-949-016-20862	Sequence 20862, A	204	13	4.2	37966	3	US-09-949-016-12566	Sequence 12566, A
C 132	13	4.2	601	3	US-09-949-016-27477	Sequence 27477, A	205	13	4.2	38052	3	US-09-949-016-13825	Sequence 13825, A
C 133	13	4.2	601	3	US-09-949-016-27478	Sequence 27478, A	206	13	4.2	38374	4	US-09-880-107-3463	Sequence 3463, App
C 134	13	4.2	601	3	US-09-949-016-27479	Sequence 27479, A	207	13	4.2	39982	3	US-09-820-924-3	Sequence 3, Appli
C 135	13	4.2	601	3	US-09-949-016-46802	Sequence 46802, A	208	13	4.2	39982	3	US-10-369-626-3	Sequence 3, Appli
C 136	13	4.2	601	3	US-09-949-016-56380	Sequence 56380, A	209	13	4.2	40398	5	US-09-543-679A-2878	Sequence 2878, App
C 137	13	4.2	601	3	US-09-949-016-66644	Sequence 66644, A	210	13	4.2	41318	3	US-09-949-016-16225	Sequence 16225, A
C 138	13	4.2	601	3	US-09-949-016-66645	Sequence 66645, A	211	13	4.2	41895	3	US-09-949-016-15135	Sequence 15135, A
C 139	13	4.2	601	3	US-09-949-016-77382	Sequence 77382, A	212	13	4.2	42250	3	US-09-949-016-17171	Sequence 17171, A
C 140	13	4.2	601	3	US-09-949-016-78138	Sequence 78138, A	213	13	4.2	42923	3	US-09-949-016-13946	Sequence 13946, A
C 141	13	4.2	601	3	US-09-949-016-92505	Sequence 92505, A	214	13	4.2	42975	3	US-09-949-016-11965	Sequence 11965, A
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C 144	13	4.2	601	3	US-09-949-016-92708	Sequence 92708, A	217	13	4.2	47032	3	US-09-949-016-16524	Sequence 16524, A
C 145	13	4.2	601	3	US-09-949-016-110209	Sequence 110209, A	218	13	4.2	51043	3	US-09-949-016-12739	Sequence 12739, A
C 146	13	4.2	601	3	US-09-949-016-113454	Sequence 113454, A	219	13	4.2	51046	3	US-09-949-016-13946	Sequence 13946, A
C 147	13	4.2	601	3	US-09-949-016-121587	Sequence 121587, A	220	13	4.2	54251	3	US-09-949-016-13702	Sequence 13702, A
C 148	13	4.2	601	3	US-09-949-016-125260	Sequence 125260, A	221	13	4.2	54252	3	US-09-949-016-11807	Sequence 11807, A
C 149	13	4.2	601	3	US-09-949-016-126249	Sequence 126249, A	222	13	4.2	54444	3	US-09-949-016-17344	Sequence 17344, A
C 150	13	4.2	601	3	US-09-949-016-140749	Sequence 140749, A	223	13	4.2	55114	3	US-09-949-016-16792	Sequence 16792, A
C 151	13	4.2	601	3	US-09-949-016-141039	Sequence 141039, A	224	13	4.2	56523	3	US-09-949-016-14297	Sequence 14297, A
C 152	13	4.2	601	3	US-09-949-016-141040	Sequence 141040, A	225	13	4.2	56665	3	US-09-949-016-14026	Sequence 14026, A
C 153	13	4.2	601	3	US-09-949-016-141041	Sequence 141041, A	226	13	4.2	58789	3	US-09-949-016-15922	Sequence 15922, A
C 154	13	4.2	601	3	US-09-949-016-141043	Sequence 141043, A	227	13	4.2	60589	3	US-09-949-016-17070	Sequence 17070, A

C 228	13	4.2	60785	3	US-09-949-016-12774	Sequence 12774, A	c 301	13	4.2	312957	3	US-09-949-001-31	Sequence 31, Appl
C 229	13	4.2	60785	3	US-09-949-016-15665	Sequence 15665, A	c 302	13	4.2	312972	3	US-09-949-001-34	Sequence 34, Appl
C 230	13	4.2	60990	3	US-09-949-016-14080	Sequence 14080, A	c 303	13	4.2	312972	3	US-09-949-016-13173	Sequence 13173, A
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C 234	13	4.2	63984	3	US-09-949-016-15254	Sequence 15254, A	c 307	13	4.2	828152	3	US-09-949-016-12777	Sequence 12777, A
C 235	13	4.2	67181	3	US-09-949-016-13102	Sequence 13102, A	c 308	13	4.2	828152	3	US-09-513-999C-18799	Sequence 18799, A
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C 237	13	4.2	69752	3	US-09-949-016-14094	Sequence 14094, A	c 310	12	3.8	133	3	US-09-513-999C-14765	Sequence 14765, A
C 238	13	4.2	71879	3	US-09-949-016-17465	Sequence 17465, A	c 311	12	3.8	141	3	US-09-513-999C-20281	Sequence 20281, A
C 239	13	4.2	74096	3	US-09-949-016-11785	Sequence 11785, A	c 312	12	3.8	159	3	US-09-513-999C-35428	Sequence 35428, A
C 240	13	4.2	74097	3	US-09-949-016-16239	Sequence 16239, A	c 313	12	3.8	181	3	US-09-513-999C-16083	Sequence 16083, A
C 241	13	4.2	74644	3	US-09-949-016-17556	Sequence 17556, A	c 314	12	3.8	200	3	US-09-513-999C-19163	Sequence 19163, A
C 242	13	4.2	74804	3	US-09-949-016-15118	Sequence 15118, A	c 315	12	3.8	206	3	US-09-513-999C-35398	Sequence 35398, A
C 243	13	4.2	76472	3	US-09-949-016-15896	Sequence 15896, A	c 316	12	3.8	208	3	US-09-513-999C-13391	Sequence 13391, A
C 244	13	4.2	80355	3	US-09-949-016-12735	Sequence 12735, A	c 317	12	3.8	209	3	US-09-513-999C-9745	Sequence 9745, Ap
C 245	13	4.2	80357	3	US-09-949-016-13272	Sequence 13272, A	c 318	12	3.8	213	3	US-09-513-999C-22014	Sequence 22014, A
C 246	13	4.2	84587	3	US-09-949-016-15733	Sequence 15733, A	c 319	12	3.8	215	3	US-09-513-999C-2518	Sequence 2518, Ap
C 247	13	4.2	85850	3	US-09-949-016-13424	Sequence 13424, A	c 320	12	3.8	245	3	US-09-513-999C-35624	Sequence 35624, A
C 248	13	4.2	86380	3	US-09-949-016-14837	Sequence 14837, A	c 321	12	3.8	249	2	US-08-687-080-100	Sequence 100, App
C 249	13	4.2	88036	3	US-09-949-016-15335	Sequence 15335, A	c 322	12	3.8	269	3	US-09-513-999C-30648	Sequence 30648, A
C 250	13	4.2	92276	3	US-09-949-016-12166	Sequence 12166, A	c 323	12	3.8	305	3	US-09-513-999C-2536	Sequence 2536, Ap
C 251	13	4.2	93894	3	US-09-949-016-13629	Sequence 13629, A	c 324	12	3.8	315	3	US-09-513-999C-9824	Sequence 9824, Ap
C 252	13	4.2	96878	3	US-09-949-016-12551	Sequence 12551, A	c 325	12	3.8	321	3	US-09-385-982-366	Sequence 366, App
C 253	13	4.2	97195	3	US-09-949-016-12212	Sequence 12212, A	c 326	12	3.8	322	3	US-09-621-976-13274	Sequence 13274, A
C 254	13	4.2	97196	3	US-09-949-016-16971	Sequence 16971, A	c 327	12	3.8	324	3	US-09-621-976-18960	Sequence 18960, A
C 255	13	4.2	97989	3	US-09-949-016-13208	Sequence 13208, A	c 328	12	3.8	351	3	US-09-621-976-2073	Sequence 2073, Ap
C 256	13	4.2	98828	3	US-09-949-016-16630	Sequence 16630, A	c 329	12	3.8	351	3	US-09-621-976-9805	Sequence 9805, Ap
C 257	13	4.2	99916	3	US-09-816-095-3	Sequence 3, Appl	c 330	12	3.8	351	3	US-09-513-999C-9390	Sequence 9390, Ap
C 258	13	4.2	101011	3	US-09-949-016-16933	Sequence 16933, A	c 331	12	3.8	352	3	US-09-621-976-17996	Sequence 17996, A
C 259	13	4.2	102409	3	US-09-949-016-15148	Sequence 15148, A	c 332	12	3.8	381	3	US-09-621-976-13923	Sequence 13923, A
C 260	13	4.2	104077	3	US-09-949-016-13593	Sequence 13593, A	c 333	12	3.8	390	3	US-09-621-976-14200	Sequence 14200, A
C 261	13	4.2	106256	3	US-09-949-016-16858	Sequence 16858, A	c 334	12	3.8	392	3	US-09-621-976-14255	Sequence 14255, A
C 262	13	4.2	110096	4	US-09-880-107-1542	Sequence 1542, Ap	c 335	12	3.8	393	3	US-09-513-999C-9097	Sequence 9097, Ap
C 263	13	4.2	112507	3	US-09-949-016-12420	Sequence 12420, A	c 336	12	3.8	400	3	US-09-621-976-18294	Sequence 18294, A
C 264	13	4.2	112507	3	US-09-949-016-12794	Sequence 12794, A	c 337	12	3.8	409	3	US-09-621-976-8750	Sequence 8750, Ap
C 265	13	4.2	112508	3	US-09-949-016-16589	Sequence 16589, A	c 338	12	3.8	416	3	US-09-621-976-14343	Sequence 14343, A
C 266	13	4.2	112508	3	US-09-949-016-16590	Sequence 16590, A	c 339	12	3.8	423	3	US-09-513-999C-3052	Sequence 3052, Ap
C 267	13	4.2	113042	3	US-09-949-016-12343	Sequence 12343, A	c 340	12	3.8	443	3	US-09-621-976-18603	Sequence 18603, A
C 268	13	4.2	113042	3	US-09-949-016-15246	Sequence 15246, A	c 341	12	3.8	443	3	US-09-513-999C-19024	Sequence 19024, A
C 269	13	4.2	114183	3	US-09-949-002-849	Sequence 849, App	c 342	12	3.8	445	3	US-09-621-976-9692	Sequence 9692, Ap
C 270	13	4.2	120727	3	US-09-949-016-15787	Sequence 15787, A	c 343	12	3.8	453	3	US-09-621-976-215	Sequence 215, App
C 271	13	4.2	120727	3	US-09-949-016-15788	Sequence 15788, A	c 344	12	3.8	459	3	US-09-621-976-15198	Sequence 15198, A
C 272	13	4.2	124480	3	US-09-949-016-15921	Sequence 15921, A	c 345	12	3.8	459	3	US-09-513-999C-13732	Sequence 13732, A
C 273	13	4.2	127546	3	US-09-949-002-624	Sequence 624, App	c 346	12	3.8	469	3	US-09-621-976-219	Sequence 219, App
C 274	13	4.2	133063	3	US-09-949-016-16293	Sequence 16293, A	c 347	12	3.8	469	3	US-09-621-976-218	Sequence 218, App
C 275	13	4.2	134434	3	US-09-949-016-17362	Sequence 17362, A	c 348	12	3.8	475	3	US-09-621-976-13778	Sequence 13778, A
C 276	13	4.2	134890	3	US-09-949-016-15602	Sequence 15602, A	c 349	12	3.8	495	3	US-09-621-976-11454	Sequence 11454, A
C 277	13	4.2	136917	3	US-09-949-016-16369	Sequence 16369, A	c 350	12	3.8	507	4	US-09-880-107-2667	Sequence 2667, Ap
C 278	13	4.2	140224	3	US-09-949-016-17002	Sequence 17002, A	c 351	12	3.8	513	3	US-09-621-976-2131	Sequence 2131, Ap
C 279	13	4.2	144596	3	US-09-949-016-11749	Sequence 11749, A	c 352	12	3.8	532	3	US-09-621-976-3687	Sequence 3687, Ap
C 280	13	4.2	144596	3	US-09-949-016-13035	Sequence 13035, A	c 353	12	3.8	601	3	US-09-691-861A-19	Sequence 19, Appl
C 281	13	4.2	147321	3	US-09-949-016-15450	Sequence 15450, A	c 354	12	3.8	601	3	US-09-949-016-17656	Sequence 17656, A
C 282	13	4.2	150780	3	US-09-949-016-14711	Sequence 14711, A	c 355	12	3.8	601	3	US-09-949-016-17657	Sequence 17657, A
C 283	13	4.2	151088	3	US-09-949-016-16240	Sequence 16240, A	c 356	12	3.8	601	3	US-09-949-016-17835	Sequence 17835, A
C 284	13	4.2	152331	3	US-09-128-155-16	Sequence 16, Appl	c 357	12	3.8	601	3	US-09-949-016-18160	Sequence 18160, A
C 285	13	4.2	152481	3	US-09-949-016-12521	Sequence 12521, A	c 358	12	3.8	601	3	US-09-949-016-18161	Sequence 18161, A
C 286	13	4.2	152798	3	US-09-949-016-12775	Sequence 12775, A	c 359	12	3.8	601	3	US-09-949-016-19127	Sequence 19127, A
C 287	13	4.2	152822	3	US-09-949-016-17518	Sequence 17518, A	c 360	12	3.8	601	3	US-09-949-016-19406	Sequence 19406, A
C 288	13	4.2	152822	3	US-09-949-016-17519	Sequence 17519, A	c 361	12	3.8	601	3	US-09-949-016-19410	Sequence 19410, A
C 289	13	4.2	154626	3	US-09-949-016-14000	Sequence 14000, A	c 362	12	3.8	601	3	US-09-949-016-20254	Sequence 20254, A
C 290	13	4.2	156942	3	US-09-949-016-12227	Sequence 12227, A	c 363	12	3.8	601	3	US-09-949-016-20274	Sequence 20274, A
C 291	13	4.2	156950	3	US-09-949-016-15946	Sequence 15946, A	c 364	12	3.8	601	3	US-09-949-016-20677	Sequence 20677, A
C 292	13	4.2	167373	3	US-09-128-155-17	Sequence 17, Appl	c 365	12	3.8	601	3	US-09-949-016-20678	Sequence 20678, A
C 293	13	4.2	187580	3	US-09-949-016-13266	Sequence 13266, A	c 366	12	3.8	601	3	US-09-949-016-20983	Sequence 20983, A
C 294	13	4.2	187595	3	US-09-949-016-15546	Sequence 15546, A	c 367	12	3.8	601	3	US-09-949-016-21045	Sequence 21045, A
C 295	13	4.2	263693	3	US-09-949-016-12386	Sequence 12386, A	c 368	12	3.8	601	3	US-09-949-016-21470	Sequence 21470, A
C 296	13	4.2	263694	3	US-09-949-016-16915	Sequence 16915, A	c 369	12	3.8	601	3	US-09-949-016-21471	Sequence 21471, A
C 297	13	4.2	264358	3	US-09-949-016-15725	Sequence 15725, A	c 370	12	3.8	601	3	US-09-949-016-21737	Sequence 21737, A
C 298	13	4.2	271134	3	US-09-949-016-12705	Sequence 12705, A	c 371	12	3.8	601	3	US-09-949-016-21738	Sequence 21738, A
C 299	13	4.2	283538	3	US-09-949-016-13506	Sequence 13506, A	c 372	12	3.8	601	3	US-09-949-016-21739	Sequence 21739, A
C 300	13	4.2	305491	3	US-09-949-016-17550	Sequence 17550, A	c 373	12	3.8	601	3	US-09-949-016-22560	Sequence 22560, A

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C 375	12	3.8	601	3	US-09-949-016-23062	Sequence 23062, A	448	12	3.8	601	3	US-09-949-016-38753	Sequence 38753, A
C 376	12	3.8	601	3	US-09-949-016-23183	Sequence 23183, A	449	12	3.8	601	3	US-09-949-016-38754	Sequence 38754, A
C 377	12	3.8	601	3	US-09-949-016-23184	Sequence 23184, A	450	12	3.8	601	3	US-09-949-016-38755	Sequence 38755, A
C 378	12	3.8	601	3	US-09-949-016-23815	Sequence 23815, A	451	12	3.8	601	3	US-09-949-016-38756	Sequence 38756, A
C 379	12	3.8	601	3	US-09-949-016-24160	Sequence 24160, A	C 452	12	3.8	601	3	US-09-949-016-38813	Sequence 38813, A
C 380	12	3.8	601	3	US-09-949-016-24160	Sequence 24160, A	C 453	12	3.8	601	3	US-09-949-016-38814	Sequence 38814, A
C 381	12	3.8	601	3	US-09-949-016-24816	Sequence 24816, A	C 454	12	3.8	601	3	US-09-949-016-38815	Sequence 38815, A
C 382	12	3.8	601	3	US-09-949-016-24817	Sequence 24817, A	C 455	12	3.8	601	3	US-09-949-016-38816	Sequence 38816, A
C 383	12	3.8	601	3	US-09-949-016-26336	Sequence 26336, A	456	12	3.8	601	3	US-09-949-016-38973	Sequence 38973, A
C 384	12	3.8	601	3	US-09-949-016-26337	Sequence 26337, A	457	12	3.8	601	3	US-09-949-016-38974	Sequence 38974, A
C 385	12	3.8	601	3	US-09-949-016-26610	Sequence 26610, A	458	12	3.8	601	3	US-09-949-016-39673	Sequence 39673, A
C 386	12	3.8	601	3	US-09-949-016-26680	Sequence 26680, A	C 459	12	3.8	601	3	US-09-949-016-39674	Sequence 39674, A
C 387	12	3.8	601	3	US-09-949-016-27126	Sequence 27126, A	460	12	3.8	601	3	US-09-949-016-39999	Sequence 39999, A
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C 389	12	3.8	601	3	US-09-949-016-27234	Sequence 27234, A	C 462	12	3.8	601	3	US-09-949-016-40252	Sequence 40252, A
C 390	12	3.8	601	3	US-09-949-016-27333	Sequence 27333, A	463	12	3.8	601	3	US-09-949-016-41075	Sequence 41075, A
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C 392	12	3.8	601	3	US-09-949-016-27457	Sequence 27457, A	465	12	3.8	601	3	US-09-949-016-41321	Sequence 41321, A
C 393	12	3.8	601	3	US-09-949-016-27758	Sequence 27758, A	C 466	12	3.8	601	3	US-09-949-016-41321	Sequence 41321, A
C 394	12	3.8	601	3	US-09-949-016-27759	Sequence 27759, A	467	12	3.8	601	3	US-09-949-016-41705	Sequence 41705, A
C 395	12	3.8	601	3	US-09-949-016-27760	Sequence 27760, A	C 468	12	3.8	601	3	US-09-949-016-41884	Sequence 41884, A
C 396	12	3.8	601	3	US-09-949-016-27761	Sequence 27761, A	469	12	3.8	601	3	US-09-949-016-41885	Sequence 41885, A
C 397	12	3.8	601	3	US-09-949-016-27762	Sequence 27762, A	470	12	3.8	601	3	US-09-949-016-41886	Sequence 41886, A
C 398	12	3.8	601	3	US-09-949-016-29079	Sequence 29079, A	C 471	12	3.8	601	3	US-09-949-016-42464	Sequence 42464, A
C 399	12	3.8	601	3	US-09-949-016-29279	Sequence 29279, A	C 472	12	3.8	601	3	US-09-949-016-43131	Sequence 43131, A
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C 404	12	3.8	601	3	US-09-949-016-29699	Sequence 29699, A	C 477	12	3.8	601	3	US-09-949-016-43360	Sequence 43360, A
C 405	12	3.8	601	3	US-09-949-016-29782	Sequence 29782, A	C 478	12	3.8	601	3	US-09-949-016-43361	Sequence 43361, A
C 406	12	3.8	601	3	US-09-949-016-29783	Sequence 29783, A	C 479	12	3.8	601	3	US-09-949-016-43362	Sequence 43362, A
C 407	12	3.8	601	3	US-09-949-016-30352	Sequence 30352, A	C 480	12	3.8	601	3	US-09-949-016-43549	Sequence 43549, A
C 408	12	3.8	601	3	US-09-949-016-30456	Sequence 30456, A	C 481	12	3.8	601	3	US-09-949-016-43571	Sequence 43571, A
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C 410	12	3.8	601	3	US-09-949-016-31242	Sequence 31242, A	C 483	12	3.8	601	3	US-09-949-016-43590	Sequence 43590, A
C 411	12	3.8	601	3	US-09-949-016-31243	Sequence 31243, A	C 484	12	3.8	601	3	US-09-949-016-43591	Sequence 43591, A
C 412	12	3.8	601	3	US-09-949-016-31489	Sequence 31489, A	C 485	12	3.8	601	3	US-09-949-016-43778	Sequence 43778, A
C 413	12	3.8	601	3	US-09-949-016-31782	Sequence 31782, A	C 486	12	3.8	601	3	US-09-949-016-43800	Sequence 43800, A
C 414	12	3.8	601	3	US-09-949-016-31814	Sequence 31814, A	C 487	12	3.8	601	3	US-09-949-016-44480	Sequence 44480, A
C 415	12	3.8	601	3	US-09-949-016-31948	Sequence 31948, A	C 488	12	3.8	601	3	US-09-949-016-44578	Sequence 44578, A
C 416	12	3.8	601	3	US-09-949-016-32087	Sequence 32087, A	C 489	12	3.8	601	3	US-09-949-016-45256	Sequence 45256, A
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C 419	12	3.8	601	3	US-09-949-016-33506	Sequence 33506, A	C 492	12	3.8	601	3	US-09-949-016-46142	Sequence 46142, A
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C 422	12	3.8	601	3	US-09-949-016-33823	Sequence 33823, A	C 495	12	3.8	601	3	US-09-949-016-46424	Sequence 46424, A
C 423	12	3.8	601	3	US-09-949-016-34011	Sequence 34011, A	C 496	12	3.8	601	3	US-09-949-016-46633	Sequence 46633, A
C 424	12	3.8	601	3	US-09-949-016-34058	Sequence 34058, A	C 497	12	3.8	601	3	US-09-949-016-46634	Sequence 46634, A
C 425	12	3.8	601	3	US-09-949-016-34376	Sequence 34376, A	C 498	12	3.8	601	3	US-09-949-016-47654	Sequence 47654, A
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C 433	12	3.8	601	3	US-09-949-016-36412	Sequence 36412, A	C 506	12	3.8	601	3	US-09-949-016-52630	Sequence 52630, A
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c 522	12	3.8	601	3	US-09-949-016-54227	Sequence 54227, A	c 595	12	3.8	601	3	US-09-949-016-72145	Sequence 72145, A
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c 573	12	3.8	601	3	US-09-949-016-68552	Sequence 68552, A	c 646	12	3.8	601	3	US-09-949-016-83071	Sequence 83071, A
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C 732	12	3.8	601	3	US-09-949-016-105770	Sequence 105770, A	C 805	12	3.8	601	3	US-09-949-016-123793	Sequence 123793,
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c1007	12	3.8	601	3	US-09-949-016-163894	Sequence 163894,	c1080	12	3.8	601	3	US-09-949-016-180693	Sequence 180693,
c1008	12	3.8	601	3	US-09-949-016-163895	Sequence 163895,	c1081	12	3.8	601	3	US-09-949-016-180854	Sequence 180854,
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c1107	12	3.8	601	3	US-09-949-016-186345	Sequence 186345,	c1180	12	3.8	601	3	US-09-949-016-206973	Sequence 206973,
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c1109	12	3.8	601	3	US-09-949-016-186347	Sequence 186347,	c1182	12	3.8	601	3	US-09-949-001-96	Sequence 96, Appl
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c1111	12	3.8	601	3	US-09-949-016-186349	Sequence 186349,	c1184	12	3.8	601	3	US-09-949-001-842	Sequence 842, App
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c1142	12	3.8	601	3	US-09-949-016-195739	Sequence 195739,	c1215	12	3.8	683	3	US-09-735-271-314	Sequence 314, App
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c1149	12	3.8	601	3	US-09-949-016-200305	Sequence 200305,	c1222	12	3.8	885	5	US-09-641-638-277	Sequence 277, App
c1150	12	3.8	601	3	US-09-949-016-200497	Sequence 200497,	c1223	12	3.8	990	3	US-09-641-638-312	Sequence 312, App
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c1157	12	3.8	601	3	US-09-949-016-202185	Sequence 202185,	c1230	12	3.8	1051	3	US-09-997-333-372	Sequence 372, App
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c1159	12	3.8	601	3	US-09-949-016-202314	Sequence 202314,	c1232	12	3.8	1281	3	US-09-989-728-372	Sequence 372, App
c1160	12	3.8	601	3	US-09-949-016-202315	Sequence 202315,	c1233	12	3.8	1281	3	US-09-989-728-372	Sequence 372, App
c1161	12	3.8	601	3	US-09-949-016-202316	Sequence 202316,	c1234	12	3.8	1281	3	US-09-997-349-372	Sequence 372, App
c1162	12	3.8	601	3	US-09-949-016-202317	Sequence 202317,	c1235	12	3.8	1281	3	US-09-997-653-372	Sequence 372, App
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US-10-785-221-9 (1-312) x US-09-907-794A-63 (1-1295)

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/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
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/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 63
/ LENGTH: 1295
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-904-920A-63

Alignment Scores:
Pred. No.: 3,64e-292 Length: 1295
Score: 312.00 Matches: 312
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
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US-10-785-221-9 (1-312) x US-09-904-920A-63 (1-1295)

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/ Patent No. 6818449
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/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/909,064
/ CURRENT FILING DATE: 2001-07-18
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
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; ORGANISM: Homo sapiens
; US-09-905-381A-63

Alignment Scores:
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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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US-10-785-221-9 (1-312) x US-09-905-381A-63 (1-1295)

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RESULT 10
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; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594

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RESULT 12

US-09-906-646-63

; Sequence 63, Application US/09906646

; Patent No. 6852848

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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,646
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 63
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-906-646-63
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GenCore version 5.1.8
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Run on: May 17, 2006, 20:00:41 ; Search time 6941 Seconds
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Title: US-10-785-221-8

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Minimum DB seq length: 0

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Post-processing: Listing first 1500 summaries

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- 14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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135	176	13.6	464	1	AI140139	qB87e10.x	AI140139	qB87e10.x	208	50	222	2	BF879039	BF879039 RCL-ET013	
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154	114	8.8	563	9	DA227018	DA227018	DA227018	DA227018	227	50	521	11	AQ335633	AQ335633 HS-5015.B	
155	114	8.8	566	9	DA305734	DA305734	DA305734	DA305734	228	50	522	4	BY798624	BY798624 BY798624	
156	110	8.5	717	14	AG009139	Homo sapi	AG009139	Homo sapi	229	50	544	9	DB346740	DB346740 DB346740	
157	110	8.5	724	14	AG009128	Homo sapi	AG009128	Homo sapi	230	50	546	11	AQ890485	AQ890485 HS-3198.A	
158	106	8.2	723	14	AG009141	Homo sapi	AG009141	Homo sapi	231	50	557	9	DB362195	DB362195 DB362195	
159	101	7.8	355	1	AI052637	Oz18a04.x	AI052637	Oz18a04.x	232	50	558	9	DB212269	DB212269 DB212269	
160	101	7.8	700	14	AG012829	Homo sapi	AG012829	Homo sapi	233	50	558	9	DB304179	DB304179 DB304179	
161	100	7.7	843	4	BX332036	BX332036	BX332036	BX332036	234	50	570	11	AQ454449	AQ454449 HS-5195.A	
162	93	7.2	876	1	AL553676	AL553676	AL553676	AL553676	235	50	581	9	DA239774	DA239774 DA239774	
163	87	6.7	556	9	CX593621	CT020005B	CX593621	CT020005B	236	50	601	9	DA136272	DA136272 DA136272	
164	86	6.6	311	4	CB137090	K-EST0189	CB137090	K-EST0189	237	50	603	1	AV602516	AV6	

c 239	50	3.9	676	14	AG056016	Pan trogl	c 312	47	3.6	549	1	AI935088	AI935088 wpl3e01.x
c 240	50	3.9	713	14	AG009140	Homo sapi	c 313	47	3.6	554	9	DB301407	DB301407 DB301407
c 241	50	3.9	719	14	AG164523	Pan trogl	c 314	47	3.6	605	11	AQ535932	AQ535932 RPCI-11-3
c 242	50	3.9	750	3	BM678700	UI-E-E00-	c 315	47	3.6	631	3	BM990829	BM990829 UI-H-D10-
c 243	50	3.9	906	3	BQ708007	AGENCOURT	c 316	47	3.6	678	11	AQ019299	AQ019299 CIT-HSP-2
c 244	50	3.9	913	3	BQ708875	AGENCOURT	c 317	47	3.6	686	3	BM979228	BM979228 UI-CF-DU1
c 245	50	3.9	1006	3	BQ710740	AGENCOURT	c 318	47	3.6	749	13	CL983261	CL983261 HSC 01074
c 246	50	3.9	1762	6	BC018833	Homo sapi	c 319	47	3.6	828	14	CR957853	CR957853 Homo sapi
c 247	49	3.8	132	2	BF914929	IL3-UT01.1	c 320	47	3.6	889	2	BI093475	BI093475 602859669
c 248	49	3.8	267	1	AA640511	nt69c09.8	c 321	47	3.6	913	4	BM930218	BM930218 BX390218
c 249	49	3.8	268	1	AA228459	nc39h01.r	c 322	47	3.6	1715	6	BC000744	BC000744 Homo sapi
c 250	49	3.8	296	1	AI791336	ng90f06.y	c 323	47	3.6	1715	6	BC004437	BC004437 Homo sapi
c 251	49	3.8	320	1	AI732476	nk36a01.x	c 324	46	3.6	256	3	BM874680	BM874680 laa06h10.
c 252	49	3.8	326	7	AV743973	AV743973	c 325	46	3.6	272	1	AA665213	AA665213 nu82c08.s
c 253	49	3.8	389	11	AQ138330	HS 3078.A	c 326	46	3.6	310	10	DW416234	DW416234 HHAGE0169
c 254	49	3.8	419	11	AQ404030	HS 5050.B	c 327	46	3.6	335	8	CN268424	CN268424 170005319
c 255	49	3.8	430	11	AQ402943	HS 5066.A	c 328	46	3.6	381	1	AI923151	AI923151 wt29d01.x
c 256	49	3.8	455	7	BE301492	b74b03.x	c 329	46	3.6	508	1	AV720063	AV720063 wv20063
c 257	49	3.8	471	11	AQ241211	RPCI11-66	c 330	46	3.6	518	11	AQ139262	AQ139262 HS 3079.A
c 258	49	3.8	477	7	AW467978	he29g09.x	c 331	46	3.6	558	1	AL600875	AL600875 DKF2p313K
c 259	49	3.8	521	7	AI668679	zb55g05.x	c 332	46	3.6	574	9	DB168358	DB168358 DB168358
c 260	49	3.8	524	7	AW971361	EST383450	c 333	46	3.6	668	14	AG012169	AG012169 Homo sapi
c 261	49	3.8	535	9	DB296746	DB296746	c 334	46	3.6	679	14	AG012159	AG012159 Homo sapi
c 262	49	3.8	539	1	AI734264	zb55g05.y	c 335	46	3.6	725	14	AG031448	AG031448 Pan trogl
c 263	49	3.8	550	9	DB350558	DB350558	c 336	46	3.6	748	14	AG099815	AG099815 Pan trogl
c 264	49	3.8	615	1	AV704497	AV704497	c 337	46	3.6	795	14	DU836637	DU836637 MUQC.CH25
c 265	49	3.8	620	1	AV723620	AV723620	c 338	46	3.6	810	8	CO582159	CO582159 ILLUMIGEN
c 266	49	3.8	620	5	CD515260	AGENCOURT	c 339	46	3.6	913	13	CZ453074	CZ453074 MCF734k21
c 267	49	3.8	622	14	AG054744	Pan trogl	c 340	45	3.5	240	10	DW439827	DW439827 HHAG80385
c 268	49	3.8	651	7	BE886807	601506975	c 341	45	3.5	282	7	AW376674	AW376674 IL3-CY021
c 269	49	3.8	698	12	BZ608385	WHAC867TF	c 342	45	3.5	282	7	AW848596	AW848596 IL3-CY021
c 270	49	3.8	738	4	CD104520	AGENCOURT	c 343	45	3.5	309	7	AW850047	AW850047 IL3-CY021
c 271	49	3.8	789	12	CC466113	HSC 00562	c 344	45	3.5	327	1	AI669798	AI669798 tu31d09.x
c 272	49	3.8	894	3	BQ922501	AGENCOURT	c 345	45	3.5	329	5	CD519025	CD519025 AGENCOURT
c 273	49	3.8	933	3	BQ959144	AGENCOURT	c 346	45	3.5	335	7	BF091146	BF091146 PM2-TN002
c 274	49	3.8	945	3	BUS27620	BUS27620	c 347	45	3.5	371	11	B45364	B45364 HS-1061-A1-
c 275	48	3.7	160	11	B15004	343K21.TP.C	c 348	45	3.5	374	4	BX101318	BX101318 HM101318
c 276	48	3.7	195	1	AA653500	ag66e03.s	c 349	45	3.5	379	11	AQ550891	AQ550891 RPCI-11-4
c 277	48	3.7	207	7	AV748678	AV748678	c 350	45	3.5	419	8	CV383504	CV383504 QVO-HT057
c 278	48	3.7	286	10	M85415	EST01930.Fe	c 351	45	3.5	426	7	BE147173	BE147173 PM2-HT022
c 279	48	3.7	308	8	CR546354	DKF2p459J	c 352	45	3.5	426	7	BE147173	BE147173 PM2-HT022
c 280	48	3.7	317	11	AQ018995	CIT-HSP-2	c 353	45	3.5	444	11	AQ603856	AQ603856 HS 2131.A
c 281	48	3.7	339	1	AI573470	AJ573470	c 354	45	3.5	456	11	B53517	B53517 CIT-HSP-201
c 282	48	3.7	406	13	CZ456787	MCF739ML3	c 355	45	3.5	501	1	AA460880	AA460880 zx69e01.r
c 283	48	3.7	456	7	AW151713	x668c07.x	c 356	45	3.5	532	9	DB064967	DB064967 DB064967
c 284	48	3.7	514	1	AW773476	ab61h07.B	c 357	45	3.5	544	9	DB069935	DB069935 DB069935
c 285	48	3.7	532	3	BQ270670	ik06h09.x	c 358	45	3.5	548	1	AL707753	AL707753 DKF2p866H
c 286	48	3.7	535	8	CR773559	DKF2p459G	c 359	45	3.5	556	3	BP417345	BP417345 BP417345
c 287	48	3.7	540	11	AQ416183	RPCI-11-1	c 360	45	3.5	572	9	DB355733	DB355733 DB355733
c 288	48	3.7	542	9	DA374553	DA374553	c 361	45	3.5	620	4	BX642603	BX642603 DKF2p5860
c 289	48	3.7	563	9	DA918447	DA918447	c 362	45	3.5	629	4	CB555128	CB555128 MNSP0044
c 290	48	3.7	578	9	DA541598	DA541598	c 363	45	3.5	673	8	CN275193	CN275193 170006000
c 291	48	3.7	593	9	DB356324	DB356324	c 364	45	3.5	675	14	AG087601	AG087601 Pan trogl
c 292	48	3.7	707	11	AQ308715	CITBT-E1-	c 365	45	3.5	691	13	CZ448878	CZ448878 MCF729a20
c 293	48	3.7	801	5	CF887485	UI-CF-EN1	c 366	45	3.5	700	1	AJ942995	AJ942995 AJ942995
c 294	48	3.7	830	10	DT809612	LB0164.CR	c 367	45	3.5	715	4	BM920450	BM920450 BX920450
c 295	48	3.7	849	4	CB991080	AGENCOURT	c 368	45	3.5	727	9	DR159303	DR159303 HESC.100
c 296	47	3.6	125	10	DR980865	SN016960	c 369	45	3.5	852	11	AQ748478	AQ748478 HS 5340.A
c 297	47	3.6	257	10	N77295	yv43d03.r1	c 370	45	3.5	859	1	AL546812	AL546812 AL546812
c 298	47	3.6	274	3	BU729074	UI-E-CQ1-	c 371	45	3.5	879	11	AQ741563	AQ741563 HS 5567.B
c 299	47	3.6	278	11	AQ585869	RPCI-11-4	c 372	45	3.5	973	4	BM460718	BM460718 BX460718
c 300	47	3.6	298	11	AQ588020	CITBT-E1-	c 373	44	3.4	263	1	AA335846	AA335846 ESP40323
c 301	47	3.6	291	10	H62550	yr43d03.81	c 374	44	3.4	265	2	BP756200	BP756200 IL2-CY051
c 302	47	3.6	305	3	BU902217	AGENCOURT	c 375	44	3.4	312	1	AA974715	AA974715 op29f01.8
c 303	47	3.6	320	10	DW413473	HHAG80142	c 376	44	3.4	328	1	AA523614	AA523614 n143c12.8
c 304	47	3.6	322	10	DW412986	DW412986 HHAG80137	c 377	44	3.4	328	9	DN391113	DN391113 LTB3924-0
c 305	47	3.6	456	11	AQ783939	HS 3023.A	c 378	44	3.4	360	11	AQ442984	AQ442984 HS 5055.B
c 306	47	3.6	483	1	AI199816	qf95d03.x	c 379	44	3.4	370	11	AQ316623	AQ316623 RPCI11-2J
c 307	47	3.6	484	1	AL702580	DKF2p866F	c 380	44	3.4	374	1	AA642445	AA642445 nb30b04.8
c 308	47	3.6	490	7	AW856326	RC6-CY028	c 381	44	3.4	392	7	AW261924	AW261924 xp87g02.x
c 309	47	3.6	523	7	AW245054	2819732.3	c 382	44	3.4	393	11	AQ207153	AQ207153 HS 3235.A
c 310	47	3.6	535	11	AQ530411	RPCI-11-3	c 383	44	3.4	411	9	DN345547	DN345547 LTB34551-0
c 311	47	3.6	548	9	DA107776	DA107776	c 384	44	3.4	426	7	AW956077	AW956077 EST368147

C 385	44	3.4	431	1	AA179707	AA179707 zps3b06.8	458	43	3.3	326	10	DW411936	DW411936 HHAGE0126
C 386	44	3.4	439	11	AQ625250	AQ625250 CITBI-EI-	C 459	43	3.3	327	1	AA721645	AA721645 DY87609.8
C 387	44	3.4	456	10	R67714	R67714 Y124n03.r1	460	43	3.3	327	2	BG219298	BG219298 RST39052
C 388	44	3.4	461	11	AQ783964	AQ783964 HS_3023.A	461	43	3.3	330	11	AQ72868	AQ72868 HS_2267.B
C 389	44	3.4	485	3	BM992299	BM992299 UT-H-DFT-	C 462	43	3.3	337	4	BX954396	BX954396 DKF2P781H
C 390	44	3.4	510	10	R76999	R76999 Y166f07.r1	C 463	43	3.3	338	7	BF031551	BF031551 601559390
C 391	44	3.4	513	9	DB351588	DB351588 DB351588	464	43	3.3	338	10	DW409626	DW409626 HHAGE0103
C 392	44	3.4	515	2	BI712061	BI712061 i601b05.x	C 465	43	3.3	339	10	N72812	N72812 Yv50b12.r1
C 393	44	3.4	519	1	AU146536	AU146536 AU146536	C 466	43	3.3	341	1	AI803827	AI803827 fp30402.x
C 394	44	3.4	519	9	DB311550	DB311550 DB311550	C 467	43	3.3	341	7	AW518758	AW518758 ha39f09.x
C 395	44	3.4	521	11	AQ792960	AQ792960 HS_5304.A	C 468	43	3.3	342	7	AV730214	AV730214 AV730214
C 396	44	3.4	524	9	DN394857	DN394857 LIB3934-0	C 469	43	3.3	345	1	AA486829	AA486829 ab19409.r
C 397	44	3.4	536	9	DB303518	DB303518 DB303518	C 470	43	3.3	345	1	AA438765	AA438765 xC03f07.x
C 398	44	3.4	546	9	DB345177	DB345177 DB345177	C 471	43	3.3	346	7	AA438765	AA438765 xC03f07.x
C 399	44	3.4	556	2	BMS11860	BMS11860 J74912.x	C 472	43	3.3	349	10	DW466845	DW466845 HHAGE0081
C 400	44	3.4	575	11	AQ381165	AQ381165 RPC111-13	C 473	43	3.3	350	8	CV311243	CV311243 CMO-HT074
C 401	44	3.4	579	9	DB123950	DB123950 DB123950	C 474	43	3.3	351	7	AV732274	AV732274 AV732274
C 402	44	3.4	594	11	AQ313134	AQ313134 RPC111-10	C 475	43	3.3	352	7	BE739174	BE739174 601556333
C 403	44	3.4	611	3	BQ447267	BQ447267 UT-H-EUI-	C 476	43	3.3	352	13	CZ442549	CZ442549 ID8C4.fwd
C 404	44	3.4	628	4	BY796440	BY796440 BY796440	C 477	43	3.3	354	10	DW465947	DW465947 HHAGE0072
C 405	44	3.4	651	9	DN864800	DN864800 nac12b02..	C 478	43	3.3	357	1	AA487150	AA487150 ab19409.8
C 406	44	3.4	676	3	BU661559	BU661559 CL73f08.z	C 479	43	3.3	359	11	AQ085420	AQ085420 HS_2270.B
C 407	44	3.4	681	11	AQ779588	AQ779588 HS_5567.B	C 480	43	3.3	360	1	AA532594	AA532594 rj54609.8
C 408	44	3.4	712	14	AG002410	AG002410 Homo sapi	C 481	43	3.3	361	11	B18131	B18131 A-57G9.TV C
C 409	44	3.4	739	8	CR7950836	CR7950836 DKF2P468C	C 482	43	3.3	364	2	BG210364	BG210364 RST29901
C 410	44	3.4	751	9	CX984480	CX984480 DOG_EST_P	C 483	43	3.3	364	10	M77858	M77858 EST01442.Fe
C 411	44	3.4	752	14	AG186943	AG186943 Pan trogl	C 484	43	3.3	364	11	AQ100325	AQ100325 HS_3054.A
C 412	44	3.4	773	3	BU750529	BU750529 CH3#034.A	C 485	43	3.3	365	5	CD868147	CD868147 EST4669.h
C 413	44	3.4	780	9	CX984497	CX984497 DOG_EST_P	C 486	43	3.3	366	2	BG942867	BG942867 ax30f02.x
C 414	44	3.4	791	12	BZ611781	BZ611781 WHACP3TfF	C 487	43	3.3	366	3	BQ024136	BQ024136 UI-1-BB1P
C 415	44	3.4	801	3	BU748394	BU748394 CH3#019.G	C 488	43	3.3	367	2	BF741814	BF741814 QV1-HB003
C 416	44	3.4	846	11	AQ750315	AQ750315 HS_5573.B	C 489	43	3.3	370	2	BG199966	BG199966 RST19262
C 417	44	3.4	854	11	AQ741165	AQ741165 HS_2273.A	C 490	43	3.3	370	14	AG266004	AG266004 Homo sapi
C 418	44	3.4	2304	6	BC029803	BC029803 Homo sapi	C 491	43	3.3	371	2	BG205639	BG205639 RST25086
C 419	44	3.4	2795	6	CR749794	CR749794 Homo sapi	C 492	43	3.3	371	9	DB311717	DB311717 DB311717
C 420	43	3.3	132	10	R07403	R07403 ye96f02.r1	C 493	43	3.3	376	4	EA091821	EA091821 BX091821
C 421	43	3.3	148	2	BG204887	BG204887 RST24303	C 494	43	3.3	377	11	AQ424584	AQ424584 CITBI-EI-
C 422	43	3.3	149	2	BG208583	BG208583 RST28086	C 495	43	3.3	378	11	B13991	B13991 A-57G9.TVB
C 423	43	3.3	150	2	BG198048	BG198048 RST17432	C 496	43	3.3	380	1	AA814530	AA814530 ob96f04.8
C 424	43	3.3	151	2	BG194658	BG194658 RST13822	C 497	43	3.3	381	1	AA113367	AA113367 zn70404.8
C 425	43	3.3	159	10	DM457917	DM457917 HHAGE0546	C 498	43	3.3	384	2	BF955722	BF955722 CM2-NN024
C 426	43	3.3	166	5	CK824734	CK824734 ig33c04.y	C 499	43	3.3	388	4	EA471272	EA471272 DKF2P686H
C 427	43	3.3	201	1	AA653250	AA653250 ag49b06.8	C 500	43	3.3	388	11	AQ212798	AQ212798 HS_3118.B
C 428	43	3.3	209	10	W39897	W39897 z828h11.r1	C 501	43	3.3	392	7	AW811226	AW811226 CM4-ST013
C 429	43	3.3	225	8	CR544860	CR544860 DKF2P470C	C 502	43	3.3	393	10	N64842	N64842 za22a09.81
C 430	43	3.3	228	1	AA806653	AA806653 OB89G03.8	C 503	43	3.3	395	10	N71033	N71033 za35e02.81
C 431	43	3.3	234	1	AA610803	AA610803 np92e03.8	C 504	43	3.3	396	1	AA626823	AA626823 ab52903.r
C 432	43	3.3	241	7	BE154457	BE154457 PMO-HT034	C 505	43	3.3	397	7	AW276408	AW276408 xrl2g10.x
C 433	43	3.3	241	10	DM439499	DM439499 HHAGE0382	C 506	43	3.3	400	2	AA856866	AA856866 od83f01.8
C 434	43	3.3	260	7	BE154526	BE154526 PMO-HT034	C 507	43	3.3	402	2	BG527479	BG527479 602557284
C 435	43	3.3	261	7	BE154518	BE154518 PMO-HT034	C 508	43	3.3	404	3	BU899189	BU899189 AGENCOURT
C 436	43	3.3	262	7	BE154524	BE154524 PMO-HT034	C 509	43	3.3	408	10	R53899	R53899 Y103d11.r1
C 437	43	3.3	263	5	CD518698	CD518698 AGENCOURT	C 510	43	3.3	408	11	AQ240405	AQ240405 CIT-HSP-2
C 438	43	3.3	265	3	BQ005096	BQ005096 UT-H-EIO-	C 511	43	3.3	410	7	AV744364	AV744364 AV744364
C 439	43	3.3	270	10	DM431080	DM431080 HHAGE0298	C 512	43	3.3	410	10	H65404	H65404 Yv63a12.r1
C 440	43	3.3	274	1	AA054055	AA054055 zf46b07.r	C 513	43	3.3	411	1	AI216054	AI216054 CM34e09.x
C 441	43	3.3	274	7	BE154459	BE154459 PMO-HT034	C 514	43	3.3	412	2	BF843910	BF843910 CM4-HT115
C 442	43	3.3	277	10	DM427904	DM427904 HHAGE0276	C 515	43	3.3	412	7	AV735885	AV735885 AV735885
C 443	43	3.3	279	1	AA296002	AA296002 EST101223	C 516	43	3.3	412	11	AQ213220	AQ213220 HS_3243.A
C 444	43	3.3	281	2	BF922017	BF922017 CM0-HT018	C 517	43	3.3	423	7	AW572140	AW572140 xql4d04.x
C 445	43	3.3	285	7	BE154446	BE154446 PMO-HT034	C 518	43	3.3	423	11	AQ436197	AQ436197 HS_5049.B
C 446	43	3.3	296	3	BU566987	BU566987 AGENCOURT	C 519	43	3.3	425	1	AA628606	AA628606 af40a03.b
C 447	43	3.3	296	7	BE154589	BE154589 PMO-HT034	C 520	43	3.3	425	10	H45136	H45136 Y066G04.r1
C 448	43	3.3	298	7	AW901135	AW901135 CMO-NN101	C 521	43	3.3	426	2	BF978162	BF978162 602148094
C 449	43	3.3	300	3	BU564352	BU564352 AGENCOURT	C 522	43	3.3	429	4	CB068634	CB068634 l830g08.x
C 450	43	3.3	301	7	BE154584	BE154584 PMO-HT034	C 523	43	3.3	432	1	AA689520	AA689520 nbl7h04.r
C 451	43	3.3	307	11	AQ477601	AQ477601 CITBI-EI-	C 524	43	3.3	432	11	AQ061934	AQ061934 CIT-HSP-2
C 452	43	3.3	311	10	DM415840	DM415840 HHAGE0165	C 525	43	3.3	437	8	CR788222	CR788222 DKF2P459H
C 453	43	3.3	311	11	AQ530386	AQ530386 RPCI-11-3	C 526	43	3.3	439	7	BE155980	BE155980 QV0-HT036
C 454	43	3.3	316	10	DM414285	DM414285 HHAGE0150	C 527	43	3.3	441	2	BF740656	BF740656 QV1-HB003
C 455	43	3.3	319	3	BU533187	BU533187 AGENCOURT	C 528	43	3.3	444	1	AL712426	AL712426 qm28f04.x
C 456	43	3.3	319	8	CN386283	CN386283 170006002	C 529	43	3.3	444	9	DB302709	DB302709 DKF2P686A
C 457	43	3.3	323	1	AA613966	AA613966 no78d10.8	C 530	43	3.3	448	3	BQ777737	BQ777737 1140c06.x

C 531	43	3.3	448	10	R64640	R64640 y19f11..s1	C 604	43	3.3	558	8	CN300035	CN300035 170004241
C 532	43	3.3	450	10	N92091	N92091 za22b10..r1	C 605	43	3.3	559	2	BI712523	BI712523 ie09a02..x
C 533	43	3.3	451	1	AA424438	AA424438 zv83c08..r	C 606	43	3.3	559	9	DB345040	DB345040 DB345040
C 534	43	3.3	451	7	AW006124	AW006124 w22f07..x	C 607	43	3.3	561	9	DA372313	DA372313 DA372313
C 535	43	3.3	453	1	AA713658	AA713658 nv69b02..s	C 608	43	3.3	561	9	DB324952	DB324952 DB324952
C 536	43	3.3	453	7	BF691653	BF691653 602248383	C 609	43	3.3	564	9	DA479779	DA479779 DA479779
C 537	43	3.3	454	8	CN343309	CN343309 170006001	C 610	43	3.3	565	9	DB329981	DB329981 DB329981
C 538	43	3.3	456	7	BE176581	BE176581 RC3-HT058	C 611	43	3.3	565	9	DB361551	DB361551 DB361551
C 539	43	3.3	457	1	AI340280	AI340280 qp85a11..x	C 612	43	3.3	566	9	DA087351	DA087351 DA087351
C 540	43	3.3	457	11	B49501	B49501 RPC111-6M10	C 613	43	3.3	567	9	DA928501	DA928501 DA928501
C 541	43	3.3	462	11	AQ320535	AQ320535 RRC111-97	C 614	43	3.3	567	9	DA967662	DA967662 DA967662
C 542	43	3.3	464	4	BA483591	BA483591 DKF2p6861	C 615	43	3.3	568	9	DA927540	DA927540 DA927540
C 543	43	3.3	464	7	AW001268	AW001268 wu36h10..x	C 616	43	3.3	569	1	AL048969	AL048969 DKF2p434M
C 544	43	3.3	465	11	AQ536566	AQ536566 RPC1-11-3	C 617	43	3.3	569	9	DB361859	DB361859 DB361859
C 545	43	3.3	467	1	AU147182	AU147182 AU147182	C 618	43	3.3	570	9	DA012227	DA012227 DA012227
C 546	43	3.3	468	1	AA115656	AA115656 z186c09..s	C 619	43	3.3	572	9	DB299400	DB299400 DB299400
C 547	43	3.3	473	3	AW075979	AW075979 za82e09..x	C 620	43	3.3	572	9	DB362114	DB362114 DB362114
C 548	43	3.3	474	3	BU076951	BU076951 in19e02..x	C 621	43	3.3	573	2	BG221264	BG221264 R541067
C 549	43	3.3	477	10	H73925	H73925 y815e04..s1	C 622	43	3.3	573	4	CB265259	CB265259 1004164 H
C 550	43	3.3	477	10	T85040	T85040 yd55g12..r1	C 623	43	3.3	573	9	DA240148	DA240148 DA240148
C 551	43	3.3	480	7	AW503991	AW503991 UI-HF-BN0	C 624	43	3.3	573	9	DB098205	DB098205 DB098205
C 552	43	3.3	481	9	DB347454	DB347454 DB347454	C 625	43	3.3	574	9	DB354833	DB354833 DB354833
C 553	43	3.3	484	7	AW975544	AW975544 EST387653	C 626	43	3.3	576	4	CA943357	CA943357 ip38d10..x
C 554	43	3.3	485	1	AA601400	AA601400 no16f05..s	C 627	43	3.3	576	9	DA241266	DA241266 DA241266
C 555	43	3.3	490	11	AQ432147	AQ432147 HS 5050..A	C 628	43	3.3	576	9	DA310642	DA310642 DA310642
C 556	43	3.3	493	9	DB059913	DB059913 DB059913	C 629	43	3.3	579	9	DA853516	DA853516 DB053516
C 557	43	3.3	497	11	AQ485536	AQ485536 RPC1-11-2	C 630	43	3.3	580	7	AW978114	AW978114 EST390223
C 558	43	3.3	498	1	AU146929	AU146929 AU146929	C 631	43	3.3	581	13	CZ464348	CZ464348 MCF755e21
C 559	43	3.3	502	2	BF819354	BF819354 ILO-RT001	C 632	43	3.3	582	7	AW993293	AW993293 RC2-BN003
C 560	43	3.3	509	7	BF183045	BF183045 601809614	C 633	43	3.3	583	9	DA633515	DA633515 DA633515
C 561	43	3.3	509	11	AZ254648	AZ254648 UP 467-14	C 634	43	3.3	584	9	DA190471	DA190471 DA190471
C 562	43	3.3	510	4	BX488002	BX488002 DKF2p686H	C 635	43	3.3	586	2	BG494803	BG494803 602540803
C 563	43	3.3	511	11	AQ475747	AQ475747 CJTBI-E1-	C 636	43	3.3	586	9	DA402809	DA402809 DB402809
C 564	43	3.3	512	11	AQ585840	AQ585840 RRC1-11-4	C 637	43	3.3	589	5	CK825911	CK825911 ik35c01..x
C 565	43	3.3	513	11	AQ154602	AQ154602 HS 3017..B	C 638	43	3.3	589	9	DA671979	DA671979 DA671979
C 566	43	3.3	514	9	DA434720	DA434720 DA434720	C 639	43	3.3	590	11	B56895	B56895 CIT-HSP-200
C 567	43	3.3	516	3	BQ928633	BQ928633 AGNCNCURT	C 640	43	3.3	592	11	B56414	B56414 CIT-HSP-200
C 568	43	3.3	516	7	BF244176	BF244176 601863116	C 641	43	3.3	594	7	AW959279	AW959279 EST371349
C 569	43	3.3	517	7	AW130591	AW130591 xf56b05..x	C 642	43	3.3	595	9	DA942293	DA942293 DA942293
C 570	43	3.3	517	3	BU541876	BU541876 AGNCNCURT	C 643	43	3.3	598	8	CN278949	CN278949 170004241
C 571	43	3.3	518	2	BF819365	BF819365 ILO-RT001	C 644	43	3.3	603	4	BX502511	BX502511 DKF2p779H
C 572	43	3.3	518	3	BG661361	BG661361 cl170h11..z	C 645	43	3.3	606	10	R77158	R77158 y165a06..r1
C 573	43	3.3	520	9	BX481617	BX481617 DKF2p686A	C 646	43	3.3	609	8	CN395084	CN395084 170006000
C 574	43	3.3	520	9	DB351807	DB351807 DB351807	C 647	43	3.3	610	3	BU178885	BU178885 AGNCNCURT
C 575	43	3.3	521	7	AW473996	AW473996 hb12903..x	C 648	43	3.3	613	8	CN387947	CN387947 170006001
C 576	43	3.3	526	1	AA224145	AA224145 zr15e04..s	C 649	43	3.3	620	7	BE748457	BE748457 601571951
C 577	43	3.3	527	9	DB313687	DB313687 DB313687	C 650	43	3.3	623	8	CN386284	CN386284 170006000
C 578	43	3.3	530	4	BX502371	BX502371 DKF2p779K	C 651	43	3.3	623	11	AQ377046	AQ377046 RRC111-15
C 579	43	3.3	530	9	DB363708	DB363708 DB363708	C 652	43	3.3	624	7	AW606333	AW606333 QV0-HT036
C 580	43	3.3	531	11	AQ0707882	AQ0707882 HS 5561..B	C 653	43	3.3	624	14	AG051410	AG051410 Pan trog1
C 581	43	3.3	533	9	DB351688	DB351688 DB351688	C 654	43	3.3	627	2	BF810146	BF810146 MR2-CI018
C 582	43	3.3	534	9	DB302217	DB302217 DB302217	C 655	43	3.3	629	5	CK005213	CK005213 AGNCNCURT
C 583	43	3.3	535	9	DB330031	DB330031 DB330031	C 656	43	3.3	630	7	AW993000	AW993000 RC2-BN003
C 584	43	3.3	536	3	BQ887587	BQ887587 AGNCNCURT	C 657	43	3.3	633	1	AL1707626	AL1707626 DKF2p6860
C 585	43	3.3	537	7	AW978041	AW978041 EST390150	C 658	43	3.3	638	2	BG500685	BG500685 60254078
C 586	43	3.3	538	4	BX479164	BX479164 DKF2p686E	C 659	43	3.3	639	14	AG039038	AG039038 Pan trog1
C 587	43	3.3	542	9	DA807650	DA807650 DA807650	C 660	43	3.3	643	7	BF212465	BF212465 601813237
C 588	43	3.3	543	7	BE961047	BE961047 601648422	C 661	43	3.3	644	4	BX499109	BX499109 DKF2p779J
C 589	43	3.3	543	9	DB343441	DB343441 DB343441	C 662	43	3.3	645	3	BU174477	BU174477 AGNCNCURT
C 590	43	3.3	546	9	DA623293	DA623293 DA623293	C 663	43	3.3	645	4	BX646005	BX646005 DKF2p781H
C 591	43	3.3	547	9	DA511741	DA511741 DA511741	C 664	43	3.3	646	3	BQ685362	BQ685362 AGNCNCURT
C 592	43	3.3	547	9	DB361960	DB361960 DB361960	C 665	43	3.3	646	3	BQ689795	BQ689795 AGNCNCURT
C 593	43	3.3	549	9	DB333449	DB333449 DB333449	C 666	43	3.3	646	3	BQ690462	BQ690462 AGNCNCURT
C 594	43	3.3	550	3	BQ417219	BQ417219 ik35c01..y	C 667	43	3.3	646	3	BQ879595	BQ879595 AGNCNCURT
C 595	43	3.3	551	1	AL698703	AL698703 DKF2p686A	C 668	43	3.3	646	3	BQ890428	BQ890428 AGNCNCURT
C 596	43	3.3	551	9	DA106623	DA106623 DA106623	C 669	43	3.3	646	3	BQ897724	BQ897724 AGNCNCURT
C 597	43	3.3	551	9	DB017652	DB017652 DB017652	C 670	43	3.3	646	3	BU168612	BU168612 AGNCNCURT
C 598	43	3.3	551	9	DB122185	DB122185 DB122185	C 671	43	3.3	646	3	BU168693	BU168693 AGNCNCURT
C 599	43	3.3	553	2	BG527806	BG527806 602556755	C 672	43	3.3	646	3	BU185413	BU185413 AGNCNCURT
C 600	43	3.3	555	9	DB348891	DB348891 DB348891	C 673	43	3.3	646	3	BU196435	BU196435 AGNCNCURT
C 601	43	3.3	556	9	DA478085	DA478085 DA478085	C 674	43	3.3	646	3	BF694141	BF694141 602082755
C 602	43	3.3	557	9	DA257791	DA257791 DA257791	C 675	43	3.3	646	14	AG138843	AG138843 Pan trog1
C 603	43	3.3	558	2	BI791900	BI791900 ie10b02..x	C 676	43	3.3	649	14	DU840232	DU840232 MUGO_CH25

C 677	43	3.3	649	14	CR960737	CR960737 Homo sapi	C 750	43	3.3	789	2	BI457961	BI457961 603198954
C 678	43	3.3	650	4	BXS06899	BXS06899 DXF2P779E	751	43	3.3	790	11	AQ740405	AQ740405 HS_5502_A
C 679	43	3.3	650	4	CB044631	CB044631 NISC_gc05	752	43	3.3	791	9	DR158777	DR158777 HESC2_94_A
C 680	43	3.3	651	7	BE870750	BE870750 601448590	753	43	3.3	794	2	BG527708	BG527708 602556647
C 681	43	3.3	651	14	AG037056	AG037056 Pan trogl	C 754	43	3.3	794	11	AQ745990	AQ745990 HS_2277_A
C 682	43	3.3	652	14	AG149791	AG149791 Pan trogl	C 755	43	3.3	803	2	BM006287	BM006287 603614960
C 683	43	3.3	654	7	BE148618	BE148618 MRO-HT024	C 756	43	3.3	804	5	CD521201	CD521201 AGENCOURT
C 684	43	3.3	657	14	AG106995	AG106995 Pan trogl	C 757	43	3.3	809	3	BUS85423	BUS85423 AGENCOURT
C 685	43	3.3	660	4	BX952602	BX952602 DXF2P781A	758	43	3.3	810	12	BZ602315	BZ602315 WHADU55TF
C 686	43	3.3	660	11	AQ376970	AQ376970 RPC111-15	759	43	3.3	811	14	DU796969	DU796969 fvo1_fp00
C 687	43	3.3	665	2	BG534555	BG534555 602553403	760	43	3.3	812	2	BF977345	BF977345 602146328
C 688	43	3.3	666	14	AG137931	AG137931 Pan trogl	761	43	3.3	814	5	BG495595	BG495595 602539928
C 689	43	3.3	668	14	AG068901	AG068901 Pan trogl	762	43	3.3	814	5	CD656590	CD656590 AGENCOURT
C 690	43	3.3	668	14	CR958509	CR958509 Homo sapi	763	43	3.3	818	14	CR957848	CR957848 Homo sapi
C 691	43	3.3	670	14	AG100015	AG100015 Pan trogl	764	43	3.3	822	2	BG527852	BG527852 602556808
C 692	43	3.3	671	14	AG124814	AG124814 Pan trogl	C 765	43	3.3	822	2	BG574820	BG574820 602596877
C 693	43	3.3	672	3	BQ685662	BQ685662 AGENCOURT	766	43	3.3	823	13	CZ459657	CZ459657 MCF748a18
C 694	43	3.3	672	8	CR278103	CR278103 170006001	C 767	43	3.3	824	3	BQ429278	BQ429278 AGENCOURT
C 695	43	3.3	673	2	BG493959	BG493959 602542239	768	43	3.3	829	7	BF211406	BF211406 601812461
C 696	43	3.3	676	14	AG116016	AG116016 Pan trogl	769	43	3.3	830	2	BF976942	BF976942 602147025
C 697	43	3.3	676	14	AG143659	AG143659 Pan trogl	C 770	43	3.3	832	2	BI461849	BI461849 603207565
C 698	43	3.3	677	14	AG104194	AG104194 Pan trogl	C 771	43	3.3	832	7	BE564077	BE564077 601348039
C 699	43	3.3	679	14	AG111125	AG111125 Pan trogl	C 772	43	3.3	842	7	BF130674	BF130674 601819276
C 700	43	3.3	684	3	BQ007969	BQ007969 UT-H-E10	773	43	3.3	847	3	BU570488	BU570488 AGENCOURT
C 701	43	3.3	686	2	BI820814	BI820814 603034026	774	43	3.3	849	2	BF977071	BF977071 602146984
C 702	43	3.3	686	4	BX104493	BX104493 BX104493	C 775	43	3.3	853	7	BF103893	BF103893 601647105
C 703	43	3.3	686	8	CN267011	CN267011 170004706	776	43	3.3	854	9	CF213033	CF213033 601844261
C 704	43	3.3	687	2	BG777306	BG777306 602664547	C 777	43	3.3	858	9	CF213033	CF213033 601844261
C 705	43	3.3	689	14	AG141493	AG141493 Pan trogl	778	43	3.3	860	7	BF238352	BF238352 601904621
C 706	43	3.3	691	11	AQ321183	AQ321183 RPC111-10	C 779	43	3.3	860	7	BF238352	BF238352 601904621
C 707	43	3.3	694	2	BG776604	BG776604 602663748	C 780	43	3.3	863	2	BQ221300	BQ221300 AGENCOURT
C 708	43	3.3	701	14	AG007987	AG007987 Homo sapi	C 781	43	3.3	866	2	BG615534	BG615534 602642849
C 709	43	3.3	702	14	AG007989	AG007989 Homo sapi	782	43	3.3	869	2	BF979045	BF979045 602147547
C 710	43	3.3	706	14	AG007988	AG007988 Homo sapi	C 783	43	3.3	873	7	BF690603	BF690603 602246520
C 711	43	3.3	708	2	BF978936	BF978936 602147612	784	43	3.3	875	7	BF132767	BF132767 601645890
C 712	43	3.3	709	2	BG777231	BG777231 602664458	785	43	3.3	878	7	BE961172	BE961172 601648383
C 713	43	3.3	712	2	BG527680	BG527680 602556617	786	43	3.3	880	7	BF209356	BF209356 601872588
C 714	43	3.3	715	11	AQ626621	AQ626621 CITB1-E1	787	43	3.3	880	7	BF209356	BF209356 602249024
C 715	43	3.3	717	14	AG002409	AG002409 Homo sapi	788	43	3.3	882	7	BF572980	BF572980 602078982
C 716	43	3.3	723	14	AG008021	AG008021 Homo sapi	C 789	43	3.3	888	7	BF184128	BF184128 601843165
C 717	43	3.3	725	2	BG400733	BG400733 602464120	C 790	43	3.3	891	8	CV815612	CV815612 AGENCOURT
C 718	43	3.3	725	4	CA427862	CA427862 UT-H-DF0	791	43	3.3	892	2	BG571845	BG571845 602593184
C 719	43	3.3	721	8	CN278948	CN278948 170005318	C 792	43	3.3	897	2	BG437057	BG437057 602488653
C 720	43	3.3	732	11	AG630973	AG630973 RPC1-11-4	C 793	43	3.3	897	2	BG529519	BG529519 602557910
C 721	43	3.3	733	7	BF571687	BF571687 602076244	794	43	3.3	899	7	BF670203	BF670203 602144353
C 722	43	3.3	734	11	AQ744948	AQ744948 HS_5506_A	C 795	43	3.3	900	2	BI462448	BI462448 603203929
C 723	43	3.3	735	14	DU839791	DU839791 MUGO_CH25	796	43	3.3	902	7	BF571004	BF571004 602075926
C 724	43	3.3	736	11	BQ0090	BQ0090 cSRL-102b6-	797	43	3.3	909	7	BF184981	BF184981 601843479
C 725	43	3.3	738	2	BG527374	BG527374 602557360	C 798	43	3.3	909	7	BF692099	BF692099 60247879
C 726	43	3.3	741	2	BG574902	BG574902 602596977	799	43	3.3	910	2	BG574813	BG574813 602596869
C 727	43	3.3	742	4	BX094930	BX094930 BX094930	800	43	3.3	911	7	BF185127	BF185127 601843973
C 728	43	3.3	746	14	AG179326	AG179326 Pan trogl	801	43	3.3	914	7	BF692045	BF692045 602247810
C 729	43	3.3	748	9	CX783820	CX783820 HESC3_26	C 802	43	3.3	914	7	BF775568	BF775568 601348459
C 730	43	3.3	750	2	BF978010	BF978010 602147903	803	43	3.3	921	3	BQ951062	BQ951062 AGENCOURT
C 731	43	3.3	753	3	BQ650742	BQ650742 AGENCOURT	C 804	43	3.3	928	3	BUS85649	BUS85649 AGENCOURT
C 732	43	3.3	755	4	BX111779	BX111779 BX111779	805	43	3.3	936	4	BX369732	BX369732 AKJ58732
C 733	43	3.3	758	9	CX761251	CX761251 AGENCOURT	C 806	43	3.3	938	1	AL558872	AL558872 AL558872
C 734	43	3.3	759	8	CN352185	CN352185 170005830	807	43	3.3	940	2	BG615524	BG615524 602620388
C 735	43	3.3	766	10	DR759801	DR759801 HESC4_108	C 808	43	3.3	944	2	BG674392	BG674392 602620388
C 736	43	3.3	775	4	CB958647	CB958647 AGENCOURT	809	43	3.3	967	2	BG687417	BG687417 602639577
C 737	43	3.3	775	7	BG631393	BG631393 602247448	C 810	43	3.3	975	3	BQ927418	BQ927418 AGENCOURT
C 738	43	3.3	776	2	BG170055	BG170055 602321515	811	43	3.3	984	2	BG393529	BG393529 602411920
C 739	43	3.3	776	5	CJ485268	CJ485268 CJ485268	812	43	3.3	984	2	BG483751	BG483751 602033390
C 740	43	3.3	778	12	BZ598488	BZ598488 WHADS65TF	C 813	43	3.3	985	2	BM459102	BM459102 AGENCOURT
C 741	43	3.3	782	4	BX644719	BX644719 DXF2P781N	814	43	3.3	987	12	BE733044	BE733044 601569538
C 742	43	3.3	782	7	BE777501	BE777501 601348551	815	43	3.3	1007	12	BZ611150	BZ611150 WHACI165TF
C 743	43	3.3	782	8	CN395087	CN395087 170005977	816	43	3.3	1131	3	BU180351	BU180351 AGENCOURT
C 744	43	3.3	783	2	BF977222	BF977222 602146780	817	43	3.3	1266	3	BM805892	BM805892 AGENCOURT
C 745	43	3.3	783	2	BF978508	BF978508 602148727	818	43	3.3	1766	6	BC030999	BC030999 full-leng
C 746	43	3.3	785	8	CV816090	CV816090 AGENCOURT	C 819	43	3.3	1876	6	BC039023	BC039023 Homo sapi
C 747	43	3.3	785	13	CZ450677	CZ450677 MCF731h18	820	43	3.3	2533	6	CR857108	CR857108 Pongo pyg
C 748	43	3.3	787	9	CX786428	CX786428 HESC3_60	821	43	3.3	2717	6	CR627095	CR627095 Homo sapi
C 749	43	3.3	788	7	BF691774	BF691774 602248315	C 822	43	3.3	8421	6	HSN808381	HSN808381 Homo sapi

C 823	42	3.2	177	2	BI037335	BI037335 CM4-NT029	896	42	3.2	592	9	DA388143
C 824	42	3.2	257	7	AW250080	AW250080 DB21192.5	897	42	3.2	596	9	DA390952
C 825	42	3.2	257	9	DB310593	DB310593 DB310593	898	42	3.2	620	4	CA942424
C 826	42	3.2	269	4	DA432984	DA432984 HHAGE0317	899	42	3.2	651	7	BE264453
C 827	42	3.2	264	4	CB070394	CB070394 i836f04.y	900	42	3.2	664	4	CA4115974
C 828	42	3.2	287	2	BF935672	BF935672 PMI-NT023	C 901	42	3.2	666	3	EU629609
C 829	42	3.2	294	1	AA340602	AA340602 EST45863	C 902	42	3.2	670	4	CA774921
C 830	42	3.2	294	1	AA528312	AA528312 nh26h01.s	C 903	42	3.2	677	13	CZ460709
C 831	42	3.2	300	10	DA420655	DA420655 HHAGE0203	C 904	42	3.2	679	11	AQ742113
C 832	42	3.2	312	2	BT049539	BT049539 ILS-GN024	C 905	42	3.2	680	14	AQ132760
C 833	42	3.2	312	10	DA415493	DA415493 HHAGE0162	C 906	42	3.2	696	7	AW975615
C 834	42	3.2	332	9	DB130822	DB130822 DB130822	C 907	42	3.2	705	4	EX107187
C 835	42	3.2	337	3	BM686391	BM686391 UI-E-CR0-	C 908	42	3.2	714	9	DA833871
C 836	42	3.2	344	1	AA341120	AA341120 EST46728	C 909	42	3.2	723	8	CR789947
C 837	42	3.2	354	1	AI702522	AI702522 t267g08.x	C 910	42	3.2	727	8	CN267171
C 838	42	3.2	359	7	AV763057	AV763057 AV763057	C 911	42	3.2	739	3	BU570447
C 839	42	3.2	363	1	AA302952	AA302952 EST113100	C 912	42	3.2	756	8	CR548885
C 840	42	3.2	386	2	BF809190	BF809190 QVO-C1019	C 913	42	3.2	882	7	BF239251
C 841	42	3.2	390	11	AQ031652	AQ031652 HS 2225.B	C 914	42	3.2	904	7	BE792161
C 842	42	3.2	394	9	DB212796	DB212796 DB212796	C 915	42	3.2	959	3	BQ706685
C 843	42	3.2	395	10	H12972	H12972 y169g09.r1	C 916	42	3.2	963	3	BQ884019
C 844	42	3.2	398	11	AQ148150	AQ148150 HS 3109.A	C 917	42	3.2	1008	3	BM907147
C 845	42	3.2	407	9	DA708042	DA708042 DA708042	C 918	42	3.2	3245	6	HSM805849
C 846	42	3.2	412	1	AA720782	AA720782 nw07C10.s	C 919	42	3.2	4585	6	CR859606
C 847	42	3.2	417	2	BI043989	BI043989 PM3-OT020	C 920	41	3.2	144	14	AG198865
C 848	42	3.2	418	11	AQ636971	AQ636971 RPCI-11-4	C 921	41	3.2	154	5	CD522548
C 849	42	3.2	435	10	H14199	H14199 ym62d09.r1	C 922	41	3.2	156	14	DU641538
C 850	42	3.2	440	10	N22058	N22058 yw45h03.s1	C 923	41	3.2	156	14	DU641748
C 851	42	3.2	443	1	AA774105	AA774105 ac36C08.s	C 924	41	3.2	164	11	AQ391544
C 852	42	3.2	445	1	AI801505	AI801505 t09C09.x	C 925	41	3.2	179	11	AQ070832
C 853	42	3.2	447	10	R93974	R93974 yf73b08.s1	C 926	41	3.2	199	1	AA055539
C 854	42	3.2	447	7	AW243793	AW243793 x056e06.x	C 927	41	3.2	235	8	CN871609
C 855	42	3.2	450	11	AQ140170	AQ140170 HS 3109.B	C 928	41	3.2	261	1	AA618452
C 856	42	3.2	455	2	BP931073	BP931073 IL2-NT020	C 929	41	3.2	263	1	AA365624
C 857	42	3.2	458	1	AL138119	AL138119 DKFZp547D	C 930	41	3.2	283	7	BF172473
C 858	42	3.2	460	7	BE161469	BE161469 RCI-RT044	C 931	41	3.2	284	10	DA432861
C 859	42	3.2	461	10	H63443	H63443 yf53b03.r1	C 932	41	3.2	265	4	BY796113
C 860	42	3.2	463	9	DB162146	DB162146 DB162146	C 933	41	3.2	269	3	BQ369906
C 861	42	3.2	467	11	AQ062513	AQ062513 CIT-HSP-2	C 934	41	3.2	277	1	AA603767
C 862	42	3.2	469	11	BI4422	BI4422 A-672D10.TV	C 935	41	3.2	280	1	AA704383
C 863	42	3.2	482	1	AA745652	AA745652 ny69h06.s	C 936	41	3.2	282	2	BF815113
C 864	42	3.2	490	11	AQ587033	AQ587033 RPCI-11-4	C 937	41	3.2	287	1	AA333046
C 865	42	3.2	493	9	DA264751	DA264751 DA264751	C 938	41	3.2	287	7	AW880331
C 866	42	3.2	496	9	DA282974	DA282974 DA282974	C 939	41	3.2	292	1	AJ940336
C 867	42	3.2	512	7	AW165944	AW165944 xg68g06.x	C 940	41	3.2	303	10	DA419293
C 868	42	3.2	512	9	DA306675	DA306675 DA306675	C 941	41	3.2	305	10	DA417548
C 869	42	3.2	525	9	DB304305	DB304305 DB304305	C 942	41	3.2	310	1	AA579196
C 870	42	3.2	535	9	DB296479	DB296479 DB296479	C 943	41	3.2	311	1	AA226846
C 871	42	3.2	538	9	DB297068	DB297068 DB297068	C 944	41	3.2	321	3	BU752299
C 872	42	3.2	547	9	DA277280	DA277280 DA277280	C 945	41	3.2	325	10	DA412307
C 873	42	3.2	549	9	AQ613789	AQ613789 HS 5118.B	C 946	41	3.2	332	7	BE764391
C 874	42	3.2	550	11	DA348268	DA348268 DB348268	C 947	41	3.2	339	2	BF811484
C 875	42	3.2	551	9	DA341045	DA341045 DA341045	C 948	41	3.2	341	7	BE764438
C 876	42	3.2	552	9	DA341045	DA341045 DA341045	C 949	41	3.2	343	7	BE095166
C 877	42	3.2	552	11	AQ720700	AQ720700 HS 5546.B	C 950	41	3.2	344	10	T77522
C 878	42	3.2	553	11	AQ883899	AQ883899 HS 5490.A	C 951	41	3.2	346	7	BE764385
C 879	42	3.2	554	11	AQ040171	AQ040171 CIT-HSP-2	C 952	41	3.2	354	7	AW811261
C 880	42	3.2	557	9	DA820561	DA820561 DA820561	C 953	41	3.2	354	7	BE764432
C 881	42	3.2	558	11	AQ508143	AQ508143 RPCI-11-3	C 954	41	3.2	354	11	B38959
C 882	42	3.2	566	9	DA181486	DA181486 DA181486	C 955	41	3.2	356	7	BE764435
C 883	42	3.2	569	5	CK902829	CK902829 ip10e05.x	C 956	41	3.2	364	10	DA463090
C 884	42	3.2	569	9	DB172384	DB172384 DB172384	C 957	41	3.2	365	8	CV403726
C 885	42	3.2	570	11	AQ613788	AQ613788 HS 5118.B	C 958	41	3.2	366	7	BE764448
C 886	42	3.2	571	9	DA274441	DA274441 DA274441	C 959	41	3.2	370	10	H94924
C 887	42	3.2	571	9	DA390652	DA390652 DA390652	C 960	41	3.2	372	8	CR547557
C 888	42	3.2	573	1	AL047306	AL047306 DKFZp586L	C 961	41	3.2	375	7	BE764486
C 889	42	3.2	576	9	DA162943	DA162943 DA162943	C 962	41	3.2	375	8	CN871155
C 890	42	3.2	576	9	DA188246	DA188246 DA188246	C 963	41	3.2	375	8	CN871173
C 891	42	3.2	579	9	DA169840	DA169840 DA169840	C 964	41	3.2	376	8	CN272927
C 892	42	3.2	580	5	CK824655	CK824655 i930h07.y	C 965	41	3.2	379	8	CN272927
C 893	42	3.2	584	5	CK824655	CK824655 i930h07.y	C 966	41	3.2	381	10	T81786
C 894	42	3.2	587	9	DA393228	DA393228 DA393228	C 967	41	3.2	384	10	DA440762
C 895	42	3.2	590	9	DA395243	DA395243 DA395243	C 968	41	3.2	391	11	AQ138631

DA388143	DA388143	DA388143
DA390952	DA390952	DA390952
CA942424	ir57g08.y	CA942424
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CA4115974	UI-H-P80-	CA4115974
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CN267171	170004706	CN267171
BU570447	AGENCOURT	BU570447
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BF239251	601905467	BF239251
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BQ706685	AGENCOURT	BQ706685
BQ884019	AGENCOURT	BQ884019
BM907147	AGENCOURT	BM907147
BS537493	Homo sapi	BS537493
CR859606	Pongo pyg	CR859606
AG198865	Pan trogl	AG198865
CD522548	AGENCOURT	CD522548
DU641538	Ciuiffi-HI	DU641538
DU641748	Ciuiffi-HI	DU641748
AQ391544	CITBI-EI-	AQ391544
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AA618452	nn27f09.s	AA618452
AA365624	EST76430	AA365624
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BY796113	BY796113	BY796113
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DA419293	HHAGE0190	DA419293
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BE764438	PM2-NT007	BE764438
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BE764432	PM2-NT007	BE764432
B38959	HS-1048-B2-	B38959
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DA463090	HHAGE0058	DA463090
CV403726	RCO-CT042	CV403726
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CN871173	010419AAP	CN871173
CN272927	170006000	CN272927
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C 969	41	3.2	393	11	AQ152518	HS 3110_B	C1042	41	3.2	582	9	DA109327
C 970	41	3.2	396	7	AW903685	CM4-NN103	1043	41	3.2	584	11	AQ775734
C 971	41	3.2	402	4	C14044	C14044 Clon	C1044	41	3.2	585	1	AUI58130
C 972	41	3.2	405	11	B87341	B87341 RPI111-2831	1045	41	3.2	586	9	DB107097
C 973	41	3.2	406	10	W42588	ZC23h02.81	C1046	41	3.2	592	3	BU678696
C 974	41	3.2	415	1	AA569648	AA569648 nE24h10.8	1047	41	3.2	592	9	DA385878
C 975	41	3.2	416	1	AI050007	AI050007 anE22h10.x	C1048	41	3.2	592	9	DB152389
C 976	41	3.2	417	7	AW167887	AW167887 XG55G07.X	1049	41	3.2	593	9	DA081575
C 977	41	3.2	420	7	AW903764	AW903764 CM4-NN103	C1050	41	3.2	594	4	BA092636
C 978	41	3.2	427	2	BG989654	BG989654 PM2-HT093	1051	41	3.2	606	9	DA809500
C 979	41	3.2	428	11	AQ167476	AQ167476 HS 3165_A	1052	41	3.2	608	9	DA570499
C 980	41	3.2	431	8	CN414806	CN414806 170006008	1053	41	3.2	610	5	CD701702
C 981	41	3.2	433	11	AQ452488	AQ452488 HS 5176_A	1054	41	3.2	622	8	CN267604
C 982	41	3.2	439	8	CN269465	CN269465 170005999	1055	41	3.2	625	9	DA415471
C 983	41	3.2	441	1	AA601025	AA601025 nE67h02.8	1056	41	3.2	634	3	BQ277998
C 984	41	3.2	442	11	B73429	B73429 CIT-HSP-631	1057	41	3.2	635	7	AW971055
C 985	41	3.2	443	7	AW962942	AW962942 EST375015	C1058	41	3.2	647	2	BG026296
C 986	41	3.2	444	11	AQ463818	AQ463818 HS 5080_A	1059	41	3.2	652	14	AG033527
C 987	41	3.2	449	7	AW903779	AW903779 CM4-NN103	C1060	41	3.2	653	14	AG128812
C 988	41	3.2	450	11	AQ237341	AQ237341 RPI111-65	1061	41	3.2	654	14	AG102406
C 989	41	3.2	451	1	AA994451	AA994451 ou37h03.8	C1062	41	3.2	657	2	BI224566
C 990	41	3.2	451	5	C137821	C137821 UT-HF-BNO	C1063	41	3.2	661	11	B54795
C 991	41	3.2	456	8	CN804039	CN804039 ILLUMIGEN	C1064	41	3.2	674	14	AG146260
C 992	41	3.2	458	11	AQ770727	AQ770727 HS 5368_B	C1065	41	3.2	677	12	BZ608568
C 993	41	3.2	462	11	AQ262012	AQ262012 CITBI-EI-	1066	41	3.2	692	14	AG173568
C 994	41	3.2	467	1	AA991677	AA991677 OC69B06.8	C1067	41	3.2	700	1	AU252740
C 995	41	3.2	475	9	DB380777	DB380777 DB380777	C1068	41	3.2	724	11	B07038
C 996	41	3.2	477	1	AL601984	AL601984 DXF2P313H	C1069	41	3.2	735	5	CD365234
C 997	41	3.2	491	9	DA801480	DA801480 DA801480	C1070	41	3.2	741	7	BG596217
C 998	41	3.2	496	11	AZ756992	AZ756992 ew07b12.r	C1071	41	3.2	741	7	BB889051
C 999	41	3.2	497	3	BP394716	BP394716 BP394716	1072	41	3.2	753	8	CR745835
1000	41	3.2	502	7	BE961021	BE961021 601648585	C1073	41	3.2	756	4	CA428019
1001	41	3.2	504	8	CN265610	CN265610 170004247	C1074	41	3.2	760	2	BI669361
1002	41	3.2	507	3	BP422702	BP422702 BP422702	C1075	41	3.2	763	12	BZ610790
C1003	41	3.2	513	9	DB355391	DB355391 DB355391	1076	41	3.2	766	2	BG498539
C1004	41	3.2	513	11	AQ719862	AQ719862 HS 5546_A	1077	41	3.2	770	4	CB228772
1005	41	3.2	514	7	AV736191	AV736191 AV73191	1078	41	3.2	782	7	BF675039
1006	41	3.2	519	11	AZ756848	AZ756848 ew02d10.x	C1079	41	3.2	786	1	AUI19698
1007	41	3.2	520	3	BQ372742	BQ372742 PM3-FT002	C1080	41	3.2	789	14	DU797364
1008	41	3.2	521	9	DA915886	DA915886 DA915886	C1081	41	3.2	810	1	AUI20769
1009	41	3.2	524	11	AQ888656	AQ888656 HS 3251_A	C1082	41	3.2	816	4	CB991902
C1010	41	3.2	532	11	AQ581979	AQ581979 RPI11-11-4	1083	41	3.2	819	8	CX167335
1011	41	3.2	534	3	BM914647	BM914647 AGENCOURT	1084	41	3.2	820	14	CB959826
C1012	41	3.2	534	4	BA473764	BA473764 DXF2P686A	1085	41	3.2	837	11	AQ748870
C1013	41	3.2	535	9	DA809228	DA809228 DA809228	C1086	41	3.2	840	4	CB990803
C1014	41	3.2	538	7	AW974104	AW974104 EST386207	1087	41	3.2	865	14	DU798194
C1015	41	3.2	538	9	DB297680	DB297680 DB297680	C1088	41	3.2	870	4	BX453450
C1016	41	3.2	538	11	AZ757646	AZ757646 ew10f06.r	C1089	41	3.2	874	4	BA453449
C1017	41	3.2	544	8	CR525105	CR525105 DXF2P459L	C1090	41	3.2	885	6	CR623847
1018	41	3.2	551	10	H38036	H38036 ypS8a11.r1	1091	41	3.2	890	7	BE782541
1019	41	3.2	553	8	CV416455	CV416455 RC3-GN007	1092	41	3.2	891	3	BUI93015
C1020	41	3.2	554	4	BX351732	BX351732 BX351732	C1093	41	3.2	893	4	BX434534
1021	41	3.2	557	9	DB137485	DB137485 DB137485	1094	41	3.2	903	14	DU797650
1022	41	3.2	559	2	BF826079	BF826079 M32-HN003	1095	41	3.2	909	5	CF619439
1023	41	3.2	559	9	DA512161	DA512161 DA512161	1096	41	3.2	913	4	BX327054
C1024	41	3.2	559	9	DB134479	DB134479 DB134479	1097	41	3.2	928	3	BQ718071
1025	41	3.2	559	9	DB354915	DB354915 DB354915	1098	41	3.2	979	5	CD514471
C1026	41	3.2	561	9	DB231684	DB231684 DB231684	1099	41	3.2	997	3	BM558941
C1027	41	3.2	561	9	DB359867	DB359867 DB359867	1100	41	3.2	1012	7	BF676440
C1028	41	3.2	562	9	DA100027	DA100027 DA100027	1101	41	3.2	1020	7	BE784159
C1029	41	3.2	563	9	DA386065	DA386065 DA386065	C1102	41	3.2	1054	3	BU899258
C1030	41	3.2	564	1	AL597194	AL597194 DXF2P313M	C1103	41	3.2	1126	5	CD243607
1031	41	3.2	565	7	AW581679	AW581679 CM0-FT004	1104	41	3.2	1214	3	BQ225688
1032	41	3.2	565	9	DA778429	DA778429 DA778429	1105	41	3.2	1734	6	BC015819
C1033	41	3.2	566	9	DA224273	DA224273 DA224273	1106	41	3.2	2089	6	CR600418
1034	41	3.2	567	7	BE972424	BE972424 601652247	1107	41	3.2	178	1	AA526630
C1035	41	3.2	573	11	AQ519755	AQ519755 HS 5183_B	C1108	41	3.2	182	7	AW051615
C1036	41	3.2	574	11	AQ356602	AQ356602 CITBI-EI-	1109	41	3.2	193	1	AI792231
C1037	41	3.2	574	14	DU840107	DU840107 MUGQ_CH25	1110	41	3.2	237	10	DM441820
C1038	41	3.2	577	2	BG507069	BG507069 601861709	1111	41	3.2	282	2	BF997488
1039	41	3.2	577	11	AQ471349	AQ471349 CITBI-EI-	C1112	41	3.2	284	4	CB924053
C1040	41	3.2	578	9	DB052486	DB052486 DB052486	1113	41	3.2	285	10	DM425598
C1041	41	3.2	579	9	DB152683	DB152683 DB152683	1114	41	3.2	286	4	CB923953

1115	40	3.1	291	1	A1370877	A1370877 tal2e09.x	cl1188	40	3.1	541	9	DB349063	DB349063
1116	40	3.1	298	11	B60195	B60195 CIT-HSP-200	cl1189	40	3.1	543	11	AQ767563	AQ767563 HS 3206_A
1117	40	3.1	303	10	T89242	T89242 yel3202.r1	cl1190	40	3.1	544	9	DB270562	DB270562 DB370562_A
1118	40	3.1	311	7	B176828	B176828 RC4-HT058	cl1191	40	3.1	545	9	DB338860	DB338860 DB338860
1119	40	3.1	317	3	B0564531	B0564531 AGENCOURT	cl1192	40	3.1	545	9	DB338860	DB338860 DB338860
1120	40	3.1	319	10	T89148	T89148 yel3202.s1	cl1193	40	3.1	546	1	AW889723	AW889723 RCI-NT003
1121	40	3.1	321	2	B0617738	B0617738 602645252	cl1194	40	3.1	549	7	AW889723	AW889723 RCI-NT003
1122	40	3.1	323	11	AQ066918	AQ066918 HS 2227_B	cl1195	40	3.1	551	11	B68316	B68316 CIT978SK-A-
1123	40	3.1	325	11	AQ261413	AQ261413 CITBI-EI-	cl1196	40	3.1	552	11	B68316	B68316 CIT978SK-A-
1124	40	3.1	327	3	B0212096	B0212096 AGENCOURT	cl1197	40	3.1	559	9	DB120055	DB120055 DB120055
1125	40	3.1	331	11	AQ344344	AQ344344 RCI11-12	cl1198	40	3.1	559	11	AQ046837	AQ046837 RCI11-12
1126	40	3.1	338	11	B69648	B69648 CIT-HSP-200	cl1199	40	3.1	560	11	AQ720657	AQ720657 HS_5546_B
1127	40	3.1	344	8	CN278603	CN278603 170060003	cl1200	40	3.1	562	3	BQ632036	BQ632036 il21e10.x
1128	40	3.1	351	1	A1439910	A1439910 t157h05.x	cl1201	40	3.1	565	9	DA824485	DA824485 DA824485
1129	40	3.1	358	10	DA465294	DA465294 HHAEG0065	cl1202	40	3.1	573	7	AW954908	AW954908 EST366978
1130	40	3.1	360	1	AA516192	AA516192 ng65f01.s	cl1203	40	3.1	576	3	BU948907	BU948907 in70e12.y
1131	40	3.1	371	7	BE079595	BE079595 RCS-BT062	cl1204	40	3.1	576	13	CL423023	CL423023 RPI1-8650
1132	40	3.1	376	2	BF757711	BF757711 MR2-C7059	cl1205	40	3.1	581	9	DB322967	DB322967 DB322967
1133	40	3.1	386	11	B98825	B98825 CIT-HSP-228	cl1206	40	3.1	582	1	AA601323	AA601323 no15905.s
1134	40	3.1	399	10	R93233	R93233 yq11d09.s1	cl1207	40	3.1	591	1	AL706370	AL706370 DKF2p686H
1135	40	3.1	400	14	AG266787	AG266787 Homo sapi	cl1208	40	3.1	596	8	CR773230	CR773230 DKF2p470K
1136	40	3.1	406	11	AQ173412	AQ173412 HS 3203_B	cl1209	40	3.1	598	1	AV654060	AV654060 AV654060
1137	40	3.1	408	11	AQ221567	AQ221567 HS_3244_B	cl1210	40	3.1	601	3	BM989400	BM989400 UI-H-DP0-
1138	40	3.1	416	4	EX644331	EX644331 DKF2p781C	cl1211	40	3.1	605	9	DB233913	DB233913 DB233913
1139	40	3.1	421	11	AQ028070	AQ028070 CIT-HSP-2	cl1212	40	3.1	618	4	CB128912	CB128912 K-EST0178
1140	40	3.1	424	11	AQ818965	AQ818965 HS 5291_A	cl1213	40	3.1	622	11	B14244	B14244 A-186E11.TV
1141	40	3.1	421	11	AQ818965	AQ818965 HS 5291_A	cl1214	40	3.1	624	11	AQ760278	AQ760278 RP43-6411
1142	40	3.1	427	4	EX487434	EX487434 DKF2p6860	cl1215	40	3.1	624	11	AQ585359	AQ585359 RPCI-11-4
1143	40	3.1	430	1	A1049671	A1049671 an33a11.x	cl1216	40	3.1	627	11	AQ563364	AQ563364 HS_5335_B
1144	40	3.1	431	10	H84463	H84463 yv86e12.r1	cl1217	40	3.1	629	1	AV708349	AV708349 AV708349
1145	40	3.1	435	2	H09744	H09744 ym01b04.s1	cl1218	40	3.1	641	4	EX103667	EX103667 BX103667
1146	40	3.1	436	2	BG015814	BG015814 PMO-GN034	cl1219	40	3.1	644	11	AQ321686	AQ321686 RPCI11-96
1147	40	3.1	439	9	DB371267	DB371267 DB371267	cl1220	40	3.1	653	14	AG137048	AG137048 Pan trogl
1148	40	3.1	440	9	AW163153	AW163153 au2e2e2.y	cl1221	40	3.1	656	13	CZ692954	CZ692954 HSC 01144
1149	40	3.1	440	9	DB354549	DB354549 DB354549	cl1222	40	3.1	660	4	EX484570	EX484570 DKF2p6861
1150	40	3.1	445	11	AQ704213	AQ704213 HS 5475_B	cl1223	40	3.1	660	14	AG078171	AG078171 Pan trogl
1151	40	3.1	445	11	AA632648	AA632648 np87c01.s	cl1224	40	3.1	665	14	AG033347	AG033347 Pan trogl
1152	40	3.1	445	11	AQ022533	AQ022533 HS 2180_A	cl1225	40	3.1	669	14	AG163577	AG163577 Pan trogl
1153	40	3.1	447	2	B1042784	B1042784 CM4-OT015	cl1226	40	3.1	677	2	BG501607	BG501607 602288665
1154	40	3.1	448	10	T57774	T57774 yb98d10.s1	cl1227	40	3.1	680	2	BF980073	BF980073 602288665
1155	40	3.1	451	11	AQ223735	AQ223735 HS 2005_B	cl1228	40	3.1	689	14	CR957993	CR957993 Homo sapi
1156	40	3.1	454	2	BF7422945	BF7422945 CMO-BT086	cl1229	40	3.1	690	14	AG118081	AG118081 Pan trogl
1157	40	3.1	464	3	B0687091	B0687091 UI-CF-DU1	cl1230	40	3.1	691	14	AG151976	AG151976 Pan trogl
1158	40	3.1	466	9	DB064384	DB064384 DB064384	cl1231	40	3.1	693	7	AV764201	AV764201 AV764201
1159	40	3.1	468	3	BM705835	BM705835 UI-E-DP0-	cl1232	40	3.1	696	7	AV728445	AV728445 AV728445
1160	40	3.1	472	1	AA665250	AA665250 ac17e10.s	cl1233	40	3.1	697	14	AG056186	AG056186 Pan trogl
1161	40	3.1	476	11	AQ376566	AQ376566 RPCI-11-1	cl1234	40	3.1	700	11	AQ782298	AQ782298 HS_3384_B
1162	40	3.1	481	11	AQ002776	AQ002776 CIT978SK-	cl1235	40	3.1	701	2	BF968568	BF968568 CIT-HSP-2
1163	40	3.1	484	11	AQ336600	AQ336600 HS 5006_A	cl1236	40	3.1	704	5	CD693692	CD693692 EST10215
1164	40	3.1	485	2	BG540352	BG540352 602568851	cl1237	40	3.1	704	14	AG160647	AG160647 Pan trogl
1165	40	3.1	487	11	AQ384933	AQ384933 RCI11-13	cl1238	40	3.1	707	14	CR974543	CR974543 Homo sapi
1166	40	3.1	488	13	CZ462336	CZ462336 MCF752e08	cl1239	40	3.1	730	1	AL603316	AL603316 DKF2p686L
1167	40	3.1	490	4	EX482356	EX482356 DKF2p686E	cl1240	40	3.1	739	2	BG747665	BG747665 602705133
1168	40	3.1	491	11	AQ423145	AQ423145 CITBI-EI-	cl1241	40	3.1	754	12	BZ612108	BZ612108 WHACN02TF
1169	40	3.1	492	5	CD245533	CD245533 AGENCOURT	cl1242	40	3.1	757	3	BU930802	BU930802 AGENCOURT
1170	40	3.1	500	11	AQ709204	AQ709204 HS 5381_A	cl1243	40	3.1	773	7	BE887319	BE887319 601510144
1171	40	3.1	503	4	CB218379	CB218379 NISC rb08	cl1244	40	3.1	781	13	CZ452581	CZ452581 MCF734a09
1172	40	3.1	503	9	DB306267	DB306267 DB306267	cl1245	40	3.1	786	2	BI335374	BI335374 602997930
1173	40	3.1	513	7	AW814317	AW814317 MR3-ST020	cl1246	40	3.1	792	12	BZ600330	BZ600330 WHAAQ45TR
1174	40	3.1	513	7	AW814351	AW814351 MR3-ST020	cl1247	40	3.1	806	11	BA04526	BA04526 CSRL-36d1-u
1175	40	3.1	513	7	BE146296	BE146296 MR0-HT020	cl1248	40	3.1	816	4	CB990403	CB990403 AGENCOURT
1176	40	3.1	515	11	AQ318236	AQ318236 RCI11-11	cl1249	40	3.1	856	2	BG569986	BG569986 602590240
1177	40	3.1	517	10	H53937	H53937 yq87b10.r1	cl1250	40	3.1	856	2	BG569986	BG569986 602590240
1178	40	3.1	520	3	BQ632285	BQ632285 il25a08.x	cl1251	40	3.1	863	11	AQ780739	AQ780739 HS 3169_A
1179	40	3.1	525	9	DB317226	DB317226 DB317226	cl1252	40	3.1	872	3	BQ432626	BQ432626 AGENCOURT
1180	40	3.1	527	4	CB142810	CB142810 K-EST0196	cl1253	40	3.1	896	3	BU902385	BU902385 AGENCOURT
1181	40	3.1	529	9	DB304550	DB304550 DB304550	cl1254	40	3.1	897	3	BU161577	BU161577 AGENCOURT
1182	40	3.1	529	9	DB334237	DB334237 DB334237	cl1255	40	3.1	928	7	BE797459	BE797459 601587778
1183	40	3.1	532	9	DB346682	DB346682 DB346682	cl1256	40	3.1	941	13	CZ452944	CZ452944 MCF734i04
1184	40	3.1	533	7	BE079585	BE079585 RCS-BT062	cl1257	40	3.1	954	11	AQ743041	AQ743041 HS 5387_B
1185	40	3.1	533	11	AQ276171	AQ276171 CITBI-EI-	cl1258	40	3.1	957	2	BG169899	BG169899 602324376
1186	40	3.1	536	7	AW889782	AW889782 RCI-NT003	cl1259	40	3.1	990	7	AW600804	AW600804 N26-20 Hu
1187	40	3.1	537	7	BE079466	BE079466 RCS-BT062	cl1260	40	3.1	1026	2	BG753720	BG753720 602732921

1261	40	3.1	1083	2	BG113930	RG113930 602284396	1334	39	3.0	347	10	DM467237	DM467237 HHAGE0085
1262	40	3.1	1107	2	BG475332	RG475332 602491417	1335	39	3.0	350	10	DM466666	DM466666 HHAGE0079
1263	40	3.1	1122	6	AF927481	BF927481 Homo sapi	1336	39	3.0	351	2	BM353189	BM353189 Ig76910.x
1264	40	3.1	1204	7	BF676194	BF676194 602084194	1337	39	3.0	351	12	BZ605681	BZ605681 WHABX95TF
1265	40	3.1	2380	6	HSMB007252	BK647108 Homo sapi	1338	39	3.0	352	4	BY795160	BY795160 BY795160
1266	40	3.1	10778	6	CR936627	CR936627 Homo sapi	1339	39	3.0	352	7	AW078909	AW078909 xB19e12.x
1267	39	3.0	113	7	BE163442	BE163442 OV3-HT046	1340	39	3.0	356	1	AA857381	AA857381 Qd83104.B
1268	39	3.0	146	11	AQ054912	AQ054912 CIT-HSP-2	1341	39	3.0	358	10	DM465352	DM465352 HHAGE0066
1269	39	3.0	165	2	BF861282	BF861282 QV1-ET018	1342	39	3.0	358	11	AQ516328	AQ516328 HS-5238.A
1270	39	3.0	172	11	AQ529038	AQ529038 RPT-11-3	1343	39	3.0	361	1	AA484321	AA484321 n890102.B
1271	39	3.0	180	7	AW847328	AW847328 RCO-CT020	1344	39	3.0	364	10	N47882	N47882 Y796a10.B
1272	39	3.0	181	7	AW847327	AW847327 RCO-CT020	1345	39	3.0	371	1	AI635677	AI635677 t208f03.x
1273	39	3.0	181	7	DM454317	DM454317 HHAGE0510	1346	39	3.0	372	10	H65856	H65856 Y775a11.B
1274	39	3.0	181	1	AI354388	AI354388 Q680603.x	1347	39	3.0	373	4	CA773407	CA773407 Im63f11.y
1275	39	3.0	198	9	DB349128	DB349128 DB349128	1348	39	3.0	375	1	AA508873	AA508873 H986606.B
1276	39	3.0	201	1	AA937639	AA937639 nW88e02.B	1349	39	3.0	376	1	AI270096	AI270096 Q63c10.x
1277	39	3.0	201	1	AA547947	AA547947 nK55e05.B	1350	39	3.0	376	1	AI849051	AI849051 UT-M-AH1-
1278	39	3.0	203	7	AW847311	AW847311 RCO-CT020	1351	39	3.0	383	12	CG624186	CG624186 OST327284
1279	39	3.0	204	1	AA613197	AA613197 n019807.B	1352	39	3.0	384	9	DB359230	DB359230 DB359230
1280	39	3.0	206	11	AQ279397	AQ279397 CITBI-EI-	1353	39	3.0	386	2	BF927705	BF927705 IL2-NT018
1281	39	3.0	207	11	AQ478974	AQ478974 RPT-11-2	1354	39	3.0	387	10	H68379	H68379 Y799b09.r1
1282	39	3.0	210	1	AA385250	AA385250 EST99054	1355	39	3.0	389	1	AA551105	AA551105 nY5402.B
1283	39	3.0	211	11	B49811	B49811 RPT11-3J22	1356	39	3.0	389	4	BY508025	BY508025 BY508025
1284	39	3.0	212	7	AW847319	AW847319 RCO-CT020	1357	39	3.0	389	10	T49213	T49213 ya73c06.B
1285	39	3.0	218	10	DM466281	DM466281 HHAGE0440	1358	39	3.0	391	1	AA199771	AA199771 zq76f06.B
1286	39	3.0	221	10	DM445600	DM445600 HHAGE0433	1359	39	3.0	391	7	BE814172	BE814172 PM0-BN006
1287	39	3.0	224	7	BF460869	BF460869 UT-M-CGP	1360	39	3.0	391	11	AQ493661	AQ493661 HS-5054.B
1288	39	3.0	225	8	CN359798	CN359798 170005321	1361	39	3.0	395	11	AQ166336	AQ166336 HS-3124.B
1289	39	3.0	226	2	BF869176	BF869176 IL5-ET011	1362	39	3.0	395	11	AQ191754	AQ191754 HS-3228.A
1290	39	3.0	228	10	DM443949	DM443949 HHAGE0416	1363	39	3.0	397	11	AQ153778	AQ153778 HS-2245.B
1291	39	3.0	235	1	AA516242	AA516242 n966b12.B	1364	39	3.0	398	7	AW008089	AW008089 wv49f02.x
1292	39	3.0	239	7	BE163415	BE163415 QV3-HT046	1365	39	3.0	398	7	BE067033	BE067033 PM4-BT034
1293	39	3.0	240	10	DM439858	DM439858 HHAGE0385	1366	39	3.0	399	7	AL038705	AL038705 DKF2P566K
1294	39	3.0	242	7	BE163419	BE163419 QV3-HT046	1367	39	3.0	402	1	AI049857	AI049857 an21f11.x
1295	39	3.0	246	9	DA377050	DA377050 DA377050	1368	39	3.0	402	11	AQ215266	AQ215266 HS-3239.B
1296	39	3.0	247	7	BE163396	BE163396 QV3-HT046	1369	39	3.0	403	12	CG662492	CG662492 OST446275
1297	39	3.0	250	7	BE062239	BE062239 RCL-BT025	1370	39	3.0	408	11	A2518006	A2518006 RPT-11-2
1298	39	3.0	255	2	BF748499	BF748499 RCL-BN041	1371	39	3.0	408	11	BX954908	BX954908 DKF2P781H
1299	39	3.0	256	9	DM77881	DM77881 EST01465.Fe	1372	39	3.0	413	1	AA555311	AA555311 nK79606.B
1300	39	3.0	256	10	D56402	D56402 HUM427802B	1373	39	3.0	417	1	AI052454	AI052454 oz07g11.x
1301	39	3.0	257	4	BX633581	BX633581 BX633581	1374	39	3.0	417	8	CN332751	CN332751 170005322
1302	39	3.0	259	5	CF141674	CF141674 UT-HF-CB0	1375	39	3.0	418	1	AI887546	AI887546 wml5a02.x
1303	39	3.0	260	7	AW814396	AW814396 MR3-ST020	1376	39	3.0	423	11	B99999	B99999 CIT-HSP-217
1304	39	3.0	268	1	AA663975	AA663975 ac07c05.B	1377	39	3.0	425	2	BF948481	BF948481 CM2-NN115
1305	39	3.0	276	7	AW833848	AW833848 QV0-TT000	1378	39	3.0	426	1	AI914748	AI914748 tr01809.x
1306	39	3.0	281	7	AW833864	AW833864 QV0-TT000	1379	39	3.0	430	1	AI708848	AI708848 as27f10.x
1307	39	3.0	282	10	DM426402	DM426402 HHAGE0261	1380	39	3.0	434	10	H58585	H58585 y706f07.r1
1308	39	3.0	286	7	AW833875	AW833875 QV0-TT000	1381	39	3.0	435	1	AA133472	AA133472 z013f09.B
1309	39	3.0	287	7	AW833949	AW833949 QV0-TT000	1382	39	3.0	435	7	AW469428	AW469428 hc84b11.x
1310	39	3.0	288	10	DM424391	DM424391 HHAGE0241	1383	39	3.0	438	9	DA640553	DA640553 DA640553
1311	39	3.0	289	10	R77560	R77560 y176902.r1	1384	39	3.0	438	10	T93089	T93089 y224f03.B
1312	39	3.0	292	12	BZ609226	BZ609226 WHADP55TF	1385	39	3.0	447	11	AQ280466	AQ280466 CITBI-EI-
1313	39	3.0	294	1	AI473581	AI473581 t141c09.x	1386	39	3.0	448	1	AI952885	AI952885 wr51408.x
1314	39	3.0	298	8	CN359797	CN359797 170005322	1387	39	3.0	449	11	AQ528729	AQ528729 RPT-11-3
1315	39	3.0	288	10	DM421311	DM421311 HHAGE0210	1388	39	3.0	452	2	BF828236	BF828236 IL0-HN008
1316	39	3.0	302	11	AQ546562	AQ546562 CITBI-EI-	1389	39	3.0	452	7	AV727075	AV727075 AV727075
1317	39	3.0	303	10	DM419431	DM419431 HHAGE0191	1390	39	3.0	453	1	AI668993	AI668993 cy30601.x
1318	39	3.0	304	1	AA280427	AA280427 zt05f06.B	1391	39	3.0	455	10	DM407935	DM407935 HHAGE0006
1319	39	3.0	306	7	BF691619	BF691619 602155887	1392	39	3.0	456	8	CN484836	CN484836 hx19d06.Y
1320	39	3.0	307	2	BF844013	BF844013 MR2-HT104	1393	39	3.0	458	1	AI880554	AI880554 ae28a08.x
1321	39	3.0	318	11	B94374	B94374 CIT-HSP-217	1394	39	3.0	458	7	AW272513	AW272513 xu20c03.x
1322	39	3.0	320	2	BF927045	BF927045 CM2-NT019	1395	39	3.0	459	1	AA652882	AA652882 nb9n01.B
1323	39	3.0	324	10	R02805	R02805 ye80d10.B	1396	39	3.0	459	1	AI124584	AI124584 am59b01.x
1324	39	3.0	330	1	AA640710	AA640710 nr22g03.r	1397	39	3.0	461	2	BG654897	BG654897 lb43b09.Y
1325	39	3.0	331	7	AV739661	AV739661 AV739661	1398	39	3.0	461	9	DB350869	DB350869 DA680226
1326	39	3.0	332	10	DM410848	DM410848 HHAGE0115	1399	39	3.0	461	9	DB350869	DB350869 DB350869
1327	39	3.0	337	3	BP429068	BP429068 BP429068	1400	39	3.0	462	1	AL704594	AL704594 DKF2P686L
1328	39	3.0	339	10	DM409394	DM409394 HHAGE0101	1401	39	3.0	464	3	BU663800	BU663800 CL106n05.
1329	39	3.0	341	2	BF924464	BF924464 IL5-NT022	1402	39	3.0	468	8	CR742728	CR742728 CR742728
1330	39	3.0	342	4	BK489414	BK489414 DKF2P686P	1403	39	3.0	468	11	AQ262065	AQ262065 CITBI-EI-
1331	39	3.0	343	2	BF942053	BF942053 nae86a01	1404	39	3.0	468	11	AQ355818	AQ355818 CITBI-EI-
1332	39	3.0	343	10	N51140	N51140 Y796a10.r1	1405	39	3.0	469	13	C2463487	C2463487 MCF754a11
1333	39	3.0	347	7	AW277109	AW277109 xp62908.x	1406	39	3.0	471	11	AQ584732	AQ584732 RPT-11-4


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Db 718 TGGCATCGTTTGCTAGAAAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATACAC 777
Qy 661 AATGAATACAAAAAATCGAACTCTGCAATTTAACTAGTTTTCAAACTGGACACTGGAGA 720
Db 778 AATGAATACAAAAAATCGAACTCTGCAATTTAACTAGTTTTCAAACTGGACACTGGAGA 837
Qy 721 ATATTCTCTGTAAGCCCGCAATTCCTGTTGGATATCGCAGGTGCTCTGGGAACGAATGCA 780
Db 838 ATATTCTCTGTAAGCCCGCAATTCCTGTTGGATATCGCAGGTGCTCTGGGAACGAATGCA 897
Qy 781 AGTAGATGATCTCAACATAAGTGCATCATAGCAGCGTAGTAGTTGTGGCCTTAGTGAT 840
Db 898 AGTAGATGATCTCAACATAAGTGCATCATAGCAGCGTAGTAGTTGTGGCCTTAGTGAT 957
Qy 841 TTCCGTTTGTGGCCTTGGTGATGCTATGCTCAGAGGAAAGGCTACTTTTCAA 893
Db 958 TTCCGTTTGTGGCCTTGGTGATGCTATGCTCAGAGGAAAGGCTACTTTTCAA 1010

RESULT 3
LOCUS CR621411 1465 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DC022YA21 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).
ACCESSION CR621411.1 GI:50502218
VERSION HTC; CNSLT cdna.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1465)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1465)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
16c strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1465
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC022YA21"
/tissue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 69.0%; Score 893; DB 6; Length 1465;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCAGAGATTCAAGGGCCCCCGGCTCTCTGGCTTCCTCCGCGGGACCCCTCGACCTCCT 60
Db 335 CCCAGAGATTCAAGGGCCCCCGGCTCTCTGGCTTCCTCCGCGGGACCCCTCGACCTCCT 394
Qy 61 CAGAGCAGCGGCTGCGCGCCCCCGGAGAGATGGCAGAGAGAGCCGCCACCGCTCCTCCT 120
Db 395 CAGAGCAGCGGCTGCGCGCCCCCGGAGAGATGGCAGAGAGAGCCGCCACCGCTCCTCCT 454
Qy 121 GCTGCTGCTGCTACCTCTGGTGGTTCGCGCTTGGCTATCATAGGCGCTATGGGTTTCTGCG 180
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Db 455 GCTGCTGCTGCTACCTGCTGGTGGCTCGCCCTATCATAGGCTATGGGTTTCTGTC 514
Qy 181 CCCAAAAGACCAACAAGTAGTCAAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA 240
Db 515 CCCAAAAGACCAACAAGTAGTCAAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA 574
Qy 241 AACCCCAAGAAAGACTGTTTCTCCAGATTAGAGTGGAAAGAACTGGGTCGGAGTGTCTC 300
Db 575 AACCCCAAGAAAGACTGTTTCTCCAGATTAGAGTGGAAAGAACTGGGTCGGAGTGTCTC 634
Qy 301 CTTTGCTACTATCAACAGACTCTTTCAGAGTGATTTTAAATAATCGAGCTGAGATGATAGA 360
Db 635 CTTTGCTACTATCAACAGACTCTTTCAGAGTGATTTTAAATAATCGAGCTGAGATGATAGA 694
Qy 361 TTTTCATATCCGGATCAAAAATGTGACAAGAGTGATCGGGGAAATATCCTTGTGAAGT 420
Db 695 TTTTCATATCCGGATCAAAAATGTGACAAGAGTGATCGGGGAAATATCCTTGTGAAGT 754
Qy 421 TAGTGCCCATCTGAGCAAGGCCAAACCTTGAAGAGGATACAGTCACTCTGGAAGTATT 480
Db 755 TAGTGCCCATCTGAGCAAGGCCAAACCTTGAAGAGGATACAGTCACTCTGGAAGTATT 814
Qy 481 AGTGGCTCCAGCAGTTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 540
Db 815 AGTGGCTCCAGCAGTTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 874
Qy 541 AGAGCTACGATGTCAAGACAAAGGGAATCCAGCTCCCTGGAATACACATGTTTAAAGGA 600
Db 875 AGAGCTACGATGTCAAGACAAAGGGAATCCAGCTCCCTGGAATACACATGTTTAAAGGA 934
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Db 935 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATACAC 994
Qy 661 AATGAATACAAAAAATCTGCAACTCTGCAATTTAACTAGTTTTCAAACTGGACACTGGAGA 720
Db 995 AATGAATACAAAAAATCTGCAACTCTGCAATTTAACTAGTTTTCAAACTGGACACTGGAGA 1054
Qy 721 ATATTCTGTGAAGCCCGCAATTCCTGTTGGATATCGCAGGTGCTCTGGAAACGAATGCA 780
Db 1055 ATATTCTGTGAAGCCCGCAATTCCTGTTGGATATCGCAGGTGCTCTGGAAACGAATGCA 1114
Qy 781 AGTAGATGATCTCAACATAAGTGCATCATAGCAGCGTAGTAGTTGTGGCCTTAGTGAT 840
Db 1115 AGTAGATGATCTCAACATAAGTGCATCATAGCAGCGTAGTAGTTGTGGCCTTAGTGAT 1174
Qy 841 TTCCGTTTGTGGCCTTGGTGATGCTATGCTCAGAGGAAAGGCTACTTTTCAA 893
Db 1175 TTCCGTTTGTGGCCTTGGTGATGCTATGCTCAGAGGAAAGGCTACTTTTCAA 1227

RESULT 4
LOCUS CR599894 1489 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI025YK19 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR599894
VERSION CR599894.1 GI:50480701
KEYWORDS HTC; CNSLT cdna.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1489)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1489)
REFERENCE 2 (bases 1 to 1489)
```


AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source
1. .1489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1025YK19"
/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 69.0%; Score 893; DB 6; Length 1489;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCAGAGATTCAAGGGCCCCCGCCCTCTCGGCTCTCGCGCGGACCCCTCGACCTCCT 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
256 CCAGAGATTCAAGGGCCCCCGCCCTCTCGGCTCTCGCGCGGACCCCTCGACCTCCT 315
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 CAGAGCAGCGCGTGGCGGCCCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCTCCT 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
316 CAGAGCAGCGCGTGGCGGCCCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCTCCT 375
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 GCTGCTGCTCGCTACTGCTGGTGGCTGGCGCTATCAAGGCTATCGGTTTCTGC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
376 GCTGCTGCTCGCTACTGCTGGTGGCTGGCGCTATCAAGGCTATCGGTTTCTGC 435
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 CCCAAAGACCAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTACGCTGCAA 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
436 CCCAAAGACCAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTACGCTGCAA 495
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 AACCCCAAGAGAGCTGTTTCTCCAGATTAGAGTGGAGAAACTTGGGTGGAGTGTCTC 300
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496 AACCCCAAGAGAGCTGTTTCTCCAGATTAGAGTGGAGAAACTTGGGTGGAGTGTCTC 555
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301 CTTTGTCTACTATCAACAGACTCTTCAAGTGATTTTAAATTCGAGCTGAGATGATAGA 360
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556 CTTTGTCTACTATCAACAGACTCTTCAAGTGATTTTAAATTCGAGCTGAGATGATAGA 615
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TTTTCAATATCCGATCAAAATCTGACAAAGTGTGCGGGGAATATCGTTGTGAAGT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
616 TTTTCAATATCCGATCAAAATCTGACAAAGTGTGCGGGGAATATCGTTGTGAAGT 675
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
676 TAGTGCCCATCTGAGCAAGGCCAAACCTTGGAGAGGATACAGTCACTCTGGAAGTATT 735
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 AGTGGCTCCAGAGTTCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGAATCTGTGGT 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
736 AGTGGCTCCAGAGTTCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGAATCTGTGGT 795
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541 AGAGCTACGATGTCAGACAAAGAGGGATCCAGCTCTCGTAATACACATGTTTAAAGGA 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
796 AGAGCTACGATGTCAGACAAAGAGGGATCCAGCTCTCGTAATACACATGTTTAAAGGA 855
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856 TGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCCAAAGCAACAAAGCTCATACAC 915
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661 AATGAATACAAAACCTGGAACTCTGCAATTTAATACATGTTTCAAACTGGACACTGGAGA 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
916 AATGAATACAAAACCTGGAACTCTGCAATTTAATACATGTTTCAAACTGGACACTGGAGA 975
Qy ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 ATATTCTGTGAAGCCCGCAATTCTGTGTGATATCGCAGGTGTCTCGGGAACGAATGCA 780

Db 976 ATATTCTGTGAAGCCCGCAATTCTGTGTGATATCGCAGGTGTCTCGGGAACGAATGCA 1035
Qy 781 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGTAGTAGTTGTGSCCTTAGTGAT 840
Db 1036 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGTAGTAGTTGTGSCCTTAGTGAT 1095
Qy 841 TTCCGTTTGTGCGCTGGTGTATGCTCTCAGAGGAAGGCTACTTTTCAA 893
Db 1096 TTCCGTTTGTGCGCTGGTGTATGCTCTCAGAGGAAGGCTACTTTTCAA 1148
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CR621227 1511 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DB009YH07 of Neuroblastoma Cot
DEFINITION 10-normalized of Homo sapiens (human).
CR621227
ACCESSION CR621227.1 GI:50502034
VERSION HTC; CNSLT_cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1511)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1511)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB009YH07"
/issue_type="Neuroblastoma Cot 10-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 69.0%; Score 893; DB 6; Length 1511;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCAGAGTTCAAGGGCCCCCGCCCTCTCGGCTCTCGCGGACCCCTCGACCTCCT 60
Db 307 CCAGAGATTCAAGGGCCCCCGCCCTCTCGGCTCTCGCGGACCCCTCGACCTCCT 366
Qy 61 CAGAGCAGCGCGTGGCGGCCCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCTCCT 120
Db 367 CAGAGCAGCGCGTGGCGGCCCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCTCCT 426
Qy 121 GCTGCTGCTGCGCTACTGCTGGTGGCTGGCGCTATCATAGGCTCATGCGTTTCTGC 180
Db 427 GCTGCTGCTGCGCTACTGCTGGTGGCTGGCGCTATCATAGGCTCATGCGTTTCTGC 486
Qy 181 CCCAAAGACCAACAAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTACGCTGCAA 240
Db 487 CCCAAAGACCAACAAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTACGCTGCAA 546

Qy	241	AAACCCAAAGAACTGTTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGCTC	300
Db	547	AAACCCAAAGAACTGTTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGCTC	606
Qy	301	CTTTGCTACTATCAACAGACTCTTCAAGTGATTTTAAATAATCGAGCTGAGATAGA	360
Db	607	CTTTGCTACTATCAACAGACTCTTCAAGTGATTTTAAATAATCGAGCTGAGATAGA	666
Qy	361	TTTCAATATCCGGATCAAAATATGACAGAAAGTATGCGGGGAAATATGCTGTGAGT	420
Db	667	TTTCAATATCCGGATCAAAATATGACAGAAAGTATGCGGGGAAATATGCTGTGAGT	726
Qy	421	TAGTGCCCACTCTGAGCAAGCCAAACCTGGAAGAGATACAGTCACTCTGGAAGATT	480
Db	727	TAGTGCCCACTCTGAGCAAGCCAAACCTGGAAGAGATACAGTCACTCTGGAAGATT	786
Qy	481	AGTGGCTCCAGCAGTTTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGGT	540
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Qy	601	TGGCATCCGTTTGTAGAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATACAC	660
Db	907	TGGCATCCGTTTGTAGAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATACAC	966
Qy	661	AATGAATACAAAACCTGGAATCTGCAATTAATATCTGTTTCCAACTCGACACTGGAG	720
Db	967	AATGAATACAAAACCTGGAATCTGCAATTAATATCTGTTTCCAACTCGACACTGGAG	1026
Qy	721	ATATTCTGTGAAGCCGCAATCTGTTGGATATCGCAGTGCTCTGGGAAACGAATGCA	780
Db	1027	ATATTCTGTGAAGCCGCAATCTGTTGGATATCGCAGTGCTCTGGGAAACGAATGCA	1086
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Qy	841	TTCCGTTTGTGGCTTGGTGATGCTATGCTCAGAGAAAGGCTACTTTTCAA	893
Db	1147	TTCCGTTTGTGGCTTGGTGATGCTATGCTCAGAGAAAGGCTACTTTTCAA	1199
RESULT 6			
CR610497			
LOCUS			
DEFINITION			
full-length cDNA clone CSODI078Y002 of Placenta Cot 25-normalized			
of Homo sapiens (human).			
CR610497			
VERSION			
CR610497.1 GI:50491304			
KEYWORDS			
HTC; CNSLT_CDNA.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
REFERENCE			
1. (bases 1 to 1598)			
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
Full-length cDNA libraries and normalization			
Unpublished			
Contact : Feng Liang Email : fliang@lifetech.com URL :			
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600			
Faraday Avenue			
2 (bases 1 to 1598)			
Genoscope.			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :			
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.			
FEATURES			
source			
Location/Qualifiers			
1..1598			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="CSODI078Y002"			
/tissue type="Placenta Cot 25-normalized"			
/plasmid="pCMVSPORT_6"			
ORIGIN			
Query Match 69.0%; Score 893; DB 6; Length 1598;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CCAGAAAGTTCAAGGGCCCCCGGCTCTCTGCGCTCTCTGCGCGCGGAGACCTCTGACCTCCT	60
Db	403	CCAGAAAGTTCAAGGGCCCCCGGCTCTCTGCGCTCTCTGCGCGCGGAGACCTCTGACCTCCT	462
Qy	61	CAGAGCAGCGGCTGCGGCGCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCCT	120
Db	463	CAGAGCAGCGGCTGCGGCGCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCCT	522
Qy	121	GCTGCTGCTGCGCTACTCTGCTGCTGCGCTCTGCGCTCTCTGCGCGCGGAGCTATGAGGCTATG	180
Db	523	GCTGCTGCTGCGCTACTCTGCTGCTGCGCTCTGCGCTCTCTGCGCGCGGAGCTATGAGGCTATG	582
Qy	181	CCAAAGACCAACAAAGTAGTCAACAGTAGTACAGAGAGGCTATTTAGCGCTGCAA	240
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Qy	241	AACCCCAAGAGACACTGTTTCTCTCCAGATTAGATGGAAGAACTGGGTGGAGTGCTC	300
Db	643	AACCCCAAGAGACACTGTTTCTCTCCAGATTAGATGGAAGAACTGGGTGGAGTGCTC	702
Qy	301	CTTTGCTACTATCAACAGACTCTTCAAGTGATTTTAAATAATCGAGCTGAGATGATAGA	360
Db	703	CTTTGCTACTATCAACAGACTCTTCAAGTGATTTTAAATAATCGAGCTGAGATGATAGA	762
Qy	361	TTTCAATATCCGGATCAAAATATGGAACAGAGTATGCGGGGAAATATCTGTTGTAAGT	420
Db	763	TTTCAATATCCGGATCAAAATATGGAACAGAGTATGCGGGGAAATATCTGTTGTAAGT	822
Qy	421	TAGTGCCCATCTGAGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT	480
Db	823	TAGTGCCCATCTGAGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT	882
Qy	481	AGTGGCTCCAGCAGTTCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT	540
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Qy	541	AGAGCTACGATGTCAAGACAAAGAGGGAATCCAGCTCTCTGAAATACACATGTTTAAAGGA	600
Db	943	AGAGCTACGATGTCAAGACAAAGAGGGAATCCAGCTCTCTGAAATACACATGTTTAAAGGA	1002
Qy	601	TGGCATCCGTTTCTAGAAAATCCAGACTTGGCTCCCAAGACCAACAGCTCATACAC	660
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Qy	721	ATATTCTGTGAAGCCGCAATCTGTTGGATATCGCAGTGCTCTGGGAAACGAATGCA	780
Db	1123	ATATTCTGTGAAGCCGCAATCTGTTGGATATCGCAGTGCTCTGGGAAACGAATGCA	1182
Qy	781	AGTAGATGATCTCAACATAGTGGCATCATAGCAGCGTAGTAGTTGTGGCCTTAGTGAT	840
Db	1183	AGTAGATGATCTCAACATAGTGGCATCATAGCAGCGTAGTAGTTGTGGCCTTAGTGAT	1242


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QY      841  TTCCGTTTGGGCTTGGTGTATGCTATGCTCAGAGGAGGCTACTTTCAA 893
Db      1243  TTCCGTTTGGGCTTGGTGTATGCTATGCTCAGAGGAGGCTACTTTCAA 1295

RESULT 7
CB992775
LOCUS   CB992775      811 bp      mRNA      linear      EST 01-MAY-2003
DEFINITION AGENCOURT_13511610 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30334613 5', mRNA sequence.
ACCESSION CB992775
VERSION   CB992775.1 GI:30287295
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominoidea; Homo.
REFERENCE 1 (bases 1 to 811)
           NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
COMMENT   Email: gqapbs-rc@mail.nih.gov
           Tissue Procurement: Dr. Stefan Hansson
           cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
           and advice from Piero Carninci (RIKEN)
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           http://image.lnl.gov
           Plate: NDAM355 row: c column: 06
           High quality sequence stop: 673.
FEATURES             Location/Qualifiers
     source           1..811
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30334613"
                     /tissue_type="pre-eclamptic placenta"
                     /lab_host="DH10B Tona"
                     /clone_lib="NIH_MGC_148"
                     /notes="Organ: Placenta; Vector: pBluescriptR; Site:1:
                     all-XhoI; Site:2: BamHI; Library is oligo-dr primed and
                     directionally cloned using primer
                     5'-TTTTTTTTTTTTTTTNN-3', size-selected for average insert
                     size 2.3 kb and normalized to ROT 5. This is a primary
                     library enriched for full-length clones and constructed
                     using the Cap-trapper method (Carninci, in preparation).
                     Library constructed by M. Brownstein (NIH/NHGRI,
                     National Institutes of Health). Note: this is a NIH_MGC
                     Library."
ORIGIN
Query Match      52.5%; Score 680; DB 4; Length 811;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCAGAGATTCAAGGGCCCGCGCTCTCTGGCTCTCTGGCGCGGAGCCCTCGACCTCCT 60
Db      49  CCAGAGATTCAAGGGCCCGCGCTCTCTGGCTCTCTGGCGCGGAGCCCTCGACCTCCT 108

QY      61  CAGACAGCGCGCTGCGCGCCCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCTCCT 120
Db      109  CAGACAGCGCGCTGCGCGCCCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCTCCT 168

QY      121  GCTGCTGCTGCGCTACTCTGTGTGTGCGCCCTGGGCTATCATAGGCGCTATGGGTTTCTGC 180
Db      169  GCTGCTGCTGCGCTACTCTGTGTGTGCGCCCTGGGCTATCATAGGCGCTATGGGTTTCTGC 228

QY      181  CCCAAAAGACCAACAGTAGTACAGCAGTAGAGTACCAAGAGCGCTATTTTAGCCCTGCAA 240

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Db      229  CCCAAAAGACCAACAGTAGTACAGCAGTACAGTACCAAGAGCGCTATTTTAGCCCTGCAA 288
QY      241  AACCCCAAAGAGAGACTGTTTCTCCAGATTAGAGTGGAGAAAGAACTGGGTGGAGTGTCTC 300
Db      289  AACCCCAAAGAGAGACTGTTTCTCCAGATTAGAGTGGAGAAAGAACTGGGTGGAGTGTCTC 348
QY      301  CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATAGA 360
Db      349  CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATAGA 408
QY      361  TTTCAATATCCGGATCAAAAATGTGACAAAGAGTGTATGCGGGGAAATATCGTTTGAAGT 420
Db      409  TTTCAATATCCGGATCAAAAATGTGACAAAGAGTGTATGCGGGGAAATATCGTTTGAAGT 468
QY      421  TAGTGCCCATCTGAGCAAGGCGCAAAACCTGGAAGAGGATACAGTCACCTCTGGAAGTATT 480
Db      469  TAGTGCCCATCTGAGCAAGGCGCAAAACCTGGAAGAGGATACAGTCACCTCTGGAAGTATT 528
QY      481  AGTGGCTCCAGCAGTTCATCATGTGAAGTACCTCTCTGCTCTGAGTGGAACTGTGGT 540
Db      529  AGTGGCTCCAGCAGTTCATCATGTGAAGTACCTCTCTGCTCTGAGTGGAACTGTGGT 588
QY      541  AGAGCTACCATGTCAAGCAAAAGAGGGAATCCAGCTCTCTGAAATACACATGTTTAAAGGA 600
Db      589  AGAGCTACCATGTCAAGCAAAAGAGGGAATCCAGCTCTCTGAAATACACATGTTTAAAGGA 648
QY      601  TGGCATCCGTTTGTAGAAAAATCCAGACTTGGTCCCAAAGCACCACAGCTCATACAC 660
Db      649  TGGCATCCGTTTGTAGAAAAATCCAGACTTGGTCCCAAAGCACCACAGCTCATACAC 708
QY      661  RATGAATACAAAACTGGAA 680
Db      709  AATGAATACAAAACTGGAA 728

RESULT 8
DN994893
LOCUS   DN994893      772 bp      mRNA      linear      EST 17-MAY-2005
DEFINITION TC108217 Human adult whole brain, large insert, pcMV expression
           library Homo sapiens cDNA clone TC108217 5', similar to Homo sapiens
           junctional adhesion molecule 2 (JAM2), mRNA sequence.
ACCESSION DN994893
VERSION   DN994893.1 GI:66254724
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominoidea; Homo.
REFERENCE 1 (bases 1 to 772)
           Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
           Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
           Zhang,X., Jay,G. and He,W.
           High-throughput cloning of full-length human cDNAs directly from
           cDNA libraries optimized for large and rare transcripts
           Unpublished (2005)
JOURNAL   Contact: Kovacs, KP
COMMENT   High Throughput cDNA Cloning
           Origene Technologies, Inc. ( www.origene.com )
           6 Taft Court, Suite 100, Rockville, MD 20850, USA
           Tel: 301 340 3188
           Fax: 301 340 8606
           Email: cDNA@origene.com
           This EST submission is part of an on-going human full-length
           cloning project at Origene Technologies, Inc.
           Please contact Origene for access.
           Origene Technologies, Inc.
           6 Taft Ct. Suite 100
           Rockville, MD 20850
           Tel: (301) 340-3188
           http://www.origene.com
           Seq primer: pcMV6 5prime forward vector primer, Origene
           Technologies Inc.

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FEATURES
source
Location/Qualifiers
1. 772
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC108217"
/tissue_type="Whole brain"
/clone_lib="Human adult whole brain, large insert, pCMV
expression library"
/notes="Organ: Brain; Vector: pCMV6-XL5; Site 1: EcoRI;
Site 2: XhoI/SalI compatible end ligatio; Oligo-dr primed
reverse transcription optimized for large and GC rich mRNA
transcripts, cDNA size selection, optimized ligation for
large inserts into mammalian expression vector, random
clones selected for end sequence verification of
full-length genes"

ORIGIN
Query Match 51.4%; Score 665; DB 9; Length 772;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAGTTCAAGGGCCCCCGGCTCTGCGCTCTGCGCGGGAGCCCTCGACTCTCTCAGAG 65
Db 59 AAGTTCAAGGGCCCCCGGCTCTGCGCTCTGCGCGGGAGCCCTCGACTCTCTCAGAG 118

Qy 66 CAGCGGCTCGCGCGCGGAGAGTGGGAGGAGCGCCACCGCTCTCTGCTGC 125
Db 119 CAGCGGCTCGCGCGCGGAGAGTGGGAGGAGCGCCACCGCTCTCTGCTGC 178

Qy 126 TGCTGCGCTACCTGCTGCTCGCCCTGCGCTATCATAGGCTATGGGTCTTCTGCCCAA 185
Db 179 TGCTGCGCTACCTGCTGCTCGCCCTGCGCTATCATAGGCTATGGGTCTTCTGCCCAA 238

Qy 186 AAGACCAACAGTAGTACACAGCAGTAGAGTACCAAGAGGCTATTTAGCTGCAAAACC 245
Db 239 AAGACCAACAGTAGTACACAGCAGTAGAGTACCAAGAGGCTATTTAGCTGCAAAACC 298

Qy 246 CAAAGAGACTGTTTCTCCAGATTAGTGGAGAACTGGGTCCGAGTGTCTCCTTG 305
Db 299 CAAAGAGACTGTTTCTCCAGATTAGTGGAGAACTGGGTCCGAGTGTCTCCTTG 358

Qy 306 TCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATGATTTCA 365
Db 359 TCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCGAGCTGAGATGATGATTTCA 418

Qy 366 ATATCCGGATCAAAAATGTGACAAAGAGTGTGCGGGAAATATCGTTGTGAAGTTAGTG 425
Db 419 ATATCCGGATCAAAAATGTGACAAAGAGTGTGCGGGAAATATCGTTGTGAAGTTAGTG 478

Qy 426 CCCATCTGAGCAAGGCCAAACCTCGAAGAGGATACAGTCACTCTCGAAGTATTAGTGG 485
Db 479 CCCATCTGAGCAAGGCCAAACCTCGAAGAGGATACAGTCACTCTCGAAGTATTAGTGG 538

Qy 486 CTCAGAGTTCATCATGTGAGTACCTCTCTGCTCTGAGTGGAACTGTGTGAGC 545
Db 539 CTCAGAGTTCATCATGTGAGTACCTCTCTGCTCTGAGTGGAACTGTGTGAGC 598

Qy 546 TAGCATGTCAAGCAAAAGAGGGAATCCAGCTCTCTGTAATACATATGTTTAAAGATGGCA 605
Db 599 TAGCATGTCAAGCAAAAGAGGGAATCCAGCTCTCTGTAATACATATGTTTAAAGATGGCA 658

Qy 606 TCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGCAACCAAGCTCATACAAATGA 665
Db 659 TCCGTTTGTAGAAAATCCAGACTTGGCTCCCAAGCAACCAAGCTCATACAAATGA 718

Qy 666 ATACA 670
Db 719 ATACA 723

RESULT 9
AL548850
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QY 421 TAGTGCCTCCATCTGAGCAAGGCCAAACCTGGAAGAGATACAGTCACCTCTGGAAGTATT 480
DB 540 TAGTGCCTCCATCTGAGCAAGGCCAAACCTGGAAGAGATACAGTCACCTCTGGAAGTATT 599
QY 481 AGTGGCTCCAGAGATTCATCATGTGAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 540
DB 600 AGTGGCTCCAGAGATTCATCATGTGAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 659
QY 541 AGAGCTACGATGTCAAGACAAAGAGGAATCCAGCTCTCTGGAATACACATGTTTAAGGA 600
DB 660 AGAGCTACGATGTCAAGACAAAGAGGAATCCAGCTCTCTGGAATACACATGTTTAAGGA 719
QY 601 TGGCATCCGTTTCTAGAAAATCCAGACTTGGCTCCCAAAGCA 644
DB 720 TGGCATCCGTTTCTAGAAAATCCAGACTTGGCTCCCAAAGCA 763

RESULT 10
BI916904
LOCUS
DEFINITION
603177882F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241957 5',
mRNA sequence.
ACCESSION
BI916904
VERSION
BI916904.1 GI:16180857
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 681)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: sgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1610 row: d column: 22
High quality sequence stop: 677.
FEATURES
Location/Qualifiers
1..681
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5241957"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (Scorv site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 48.5%; Score 628; DB 2; Length 681;
Best Local Similarity 99.9%; Pred. No. 6.9e-299;
Matches 678; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCAGAGATTCAGAGGCCCGCCCTCTGCGCTCTGCGCGGAGACCTCGACCTCT 60
DB 1 CCAGAGATTCAGAGGCCCGCCCTCTGCGCTCTGCGCGGAGACCTCGACCTCT 60

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QY 61 CAGAGCAGCCGCTGCCGCCCGGAGAGATGCGAGGAGAGCCGCCACCGCTCTCTCT 120
DB 61 CAGAGCAGCCGCTGCCGCCCGGAGAGATGCGAGGAGAGCCGCCACCGCTCTCTCT 120
QY 121 GCTGCTGCTGCGCTACCTGCTGCTGCTGCTGCTGCTATCATAGGCTATAGGGTTTCTGC 180
DB 121 GCTGCTGCTGCGCTACCTGCTGCTGCTGCTGCTATCATAGGCTATAGGGTTTCTGC 180
QY 181 CCAAAAGACCAACCAAGTAGTCAAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGC 240
DB 181 CCAAAAGACCAACCAAGTAGTCAAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGC 240
QY 241 AACCCCAAGAGAGACTGTTTCTCCAGATTAGAGTGAAGAACTGGGTCGAGTCTTC 300
DB 241 AACCCCAAGAGAGACTGTTTCTCCAGATTAGAGTGAAGAACTGGGTCGAGTCTTC 300
QY 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA 360
DB 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA 360
QY 361 TTTCAATATCCGATCAAAAATGTGACAAAGTGTGCGGGAATAATATCGTTGTGAAGT 420
DB 361 TTTCAATATCCGATCAAAAATGTGACAAAGTGTGCGGGAATAATATCGTTGTGAAGT 420
QY 421 TAGTGCCCATCTGAGCAAGGCCAAACCTGGAAGAGATACAGTCACCTCTGGAAGTATT 480
DB 421 TAGTGCCCATCTGAGCAAGGCCAAACCTGGAAGAGATACAGTCACCTCTGGAAGTATT 480
QY 481 AGTGGCTCCAGAGATTCATCATGTGAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 540
DB 481 AGTGGCTCCAGAGATTCATCATGTGAGTACCTCTTCTGCTCTGAGTGGAACTGTGGT 540
QY 541 AGAGCTACGATGTCAAGACAAAGAGGAATCCAGCTCTCTGGAATACACATGTTTAAGGA 600
DB 541 AGAGCTACGATGTCAAGACAAAGAGGAATCCAGCTCTCTGGAATACACATGTTTAAGGA 600
QY 601 TGGCATCCGTTTCTAGAAAATCCAGACTTGGCTCCCAAAGCAACAGCTCATACAC 660
DB 601 TGGCATCCGTTTCTAGAAAATCCAGACTTGGCTCCCAAAGCAACAGCTCATACAC 660
QY 661 AATGAATACAAAACCTGGA 679
DB 661 AATGAATACAAAACCTGGA 679

RESULT 11
CF127652
LOCUS
DEFINITION
CF127652 753 bp mRNA linear EST 05-AUG-2003
IMAGE:30552877 5', mRNA sequence.
ACCESSION
CF127652
VERSION
CF127652.1 GI:33206105
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 753)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
PUBMED
889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix

```


cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/humanfl.html>
Seq primer: pyX-5.

FEATURES

Location/Qualifiers
1..753
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:3052877"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_MGC_214"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."

ORIGIN
Query Match 47.6%; Score 616; DB 5; Length 753;
Best Local Similarity 100.0%; Pred. No. 6e-293;
Matches 616; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCAGAGTTCAGAGGCCCGCCGCTCTCGCTCCCTGCGCGCGCGGACCCCTCGACCTCCT 60
Db 138 CCCAGAGTTCAGAGGCCCGCCGCTCTCGCTCCCTGCGCGCGGACCCCTCGACCTCCT 197
Qy 61 CAGAGCAGCCGGCTGCGCGCGCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCCT 120
Db 198 CAGAGCAGCCGGCTGCGCGCGCGGGAAGATGGCGAGGAGGAGCGCCACCGCTCTCCT 257
Qy 121 GCTGCTGCTGGCTACCTGCTGCTGCGCTGGCTATCATAGAGCCCTATGGTTTCTGC 180
Db 258 GCTGCTGCTGGCTACCTGCTGCTGCGCTGGCTATCATAGAGCCCTATGGTTTCTGC 317
Qy 181 CCCAAAAGACCAACAGTAGTCACAGCAGTAGATACCAAGAGCTATTTAGCCTGCAA 240
Db 318 CCCAAAAGACCAACAGTAGTCACAGCAGTAGATACCAAGAGCTATTTAGCCTGCAA 377
Qy 241 AACCCCAAAGAGACTGTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTC 300
Db 378 AACCCCAAAGAGACTGTTCTCCAGATTAGAGTGAAGAACTGGGTGGAGTGTCTC 437
Qy 301 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCAGCTGAGATGATAGA 360
Db 438 CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAATAATCAGCTGAGATGATAGA 497
Qy 361 TTTCATATATCCGATCAAAAATGTGACAGAGTGTATGCGGGGAAATATCGTTGTGAAT 420
Db 498 TTTCATATATCCGATCAAAAATGTGACAGAGTGTATGCGGGGAAATATCGTTGTGAAT 557
Qy 421 TAGTGCCCACTCTCAGCAAGGCCAAAACCTTGGAAAGAGATACAGTCACTCTGGAAGTATT 480
Db 558 TAGTGCCCACTCTCAGCAAGGCCAAAACCTTGGAAAGAGATACAGTCACTCTGGAAGTATT 617
Qy 481 AGTGGCTCCAGCAGTTCATCATGTGAAGTACCCTTCTTGCTCTGAGTGGAACTGTGGT 540
Db 618 AGTGGCTCCAGCAGTTCATCATGTGAAGTACCCTTCTTGCTCTGAGTGGAACTGTGGT 677
Qy 541 AGAGCTACGATGTCAAGCAAAAGAGGAATCCAGCTCCTGGAATACACATGTTTAAAGGA 600
Db 678 AGAGCTACGATGTCAAGCAAAAGAGGAATCCAGCTCCTGGAATACACATGTTTAAAGGA 737
Qy 601 TGGCATCCGTTTGCTA 616

Db 738 TGGCATCCGTTTGCTA 753

RESULT 12

DB289885

LOCUS

DEFINITION

DB289885

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

FEATURES

source

ORIGIN

Query Match

Best Local

Matches

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

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Qy

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Qy

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Qy

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Qy

Db

Qy

Db

Qy

Db

Qy

Db

587 bp mRNA linear EST 11-DEC-2005
DB289885 UTER3 Homo sapiens cDNA clone UTER3019733 5', mRNA
sequence.
DB289885
DB289885.1 GI:83558149
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1. (bases 1 to 587)
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatauma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Sugano, S.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
Location/Qualifiers
1..587
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UTER3019733"
/tissue_type="uterus"
/clone_lib="UTER3"
/note="Vector: pME18SFL3"

ORIGIN
Query Match 45.3%; Score 587; DB 9; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.3e-278;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 AGAAGTTCAAGGGCCCCCGGCTCTGCGCTCTGCGCGCGGACCCCTCGACCTCTCAG 63
Db 1 AGAAGTTCAAGGGCCCCCGGCTCTGCGCTCTGCGCGCGGACCCCTCGACCTCTCAG 60
Qy 64 AGCAGCCGGCTGCGCGCGCGGGAAGATGGCGAGGAGCGCCACCGCTCTCTCTGCT 123
Db 61 AGCAGCCGGCTGCGCGCGCGGGAAGATGGCGAGGAGCGCCACCGCTCTCTCTGCT 120
Qy 124 GCTGCTCGCTACCTGCTGCTGCGCCCTGCGCTATCATAGGCCCTATGGGTTTCTGCCCC 183
Db 121 GCTGCTCGCTACCTGCTGCTGCGCCCTGCGCTATCATAGGCCCTATGGGTTTCTGCCCC 180
Qy 184 AAAAGACCAACAAGTAGTCA CAGCAGTAGAGTACCAAGAGGCTATTTTAGCTGCAAAAC 243
Db 181 AAAAGACCAACAAGTAGTCA CAGCAGTAGAGTACCAAGAGGCTATTTTAGCTGCAAAAC 240


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QY 244 CCCAAGAGAGACTGTTCTCCAGATTAGAGTCGAGAGAACTGGTCGGAGTCTCCTT 303
Db 241 CCCAAGAGAGACTGTTCTCCAGATTAGAGTCGAGAGAACTGGTCGGAGTCTCCTT 300
QY 304 TGTCTACTATCAACAGACTCTTCAAGTGTATTTTAAAAATCGAGCTGAGATGATAGATT 363
Db 301 TGTCTACTATCAACAGACTCTTCAAGTGTATTTTAAAAATCGAGCTGAGATGATAGATT 360
QY 364 CAATATCCGGATCAAAAATGTGACAAGAGTATGCGGGGAAATATCGTTGTGAAGTAG 423
Db 361 CAATATCCGGATCAAAAATGTGACAAGAGTATGCGGGGAAATATCGTTGTGAAGTAG 420
QY 424 TGCCCATCTGACCAAGCCCAAACTGGAGAGGATACAGTCACCTCGAATATTAGT 483
Db 421 TGCCCATCTGAGCAAGCCCAAACTGGAGAGGATACAGTCACCTCGAATATTAGT 480
QY 484 GGCTCCAGCAGTTCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTCTGTGTAGA 543
Db 481 GGCTCCAGCAGTTCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTCTGTGTAGA 540
QY 544 GCTACGATGTCAAGACAAGAGGGAATCCAGCTCTCTGAATACACAT 590
Db 541 GCTACGATGTCAAGACAAGAGGGAATCCAGCTCTCTGAATACACAT 587

RESULT 13
DA293800
LOCUS
DEFINITION
DA293800 BRHIP2 Homo sapiens cDNA clone BRHIP2006083 5', mRNA
sequence.
ACCESSION
DA293800
VERSION
DA293800.1 GI:78734403
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 580)
Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kishida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanabe,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
1634560
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FLJ Project (HRI Team)
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NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan): cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
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Homo sapiens
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1 (bases 1 to 716)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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Best Local Similarity	99.9%; Pred. No. 3.8e-274;
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Job time : 7021 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 17, 2006, 17:24:08 ; Search time 5374 Seconds
(without alignments)
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Ygapop 60.0 , Ygapext 60.0
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Delop 60.0 , Delext 60.0

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 112	69	22.1	520	9	DA757224	DA757224	DA757224	C 185	30	9.6	540	1	AJ679277	AJ679277	AJ679277	AJ679277
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C 114	68	21.8	582	3	BP229524	BP229524	BP229524	C 187	30	9.6	593	1	AM017760	AM017760	AM017760	AM017760
C 115	66	21.2	583	3	BP320097	BP320097	BP320097	C 188	30	9.6	603	1	AV602516	AV602516	AV602516	AV602516
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C 120	60	19.2	464	3	BM723158	BM723158	BM723158	C 193	30	9.6	769	10	DT834338	DT834338	DT834338	DT834338
C 121	60	19.2	466	1	AI201753	AI201753	AI201753	C 194	29	9.3	486	8	CX004210	CX004210	CX004210	CX004210
C 122	60	19.2	1006	4	BX345643	BX345643	BX345643	C 195	29	9.3	524	9	DN394857	DN394857	DN394857	DN394857
C 123	59	18.9	564	9	DA810910	DA810910	DA810910	C 196	29	9.3	878	8	CX004209	CX004209	CX004209	CX004209
C 124	59	18.9	813	1	AI544740	AI544740	AI544740	C 197	28	9.0	398	9	DA850901	DA850901	DA850901	DA850901
C 125	58	18.6	464	1	AI140139	AI140139	AI140139	C 198	27	8.7	311	4	CB137090	CB137090	CB137090	CB137090
C 126	57	18.3	335	2	BP932991	BP932991	BP932991	C 199	27	8.7	715	4	BX920450	BX920450	BX920450	BX920450
C 127	57	18.3	555	9	DB133113	DB133113	DB133113	C 200	27	8.7	818	3	BP144687	BP144687	BP144687	BP144687
C 128	57	18.3	556	9	DB065689	DB065689	DB065689	C 201	27	8.7	862	4	BX343700	BX343700	BX343700	BX343700
C 129	57	18.3	565	9	DA233331	DA233331	DA233331	C 202	27	8.7	1184	6	AY610145	AY610145	AY610145	AY610145
C 130	56	17.9	553	9	DB220037	DB220037	DB220037	C 203	25	8.0	589	10	DV873456	DV873456	DV873456	DV873456
C 131	56	17.9	619	2	BG482835	BG482835	BG482835	C 204	25	8.0	876	1	AL553676	AL553676	AL553676	AL553676
C 132	55	17.6	508	9	DB233521	DB233521	DB233521	C 205	24	7.7	355	7	BF091146	BF091146	BF091146	BF091146
C 133	54	17.3	492	8	CO594463	CO594463	CO594463	C 206	24	7.7	427	2	BF709908	BF709908	BF709908	BF709908
C 134	54	17.3	498	8	CO591452	CO591452	CO591452	C 207	24	7.7	549	11	AQ441827	AQ441827	AQ441827	AQ441827
C 135	54	17.3	577	2	BM538432	BM538432	BM538432	C 208	24	7.7	605	14	AG012165	AG012165	AG012165	AG012165
C 136	54	17.3	594	8	CO658359	CO658359	CO658359	C 209	24	7.7	689	14	AG012165	AG012165	AG012165	AG012165
C 137	54	17.3	651	9	DN864800	DN864800	DN864800	C 210	23	7.4	292	1	AF940336	AF940336	AF940336	AF940336
C 138	54	17.3	666	2	BI817130	BI817130	BI817130	C 211	23	7.4	380	2	BF846977	BF846977	BF846977	BF846977
C 139	54	17.3	679	8	CO715331	CO715331	CO715331	C 212	23	7.4	639	8	CO593712	CO593712	CO593712	CO593712
C 140	54	17.3	705	9	DN743946	DN743946	DN743946	C 213	21	6.7	163	9	DB370076	DB370076	DB370076	DB370076
C 141	54	17.3	732	9	DR107648	DR107648	DR107648	C 214	21	6.7	163	9	DB370076	DB370076	DB370076	DB370076
C 142	54	17.3	772	9	DN392017	DN392017	DN392017	C 215	21	6.7	470	7	BF189965	BF189965	BF189965	BF189965
C 143	54	17.3	800	3	BU748393	BU748393	BU748393	C 216	21	6.7	488	3	BP149408	BP149408	BP149408	BP149408
C 144	54	17.3	809	9	CX988602	CX988602	CX988602	C 217	21	6.7	701	14	AG012830	AG012830	AG012830	AG012830
C 145	54	17.3	916	5	CF407265	CF407265	CF407265	C 218	20	6.4	263	12	CG495820	CG495820	CG495820	CG495820
C 146	53	17.0	245	7	AW865421	AW865421	AW865421	C 219	20	6.4	265	12	CG493686	CG493686	CG493686	CG493686
C 147	52	16.7	532	9	DB336126	DB336126	DB336126	C 220	20	6.4	269	12	CG643424	CG643424	CG643424	CG643424
C 148	52	16.7	556	9	CBX931621	CBX931621	CBX931621	C 221	20	6.4	281	12	CG515360	CG515360	CG515360	CG515360
C 149	51	16.3	449	7	AW136481	AW136481	AW136481	C 222	20	6.4	285	12	CG541092	CG541092	CG541092	CG541092
C 150	51	16.3	433	1	AI650503	AI650503	AI650503	C 223	20	6.4	287	12	CG646149	CG646149	CG646149	CG646149

224	20	6.4	327	12	CG497834	CG497834	OST38673	297	18	5.8	428	12	CG658984	CG658984	OST436033
225	20	6.4	330	12	CG495419	CG495419	OST34804	298	18	5.8	451	12	CG650844	CG650844	OST409725
226	20	6.4	339	12	CG514649	CG514649	OST68527	299	18	5.8	457	12	CG655131	CG655131	OST425078
227	20	6.4	339	12	CG598159	CG598159	OST262313	300	18	5.8	466	12	CG607524	CG607524	OST286494
228	20	6.4	343	12	CG496542	CG496542	OST36638	301	18	5.8	468	12	CG635842	CG635842	OST359320
229	20	6.4	347	12	CG514469	CG514469	OST68282	302	18	5.8	495	12	CG640726	CG640726	OST374100
230	20	6.4	364	12	CG659115	CG659115	OST336465	303	18	5.8	496	12	CG643181	CG643181	OST381341
231	20	6.4	377	12	CG498385	CG498385	OST39661	304	18	5.8	534	12	CG654462	CG654462	OST422612
232	20	6.4	386	12	CG615648	CG615648	OST306561	c 305	17	5.4	224	7	BF460869	BF460869	UI-M-CG0p
233	20	6.4	391	12	CG507979	CG507979	OST58238	c 306	17	5.4	257	4	BX633581	BX633581	UI-M-CG0p
234	20	6.4	403	12	CG572210	CG572210	OST202508	307	17	5.4	311	1	AV225976	AV225976	AV225976
235	20	6.4	408	12	CG605104	CG605104	OST281411	c 308	17	5.4	376	1	AI849051	AI849051	UI-M-AH1-
236	20	6.4	422	12	CG497261	CG497261	OST37749	c 309	17	5.4	381	1	AI556456	AI556456	UI-R-C2p-
237	20	6.4	422	12	CG504458	CG504458	OST52558	310	17	5.4	383	12	CG624186	CG624186	OST327284
238	20	6.4	422	12	CG580233	CG580233	OST219462	311	17	5.4	389	4	BY508025	BY508025	BY508025
239	20	6.4	423	12	CG535702	CG535702	OST122877	c 312	17	5.4	398	1	AI432092	AI432092	th32a12.x
240	20	6.4	423	12	CG595339	CG595339	OST254712	c 313	17	5.4	403	12	CG662492	CG662492	OST446275
241	20	6.4	424	12	CG500225	CG500225	OST42979	c 314	17	5.4	480	8	CR468808	CR468808	CR468808
242	20	6.4	426	12	CG604841	CG604841	OST280915	c 315	17	5.4	502	4	BY477702	BY477702	BY477702
243	20	6.4	435	12	CG506984	CG506984	OST56760	316	17	5.4	502	12	CG602718	CG602718	OST276379
244	20	6.4	437	12	CG541713	CG541713	OST135238	c 317	17	5.4	507	1	AJ507041	AJ507041	AJ507041
245	20	6.4	445	12	CG551037	CG551037	OST157738	c 318	17	5.4	510	3	BQ211610	BQ211610	UI-R-DY1-
246	20	6.4	445	12	CG568316	CG568316	OST195236	c 319	17	5.4	513	12	CG605974	CG605974	OST283410
247	20	6.4	445	12	CG616790	CG616790	OST309395	c 320	17	5.4	526	1	AI853724	AI853724	UI-M-BH0-
248	20	6.4	449	12	CG512231	CG512231	OST65057	321	17	5.4	533	7	BB763748	BB763748	BB763748
249	20	6.4	454	12	CG507182	CG507182	OST57042	c 322	17	5.4	545	7	AW082343	AW082343	xb65g01.x
250	20	6.4	454	12	CG523774	CG523774	OST96556	c 323	17	5.4	555	2	BI290037	BI290037	UI-R-DK0-
251	20	6.4	470	1	AI154320	udb1d06.r	324	17	5.4	580	3	BM941662	BM941662	UI-M-CG0p	
252	20	6.4	473	12	CG619438	CG619438	OST315342	c 325	17	5.4	596	3	BP770982	BP770982	BP770982
253	20	6.4	482	12	CG539560	CG539560	OST130739	c 326	17	5.4	609	2	BI732178	BI732178	603352794
254	20	6.4	489	12	CG625930	CG625930	OST333211	c 327	17	5.4	617	11	BH055189	BH055189	RPCI-24-2
255	20	6.4	503	12	CG492599	CG492599	OST30532	328	17	5.4	674	7	BB046911	BB046911	BB046911
256	20	6.4	513	12	CG625693	CG625693	OST332417	c 329	17	5.4	675	8	CO039152	CO039152	UI-M-AL1-
257	20	6.4	533	12	CG662003	CG662003	OST444083	c 330	17	5.4	731	3	BQ210314	BQ210314	UI-R-DY1-
258	20	6.4	541	12	CG570152	CG570152	OST198791	331	17	5.4	734	4	CB595085	CB595085	AGENCOURT
259	20	6.4	546	12	CG645278	CG645278	OST389673	c 332	17	5.4	745	8	CN543699	CN543699	UI-R-DZ1-
260	20	6.4	579	4	CA873574	CA873574	K0926B10-	333	17	5.4	773	5	CK477501	CK477501	AGENCOURT
261	20	6.4	589	3	BP427892	BP427892	334	17	5.4	825	4	CB573834	CB573834	AGENCOURT	
262	20	6.4	592	8	CV558990	UI-M-HZ0-	335	17	5.4	928	3	BU504526	BU504526	AGENCOURT	
263	20	6.4	600	4	CA528989	8092-83 M	c 336	16	5.1	934	7	AW825281	AW825281	PM4-CY024	
264	20	6.4	614	7	BB613061	BB613061	337	16	5.1	977	7	AW973181	AW973181	EST385279	
265	20	6.4	618	12	CG5988364	CG5988364	OST239173	338	16	5.1	998	9	CM870994	CM870994	HESC4_51
266	20	6.4	622	12	CG494247	CG494247	OST33008	339	16	5.1	713	14	AG009140	AG009140	Homo sapi
267	20	6.4	628	12	CG589793	CG589793	OST242455	c 340	16	5.1	730	14	CR913116	CR913116	Sub scrof
268	20	6.4	644	7	BB622205	BB622205	341	16	5.1	738	3	BQ207505	BQ207505	UI-R-DY1-	
269	20	6.4	665	7	BB627936	BB627936	342	16	5.1	828	2	BI157375	BI157375	602923864	
270	20	6.4	668	7	BB627619	BB627619	343	16	5.1	838	5	CK599264	CK599264	AGENCOURT	
271	20	6.4	701	7	BB642937	BB642937	344	15	4.8	318	7	BB218442	BB218442	BB218442	
272	20	6.4	700	1	AJ942995	AJ942995	345	15	4.8	357	4	CB812950	CB812950	AMGNNUC:T	
273	20	6.4	707	4	CB521570	UI-M-GH0-	346	15	4.8	376	4	CB690994	CB690994	AMGNNUC:T	
274	20	6.4	741	4	BY710270	BY710270	347	15	4.8	380	12	CG535813	CG535813	OST123088	
275	20	6.4	794	4	CB318894	CB318894	AGENCOURT	348	15	4.8	396	4	CB772835	CB772835	AMGNNUC:S
276	20	6.4	811	2	BI739594	BI739594	603361849	349	15	4.8	668	14	AG012169	AG012169	Homo sapi
277	20	6.4	812	8	CK200154	MNS00784	c 350	15	4.8	679	14	AG012159	AG012159	Homo sapi	
278	20	6.4	839	8	CK218247	CK218247	351	15	4.8	900	4	CB319992	CB319992	AGENCOURT	
279	20	6.4	923	3	BU035587	BU035587	352	14	4.5	209	4	CA439076	CA439076	UI-H-D10-	
280	20	6.4	953	3	BU035587	AGENCOURT	c 353	14	4.5	236	11	AQ543042	AQ543042	RPCI-11-3	
281	20	6.4	989	4	BY762264	BY762264	354	14	4.5	243	2	BF05962	BF05962	RC6-CI000	
282	20	6.4	1012	4	BY710030	BY710030	c 355	14	4.5	269	3	BQ369906	BQ369906	MR3-GN002	
283	20	6.4	1094	6	AK010826	AK010826	c 356	14	4.5	290	2	AA487911	AA487911	ab12d12.8	
284	20	6.4	1167	6	AK013914	Mus muscu	357	14	4.5	293	2	BA203894	BA203894	RST3286	
285	20	6.4	1195	6	AK078128	Mus muscu	358	14	4.5	299	1	AV225553	AV225553	AV225553	
286	20	6.4	1290	6	AKI53636	Mus muscu	359	14	4.5	300	10	DM420555	DM420555	HHAG80203	
287	20	6.4	1312	6	AK010616	Mus muscu	360	14	4.5	303	10	DW419293	DW419293	HHAG80190	
288	20	6.4	1999	6	AK045095	Mus muscu	361	14	4.5	305	10	DW417548	DW417548	HHAG80182	
289	20	6.4	2902	6	AK028757	Mus muscu	362	14	4.5	311	12	CG513247	CG513247	OST766533	
c 290	19	6.1	150	7	BE938414	RC0-TN007	c 363	14	4.5	312	1	AA936787	AA936787	OI50f07.8	
c 291	19	6.1	594	11	AQ313134	AQ313134	c 364	14	4.5	312	1	AA974715	AA974715	OP29f01.8	
292	18	5.8	330	12	CG571674	CG571674	365	14	4.5	315	12	CG619644	CG619644	OST315800	
293	18	5.8	332	12	CG661287	CG661287	366	14	4.5	327	11	AQ182324	AQ182324	H2-2442 B	
294	18	5.8	355	12	CG564765	OST189087	367	14	4.5	333	12	CG669324	CG669324	OST466157	
295	18	5.8	356	12	CG599907	CG599907	c 368	14	4.5	341	11	B78763	B78763	CIT-HSP-563	
296	18	5.8	408	12	CG648347	CG648347	369	14	4.5	346	1	AA488026	AA488026	ab12d12.1.r	

370	14	4.5	365	8	CV403726	CV403726 RC0-CT042	C 443	14	4.5	680	14	AG132760
C 371	14	4.5	374	11	AQ043454	AQ043454 CIT-HSP-2	444	14	4.5	685	11	AQ470681
C 372	14	4.5	385	11	AQ404280	AQ404280 HS 5071-B	445	14	4.5	696	9	DA571961
C 373	14	4.5	390	11	AQ060642	AQ060642 CIT-HSP-2	446	14	4.5	697	14	AG066960
C 374	14	4.5	391	2	BF742066	BF742066 CM4-HB002	C 447	14	4.5	700	2	BG615266
C 375	14	4.5	392	7	AW261924	AW261924 XP87902.X	C 448	14	4.5	710	9	CX757319
C 376	14	4.5	393	11	AQ152518	AQ152518 HS 3110-B	C 449	14	4.5	711	7	BF666079
C 377	14	4.5	398	11	AQ014641	AQ014641 HS-2262-B	C 450	14	4.5	714	9	DA833871
C 378	14	4.5	411	1	AI3357605	AI3357605 Qn20F04.X	C 451	14	4.5	723	2	BG502627
C 379	14	4.5	411	4	CB296117	CB296117 12B2202.X	452	14	4.5	725	4	CA427862
C 380	14	4.5	412	11	AQ0406334	AQ0406334 HS 2262-B	453	14	4.5	726	4	BA645530
C 381	14	4.5	417	1	AA599115	AA599115 a952805.B	C 454	14	4.5	730	7	BF666566
C 382	14	4.5	417	1	AA599143	AA599143 a952804.B	C 455	14	4.5	739	3	BU616284
C 383	14	4.5	417	2	BI043989	BI043989 PM3-OT020	C 456	14	4.5	741	7	BB889051
C 384	14	4.5	417	11	AQ5266818	AQ5266818 HS 5218-A	C 457	14	4.5	762	12	B2774475
C 385	14	4.5	418	1	AA075975	AA075975 zm75402.X	C 458	14	4.5	777	7	BF574535
C 386	14	4.5	418	11	AQ101128	AQ101128 HS 3064-B	C 459	14	4.5	779	5	CJ436518
C 387	14	4.5	422	11	AQ137158	AQ137158 HS 3064-B	C 460	14	4.5	786	1	AU119698
C 388	14	4.5	423	1	AA776656	AA776656 a979907.B	C 461	14	4.5	789	7	BF029924
C 389	14	4.5	428	11	AQ167476	AQ167476 HS 3165-A	C 462	14	4.5	789	12	CA466113
C 390	14	4.5	432	1	AA149033	AA149033 z003h12.B	C 463	14	4.5	792	11	AQ897192
C 391	14	4.5	443	1	AA774105	AA774105 ac36608.B	C 464	14	4.5	807	9	CX762940
C 392	14	4.5	443	11	AQ044965	AQ044965 RPC111-33	C 465	14	4.5	816	3	BU561328
C 393	14	4.5	447	7	AW243793	AW243793 x05606.X	C 466	14	4.5	816	4	CB991902
C 394	14	4.5	454	8	CN276419	CN276419 170006001	C 467	14	4.5	840	4	CB990803
C 395	14	4.5	458	7	BE148151	BE148151 RC4-HT023	C 468	14	4.5	877	9	DA647195
C 396	14	4.5	458	11	AQ770727	AQ770727 HS 5368-B	C 469	14	4.5	894	9	DA570330
C 397	14	4.5	459	2	BI060938	BI060938 I13-VT011	C 470	14	4.5	894	14	DU797934
C 398	14	4.5	462	11	AQ262012	AQ262012 CITBI-EI-	C 471	14	4.5	913	3	BU186592
C 399	14	4.5	467	1	AA991677	AA991677 ot69b06.B	C 472	14	4.5	935	2	BG531700
C 400	14	4.5	468	11	AQ592346	AQ592346 HS 5446-A	C 473	14	4.5	946	2	BG119631
C 401	14	4.5	473	11	AQ425696	AQ425696 CITBI-EI-	C 474	14	4.5	956	2	BG110329
C 402	14	4.5	480	2	BF815279	BF815279 RC5-C1014	C 475	14	4.5	979	5	CD514471
C 403	14	4.5	480	14	DU840104	DU840104 MUGQ-CH25	C 476	14	4.5	1023	3	BQ048974
C 404	14	4.5	483	1	AI831926	AI831926 wh89a12.X	C 477	14	4.5	1217	14	DU800092
C 405	14	4.5	485	3	BM992299	BM992299 UT-H-DF1-	C 478	14	4.5	1226	3	BQ895921
C 406	14	4.5	490	11	AQ146105	AQ146105 HS 2224-A	C 479	14	4.5	1266	6	CR627306
C 407	14	4.5	490	11	AQ587033	AQ587033 RPC1-11-4	C 480	13	4.2	157	7	BE154307
C 408	14	4.5	500	11	AQ114379	AQ114379 CIT-HSP-2	C 481	13	4.2	165	2	BF881282
C 409	14	4.5	503	11	AQ038737	AQ038737 CIT-HSP-2	C 482	13	4.2	165	2	BI038371
C 410	14	4.5	516	8	CR747112	CR747112 CR747112	C 483	13	4.2	172	11	AQ260677
C 411	14	4.5	517	11	AQ378622	AQ378622 RPC1-11-1	C 484	13	4.2	182	7	AW051615
C 412	14	4.5	528	11	BO6811	BO6811 CSBL-95G5-U	C 485	13	4.2	196	14	DU823819
C 413	14	4.5	533	9	DB298072	DB298072 DB298072	C 486	13	4.2	197	12	CS539407
C 414	14	4.5	534	4	BA473764	BA473764 DKF2P686A	C 487	13	4.2	208	1	AA076473
C 415	14	4.5	538	7	AW974104	AW974104 EST386207	C 488	13	4.2	214	12	CG502403
C 416	14	4.5	539	12	BZ602944	BZ602944 WHABT92TF	C 489	13	4.2	219	7	BE140860
C 417	14	4.5	541	9	DB335014	DB335014 DB335014	C 490	13	4.2	225	8	CN359798
C 418	14	4.5	545	5	CD674240	CD674240 f808007.Y	C 491	13	4.2	231	11	AZ757366
C 419	14	4.5	545	11	AQ769267	AQ769267 HS 3222-A	C 492	13	4.2	231	11	AZ757366
C 420	14	4.5	557	11	AQ387469	AQ387469 RPC111-14	C 493	13	4.2	235	8	CN871609
C 421	14	4.5	562	9	DA100027	DA100027 DA100027	C 494	13	4.2	237	10	DA441820
C 422	14	4.5	563	9	DA079516	DA079516 DA079516	C 495	13	4.2	245	2	BG008332
C 423	14	4.5	563	9	DA386065	DA386065 DA386065	C 496	13	4.2	247	11	AQ278518
C 424	14	4.5	563	9	DB298429	DB298429 DB298429	C 497	13	4.2	255	2	BF748499
C 425	14	4.5	564	2	BG502472	BG502472 602550080	C 498	13	4.2	258	12	CG425392
C 426	14	4.5	565	7	AW581679	AW581679 CM0-PT004	C 499	13	4.2	261	1	AA654212
C 427	14	4.5	565	11	AQ561039	AQ561039 HS 5342-B	C 500	13	4.2	263	8	CN276062
C 428	14	4.5	568	2	BF815598	BF815598 MR2-C1012	C 501	13	4.2	265	4	BY796113
C 429	14	4.5	569	9	DB228081	DB228081 DB228081	C 502	13	4.2	266	10	DA432193
C 430	14	4.5	573	1	AI904768	AI904768 I1-BT067-	C 503	13	4.2	267	7	AW798708
C 431	14	4.5	573	9	DB357134	DB357134 DB357134	C 504	13	4.2	282	2	BF997488
C 432	14	4.5	573	11	AQ159755	AQ159755 HS 5183-B	C 505	13	4.2	283	1	AV161763
C 433	14	4.5	574	11	AQ356602	AQ356602 CITBI-EI-	C 506	13	4.2	287	7	AW880331
C 434	14	4.5	582	7	AW993293	AW993293 RC2-BN003	C 507	13	4.2	289	7	AW169791
C 435	14	4.5	582	8	CR539972	CR539972 DKF2P4590	C 508	13	4.2	291	1	AI370877
C 436	14	4.5	602	4	CA331749	CA331749 c818602.Y	C 509	13	4.2	294	11	AQ095103
C 437	14	4.5	630	7	AW993000	AW993000 RC2-BN003	C 510	13	4.2	295	7	BE077803
C 438	14	4.5	650	9	DA863405	DA863405 DA863405	C 511	13	4.2	295	10	DA422335
C 439	14	4.5	653	11	AQ262542	AQ262542 CITBI-EI-	C 512	13	4.2	298	8	CN359797
C 440	14	4.5	653	14	AG137048	AG137048 Pan trogl	C 513	13	4.2	298	11	BG0195
C 441	14	4.5	666	11	AQ316957	AQ316957 CITBI-EI-	C 514	13	4.2	300	8	CV376371
C 442	14	4.5	676	14	AG116016	AG116016 Pan trogl	C 515	13	4.2	301	1	AA094823

516	13	4.2	302	11	AQ546562	CITBI-E1-	589	13	4.2	442	10	DR421957	DR421957 nav06b08.
C 517	13	4.2	304	10	N87454	L4284F Huma	590	13	4.2	442	11	B73429	B73429 CIT-HSP-631
C 518	13	4.2	310	7	BE151713	PM1-HT030	591	13	4.2	442	12	CG668943	CG668943 OST745402
519	13	4.2	314	3	BU927594	AGENCOURT	C 592	13	4.2	443	11	AQ478403	AQ478403 RPCI-11-2
520	13	4.2	320	11	AQ235083	HS-2052 B	C 593	13	4.2	444	11	B69124	B69124 CIT-HSP-205
521	13	4.2	324	8	CR546446	DKFZp459P	C 594	13	4.2	447	2	B1042784	B1042784 CM4-OT015
C 522	13	4.2	330	7	BE078022	CM1-BT061	C 595	13	4.2	447	10	N39004	N39004 Y221n08.e81
C 523	13	4.2	333	11	AZ757286	ew05h03.x	C 596	13	4.2	448	11	AQ592228	AQ592228 HS 5434 A
C 524	13	4.2	333	11	AZ757297	ew06a02.x	C 597	13	4.2	449	7	AW903779	AW903779 CM4-NN103
C 525	13	4.2	333	11	AZ757462	ew04f12.x	C 598	13	4.2	450	11	AQ237341	AQ237341 RPCI-11-65
526	13	4.2	338	11	B69648	CIT-HSP-200	C 599	13	4.2	451	11	AQ223735	AQ223735 HS 2005 B
527	13	4.2	344	12	CG505012		C 600	13	4.2	451	10	N25037	N25037 YW40a07.e81
528	13	4.2	346	11	AQ442886	OST59868	C 601	13	4.2	456	5	CF136608	CF136608 UI-HF-BN0
C 529	13	4.2	347	7	AW277109	XP62G08.x	C 602	13	4.2	456	8	CA484836	CA484836 hx19d06.y
530	13	4.2	348	2	B1030671	IL5-MT026	C 603	13	4.2	459	1	AI124584	AI124584 am59b01.x
531	13	4.2	349	10	H90688	YV03d01.e1	C 604	13	4.2	460	2	BF812253	BF812253 QV1-CI017
532	13	4.2	350	10	DW466666	HACG0079	C 605	13	4.2	461	1	AL707727	AL707727 DKFZp686F
C 533	13	4.2	351	1	AI439910	t157h05.x	C 606	13	4.2	462	1	AL041407	AL041407 DKFZp434C
C 534	13	4.2	358	2	BF766167	IL2-CS005	C 607	13	4.2	468	1	AV648864	AV648864 AV648864
C 535	13	4.2	362	10	N85265	J3017F Huma	C 608	13	4.2	468	11	AQ262065	AQ262065 CITBI-E1-
536	13	4.2	368	10	F35650	HSPD32475 H	C 609	13	4.2	470	7	BE653351	BE653351 UI-M-AL1-
537	13	4.2	371	7	BE079595	RCS-BT062	C 610	13	4.2	475	3	BQ682550	BQ682550 AGENCOURT
538	13	4.2	373	2	BF964305	PM3-NN117	C 611	13	4.2	475	3	BU190338	BU190338 AGENCOURT
C 539	13	4.2	374	1	AA485858	ab10h06.x	C 612	13	4.2	475	7	BE144859	BE144859 CM3-HT018
C 540	13	4.2	375	8	CN871155	010419AAP	C 613	13	4.2	476	2	BG572043	BG572043 602592510
541	13	4.2	375	8	CN871173	010419AAP	C 614	13	4.2	476	11	AQ376566	AQ376566 RPCI-11-1
C 542	13	4.2	379	8	CN871926	010201AAP	C 615	13	4.2	477	1	AL601984	AL601984 DKFZp313H
543	13	4.2	381	3	BQ303871	RC1-BT025	C 616	13	4.2	480	11	AQ352947	AQ352947 CITBI-E1-
544	13	4.2	383	7	BE144235	MRO-HT016	C 617	13	4.2	481	9	DA156104	DA156104 DA156104
545	13	4.2	383	11	AQ240777	CIT-HSP-2	C 618	13	4.2	483	4	CB164760	CB164760 K-EST0226
C 546	13	4.2	385	2	B1044592	CMO-OT021	C 619	13	4.2	484	10	W80145	W80145 me91g01.r1
C 547	13	4.2	386	11	B98825	CIT-HSP-228	C 620	13	4.2	489	11	B45405	B45405 HS-1061-A1-
548	13	4.2	388	4	CA873163	K0923C07-	C 621	13	4.2	489	11	AQ532428	AQ532428 RPCI-11-3
C 549	13	4.2	391	11	AQ138631	HS 3070 B	C 622	13	4.2	489	11	AL039515	AL039515 DKFZp434B
C 550	13	4.2	395	11	AQ081511	RPCI11-54	C 623	13	4.2	499	3	BP398601	BP398601 BP398601
C 551	13	4.2	396	7	AW903685	CM4-NN103	C 624	13	4.2	503	1	AL601843	AL601843 DKFZp313J
C 552	13	4.2	397	11	AQ043028	CIT-HSP-2	C 625	13	4.2	507	3	BP422702	BP422702 BP422702
553	13	4.2	398	7	BE067033	PM4-BT034	C 626	13	4.2	510	1	AI821342	AI821342 YC12b04.x
C 554	13	4.2	400	1	AA662986	ac52c01.8	C 627	13	4.2	510	2	BG060200	BG060200 QV4-GN025
555	13	4.2	402	3	BQ292976	MRI-AN003	C 628	13	4.2	513	7	AW814317	AW814317 MR3-ST020
556	13	4.2	402	12	CG555414	OST170007	C 629	13	4.2	513	7	AW814351	AW814351 MR0-HT020
557	13	4.2	403	2	BF821928	MRI-RT004	C 630	13	4.2	513	7	BE146296	BE146296 MRO-ST020
C 558	13	4.2	405	11	B87341	RPCI11-28J1	C 631	13	4.2	513	9	DB355391	DB355391 DB355391
559	13	4.2	409	1	AI820553	YC12b04.y	C 632	13	4.2	515	11	AQ318236	AQ318236 RPCI11-11
C 560	13	4.2	410	9	DB299527	DB299527	C 633	13	4.2	516	7	BE072633	BE072633 PM4-BT054
C 561	13	4.2	411	1	AA485767	ab10b06.x	C 634	13	4.2	518	5	CK003484	CK003484 AGENCOURT
562	13	4.2	411	11	AQ024789	HS 2182 B	C 635	13	4.2	520	3	BQ372742	BQ372742 PM3-FT002
563	13	4.2	411	1	AA720913	nm12a01.8	C 636	13	4.2	520	9	DB349546	DB349546 DB349546
C 564	13	4.2	412	12	CG585601	OST262197	C 637	13	4.2	520	11	AQ174753	AQ174753 HS 3211 A
565	13	4.2	413	1	AA555311	nk79e06.8	C 638	13	4.2	523	1	AA461475	AA461475 zx68f08.8
566	13	4.2	416	1	AA236552	nc26e11.x	C 639	13	4.2	523	9	DB327798	DB327798 DB327798
567	13	4.2	416	11	AQ066613	HS 3237 B	C 640	13	4.2	524	11	AQ019171	AQ019171 CIT-HSP-2
568	13	4.2	417	1	AA720913	nm12a01.8	C 641	13	4.2	524	11	AQ616055	AQ616055 HS 5147 A
C 569	13	4.2	417	1	AI052454	oz07g11.x	C 642	13	4.2	525	2	BI018952	BI018952 IL3-MT026
C 570	13	4.2	417	8	CN332751	170005322	C 643	13	4.2	526	9	DB059313	DB059313 DB059313
C 571	13	4.2	419	8	CN332750	170005999	C 644	13	4.2	527	11	AQ583965	AQ583965 RPCI-11-4
572	13	4.2	420	7	AW903764	CM4-NN103	C 645	13	4.2	527	11	AQ04694	AQ04694 HS 3094 A
C 573	13	4.2	423	11	B99999	CIT-HSP-217	C 646	13	4.2	531	8	CR544088	CR544088 DKFZp470L
C 574	13	4.2	426	1	AI914748	tr01e09.x	C 647	13	4.2	532	7	BE56219	BE56219 UI-M-BH0
575	13	4.2	426	11	AQ672999	HS 5460 A	C 648	13	4.2	532	11	AQ261863	AQ261863 CITBI-E1-
C 576	13	4.2	426	12	BZ611571	WHAAQ38TF	C 649	13	4.2	533	7	BE079585	BE079585 RCS-BT062
C 577	13	4.2	427	4	BA487434	DKFZp6860	C 650	13	4.2	533	11	AQ276171	AQ276171 CITBI-E1-
578	13	4.2	428	1	AA262224	nc26e11.8	C 651	13	4.2	535	9	DB325343	DB325343 DB325343
C 579	13	4.2	429	11	AQ080608	CIT-HSP-2	C 652	13	4.2	536	11	AQ702002	AQ702002 HS 5400 B
580	13	4.2	430	9	DA111706	DA111706	C 653	13	4.2	537	3	BQ287970	BQ287970 IK37g10.x
C 581	13	4.2	432	11	AQ060107	CIT-HSP-2	C 654	13	4.2	537	7	BE079466	BE079466 RCS-BT062
C 582	13	4.2	434	7	AW076036	xa83d06.x	C 655	13	4.2	537	11	AQ431177	AQ431177 HS 5127 A
583	13	4.2	435	11	AQ352406	CITBI-E1-	C 656	13	4.2	538	5	CK819362	CK819362 if14c12.y
C 584	13	4.2	436	11	AQ471844	CITBI-E1-	C 657	13	4.2	539	7	AW957572	AW957572 EST369642
C 585	13	4.2	437	11	AQ368554	HS 5037 A	C 658	13	4.2	541	11	AQ392404	AQ392404 CITBI-E1-
C 586	13	4.2	438	10	F23304	HSPD20757 H	C 659	13	4.2	542	4	BX507790	BX507790 DKFZp6860
C 587	13	4.2	439	8	CN269465	170005999	C 660	13	4.2	543	2	BM127912	BM127912 if11a06.x
C 588	13	4.2	439	9	DB371267	DB371267	C 661	13	4.2	543	2	BM128228	BM128228 if11b06.y

808	13	4.2	989	11	AQ937652	AQ937652 NB6-242C	881	12	3.8	195	2	BI055758	BI055758 PM2-GN001
809	13	4.2	1054	3	BU899258	BU899258 AGENCOURT	882	12	3.8	195	11	B76067	B76067 RPC111-13H1
810	13	4.2	1057	6	CF596895	CF596895 full-leng	c 883	12	3.8	196	10	N87943	N87943 K0843F Huma
811	13	4.2	1107	5	CD523408	CD523408 AGENCOURT	884	12	3.8	197	7	AW377702	AW377702 PMO-CT023
812	13	4.2	1129	2	EG391224	EG391224 602417258	885	12	3.8	199	11	B30819	B30819 HS-1003-A2-
813	13	4.2	1170	6	AF113695	AF113695 Homo sapi	886	12	3.8	202	7	AW903663	AW903663 CM4-NN103
814	13	4.2	1177	4	BX437751	BX437751 BX437751	887	12	3.8	205	3	AA096400	AA096400 19529.seq
815	13	4.2	1655	7	BF678975	BF678975 602153613	c 888	12	3.8	205	3	BP425903	BP425903 BP425903
816	13	4.2	1863	6	CF599842	CF599842 full-leng	c 889	12	3.8	206	1	AA652910	AA652910 ns68b09.8
817	13	4.2	10778	6	CF936627	CF936627 Homo sapi	c 890	12	3.8	206	1	AA678616	AA678616 ah03c11.8
818	12	3.8	85	14	AG199713	AG199713 Pan trogl	891	12	3.8	207	7	BF094378	BF094378 CM4-UT004
819	12	3.8	109	2	BI038245	BI038245 IL3-NT028	c 892	12	3.8	207	11	AQ584544	AQ584544 RPC11-11-4
820	12	3.8	117	1	AA228794	AA228794 nc14e03.8	c 893	12	3.8	209	1	AI719295	AI719295 ag45h01.x
821	12	3.8	119	2	BG949671	BG949671 RC4-BT068	c 894	12	3.8	210	7	BF876369	BF876369 CM4-ET009
822	12	3.8	123	2	BF884711	BF884711 PM3-ET015	c 895	12	3.8	211	10	T12047	T12047 A760F Heart
823	12	3.8	123	10	T18553	T18553 hbce2055 Hum	896	12	3.8	212	4	BX484546	BX484546 DKFZp686H
824	12	3.8	134	2	BZ601802	BZ601802 WHAC059TR	897	12	3.8	213	8	CN278330	CN278330 170006002
825	12	3.8	134	2	EG997705	EG997705 CM0-HT129	c 898	12	3.8	214	3	BQ358346	BQ358346 CM1-HT087
826	12	3.8	139	2	BI060773	BI060773 IL3-UT011	c 899	12	3.8	215	7	AW995565	AW995565 QVO-BN004
827	12	3.8	139	2	BI060777	BI060777 IL3-UT011	c 900	12	3.8	216	2	BF760249	BF760249 CM1-CT063
828	12	3.8	141	1	AI886299	AI886299 wme6f10.x	c 901	12	3.8	216	2	BF802791	BF802791 CM0-CI013
829	12	3.8	142	2	BF842772	BF842772 QV2-HT101	c 902	12	3.8	216	7	AV741309	AV741309 AV741309
830	12	3.8	142	11	AQ198305	AQ198305 RPC111-47	c 903	12	3.8	217	2	EG007863	EG007863 RC4-GN008
831	12	3.8	142	11	AQ474525	AQ474525 CITBI-EL-	c 904	12	3.8	217	2	BG984286	BG984286 PMO-CN015
832	12	3.8	143	14	AG189524	AG189524 Pan trogl	c 905	12	3.8	217	3	BQ340821	BQ340821 RC4-NN026
833	12	3.8	144	10	DM459774	DM459774 HHAGE0565	c 906	12	3.8	217	11	AQ017363	AQ017363 CIT-HSP-2
834	12	3.8	146	2	BF994639	BF994639 CM0-GN010	c 907	12	3.8	220	2	BG949673	BG949673 RC4-BT068
835	12	3.8	146	3	BQ378402	BQ378402 CM4-UT000	c 908	12	3.8	220	4	C15811	C15811 C15811 Clon
836	12	3.8	147	3	BU662499	BU662499 cl86h09.z	c 909	12	3.8	221	2	BF847991	BF847991 IL5-EN008
837	12	3.8	148	8	CN271778	CN271778 170005999	c 910	12	3.8	221	2	BG956235	BG956235 QV1-CT075
838	12	3.8	150	5	CD299176	CD299176 AGENCOURT	c 911	12	3.8	221	2	BG983430	BG983430 IL5-CN006
839	12	3.8	155	11	AQ480419	AQ480419 RPC11-11-2	c 912	12	3.8	221	7	AW947021	AW947021 RC3-CT002
840	12	3.8	156	11	B51814	B51814 CIT-HSP-384	c 913	12	3.8	222	7	BE154769	BE154769 PM3-HT034
841	12	3.8	158	3	BU960103	BU960103 AGENCOURT	c 914	12	3.8	224	1	AA364546	AA364546 EST75147
842	12	3.8	158	11	AZ576016	AZ576016 AST-T33D0	c 915	12	3.8	226	1	AA321741	AA321741 EST24270
843	12	3.8	159	1	AA077952	AA077952 7H11F08 C	c 916	12	3.8	226	2	BI011083	BI011083 QV2-EN009
844	12	3.8	164	2	BF964071	BF964071 PM4-NN120	c 917	12	3.8	227	2	BF829536	BF829536 MR2-HN003
845	12	3.8	165	14	AG192925	AG192925 Pan trogl	c 918	12	3.8	227	2	BF960188	BF960188 CM2-NN024
846	12	3.8	167	7	BF478314	BF478314 nae48b02.	c 919	12	3.8	227	2	BG982899	BG982899 PMO-CN015
847	12	3.8	168	1	AA748121	AA748121 nx79g01.8	c 920	12	3.8	227	10	DM444068	DM444068 HHAGE0417
848	12	3.8	168	1	AI989742	AI989742 wu21f02.x	c 921	12	3.8	228	2	BF935292	BF935292 CM1-NT024
849	12	3.8	168	3	BU540275	BU540275 AGENCOURT	c 922	12	3.8	228	2	BG960688	BG960688 RC4-CT065
850	12	3.8	168	7	AW364838	AW364838 QV3-DT004	c 923	12	3.8	228	7	AW571410	AW571410 xx87c03.x
851	12	3.8	169	10	DM456252	DM456252 HHAGE0529	c 924	12	3.8	228	11	AQ029673	AQ029673 RPC111-40
852	12	3.8	170	10	DM456105	DM456105 HHAGE0528	c 925	12	3.8	229	2	BF873158	BF873158 CM0-ET012
853	12	3.8	170	11	AZ537231	AZ537231 AST-2F030	c 926	12	3.8	229	10	DR980303	DR980303 SN016028
854	12	3.8	171	2	BF994638	BF994638 CM0-GN010	c 927	12	3.8	229	10	DM443350	DM443350 HHAGE0413
855	12	3.8	171	3	BQ023882	BQ023882 UT-1-BB1P	c 928	12	3.8	229	11	AQ491143	AQ491143 RPC111-2
856	12	3.8	171	8	CN294007	CN294007 170006002	c 929	12	3.8	230	1	AA483497	AA483497 ne40a01.8
857	12	3.8	172	2	BF842188	BF842188 RC6-HT084	c 930	12	3.8	230	2	BG982907	BG982907 PMO-CN015
858	12	3.8	172	2	BF994635	BF994635 CM0-GN010	c 931	12	3.8	230	10	DM443549	DM443549 HHAGE0412
859	12	3.8	172	10	DM455785	DM455785 HHAGE0525	c 932	12	3.8	231	1	AI400912	AI400912 th30h05.x
860	12	3.8	173	2	BI054142	BI054142 CM4-GN032	c 933	12	3.8	231	10	DM443349	DM443349 HHAGE0408
861	12	3.8	175	2	BG983538	BG983538 PMO-CN015	c 934	12	3.8	231	11	AQ631032	AQ631032 RPC11-11-4
862	12	3.8	176	10	DM455134	DM455134 HHAGE0518	c 935	12	3.8	232	1	AA229354	AA229354 nc47e04.x
863	12	3.8	179	1	AA403309	AA403309 zt44f02.8	c 936	12	3.8	233	10	DM442889	DM442889 HHAGE0406
864	12	3.8	179	10	DM454685	DM454685 HHAGE0514	c 937	12	3.8	234	2	BP915265	BP915265 MR3-UT012
865	12	3.8	180	1	AI821574	AI821574 zt44f02.x	c 938	12	3.8	234	3	BQ376365	BQ376365 CM1-TN014
866	12	3.8	180	7	BF108740	BF108740 7145D04.x	c 939	12	3.8	234	10	DM460572	DM460572 n4273 Hum
867	12	3.8	181	8	CR748046	CR748046 CR748046	c 940	12	3.8	234	10	DM442386	DM442386 HHAGE0401
868	12	3.8	182	7	AW979337	AW979337 EST391447	c 941	12	3.8	234	10	DM442390	DM442390 HHAGE0401
869	12	3.8	185	1	AA339714	AA339714 EST44902	c 942	12	3.8	234	11	AQ200492	AQ200492 RPC111-63
870	12	3.8	185	1	AA363216	AA363216 EST73035	c 943	12	3.8	235	7	BE076399	BE076399 CM0-BT059
871	12	3.8	186	12	BZ630096	BZ630096 UP_305-20	c 944	12	3.8	236	10	DR979854	DR979854 SN015263
872	12	3.8	187	2	BG959839	BG959839 CM2-CT077	c 945	12	3.8	238	2	BF756654	BF756654 CM0-CT012
873	12	3.8	188	11	B88207	B88207 CIT-HSP-384	c 946	12	3.8	238	2	BI014074	BI014074 CM0-ET012
874	12	3.8	191	2	BF991536	BF991536 MR3-GN014	c 947	12	3.8	238	2	BI027044	BI027044 CM3-MT029
875	12	3.8	191	14	AG192049	AG192049 Pan trogl	c 948	12	3.8	239	2	BI044291	BI044291 CM0-OT021
876	12	3.8	192	2	BF802526	BF802526 CM0-CT013	c 949	12	3.8	239	10	DM440098	DM440098 HHAGE0388
877	12	3.8	193	10	F04504	F04504 HSC2PD042 n	c 950	12	3.8	240	1	AA878416	AA878416 oel4f06.8
878	12	3.8	195	1	AA631414	AA631414 np85a06.8	c 951	12	3.8	240	1	AA494030	AA494030 ns60d03.8
879	12	3.8	195	1	AA291378	AA291378 zt44f02.x	c 952	12	3.8	240	2	BG996664	BG996664 PMO-HT091
880	12	3.8	195	2	BI036506	BI036506 RC5-NT018	c 953	12	3.8	240	10	DM440074	DM440074 HHAGE0388

954	12	3.8	240	14	AG203419	AG203419 Pan trogl	1027	12	3.8	271	14	DU637414	DU637414
955	12	3.8	241	8	CV330284	CV330284 IL2-UT007	CI028	12	3.8	272	2	BG003208	BG003208
956	12	3.8	241	10	DW439505	DW439505 HHAGE0382	CI029	12	3.8	273	1	AA381390	AA381390
957	12	3.8	241	11	AQ058830	AQ058830 RPT111-53	CI030	12	3.8	273	1	BA214045	BA214045
958	12	3.8	242	7	BF565303	BF565303 UT-R-BOL-	1031	12	3.8	273	2	BI027079	BI027079
959	12	3.8	242	10	DW439429	DW439429 HHAGE0381	1032	12	3.8	273	10	DW429121	DW429121
960	12	3.8	242	10	DW439481	DW439481 HHAGE0382	1033	12	3.8	274	1	AA603385	AA603385
961	12	3.8	243	10	DW438930	DW438930 HHAGE0376	CI034	12	3.8	274	2	BF925640	BF925640
962	12	3.8	243	10	DW438931	DW438931 HHAGE0376	CI035	12	3.8	275	1	AI348731	AI348731
963	12	3.8	244	1	AA309473	AA309473 EST180342	CI036	12	3.8	275	10	DW428447	DW428447
964	12	3.8	244	1	AA366847	AA366847 EST77847	CI037	12	3.8	275	11	AQ107577	AQ107577
965	12	3.8	244	1	AA502225	AA502225 ne94a10.s	1038	12	3.8	276	7	AW269071	AW269071
966	12	3.8	244	10	DW438743	DW438743 HHAGE0374	1039	12	3.8	276	11	AQ070290	AQ070290
967	12	3.8	245	7	BE859084	BE859084 7g47g09.x	1040	12	3.8	277	1	AA862014	AA862014
968	12	3.8	246	2	BF841555	BF841555 PM2-HT035	CI041	12	3.8	277	10	AI762237	AI762237
969	12	3.8	248	1	AA730916	AA730916 NW50e01.s	CI042	12	3.8	277	10	TS9689	TS9689
970	12	3.8	249	1	AI250080	AI250080 QX70B01.x	1043	12	3.8	278	7	BE066250	BE066250
971	12	3.8	249	2	BI015294	BI015294 PM0-ET025	1044	12	3.8	278	2	BF822300	BF822300
972	12	3.8	249	7	AW793661	AW793661 MR1-UM000	1045	12	3.8	279	7	AW839236	AW839236
973	12	3.8	249	11	AZ051317	AZ051317 sit00024	CI046	12	3.8	280	6	AY927545	AY927545
974	12	3.8	250	2	BI497386	BI497386 df135912	1047	12	3.8	280	11	AQ261477	AQ261477
975	12	3.8	250	11	AQ260459	AQ260459 CITBI-EI-	CI048	12	3.8	281	1	AA653655	AA653655
976	12	3.8	251	1	AA664148	AA664148 ac04e07.s	1049	12	3.8	281	2	BF922017	BF922017
977	12	3.8	251	1	AA442533	AA442533 zv68b06.r	CI050	12	3.8	281	10	TS6181	TS6181
978	12	3.8	251	1	AA578931	AA578931 nf26e03.s	1051	12	3.8	281	11	B06911	B06911
979	12	3.8	251	3	BQ376495	BQ376495 CM1-TN014	1052	12	3.8	282	1	AA720750	AA720750
980	12	3.8	251	10	DW436730	DW436730 HHAGE0354	1053	12	3.8	282	1	AA316905	AA316905
981	12	3.8	251	10	DW436851	DW436851 HHAGE0355	1054	12	3.8	282	2	BF823598	BF823598
982	12	3.8	252	1	AA808996	AA808996 nf31d07.r	1055	12	3.8	282	7	AW236235	AW236235
983	12	3.8	252	1	AA827281	AA827281 of31c06.s	1056	12	3.8	282	10	DW426499	DW426499
984	12	3.8	253	2	BF957856	BF957856 PM0-NN117	1057	12	3.8	283	1	AL353981	AL353981
985	12	3.8	254	2	BF827978	BF827978 MR2-RN003	1058	12	3.8	283	10	DW426191	DW426191
986	12	3.8	255	1	AI053522	AI053522 Q172803.x	1059	12	3.8	283	11	AQ285012	AQ285012
987	12	3.8	256	1	AA626637	AA626637 ab51d07.r	1060	12	3.8	284	2	BG984284	BG984284
988	12	3.8	257	4	BX092806	BX092806 BX092806	1061	12	3.8	284	2	BI043646	BI043646
989	12	3.8	258	5	CK816229	CK816229 AGENCOURT	CI062	12	3.8	284	7	BE149223	BE149223
990	12	3.8	258	7	BE552064	BE552064 hy03d03.x	1063	12	3.8	284	10	DW425781	DW425781
991	12	3.8	258	11	AQ080118	AQ080118 CIT-HSP-2	1064	12	3.8	284	10	T39841	T39841
992	12	3.8	258	11	AQ096873	AQ096873 HS 3040 A	1065	12	3.8	284	11	BF927013	BF927013
993	12	3.8	259	1	AA077052	AA077052 7b07B04 C	1066	12	3.8	285	2	BF927013	BF927013
994	12	3.8	259	14	DU640659	DU640659 Cluffi-HI	CI067	12	3.8	285	3	BQ354660	BQ354660
995	12	3.8	259	14	DU641621	DU641621 Cluffi-HI	1068	12	3.8	285	4	BX099465	BX099465
996	12	3.8	259	14	DU641621	DU641621 Cluffi-HI	1069	12	3.8	286	2	BF897667	BF897667
997	12	3.8	260	2	BF956628	BF956628 602260315	CI070	12	3.8	286	7	BE148565	BE148565
998	12	3.8	260	8	CN277926	CN277926 170006001	1071	12	3.8	287	2	BF829109	BF829109
999	12	3.8	261	1	AI240919	AI240919 QK01804.x	1072	12	3.8	287	2	BI054859	BI054859
1000	12	3.8	261	13	CZ462743	CZ462743 MCF752n24	CI073	12	3.8	288	1	AI821185	AI821185
1001	12	3.8	262	10	DW433341	DW433341 HHAGE0320	1074	12	3.8	288	1	AA353897	AA353897
1002	12	3.8	262	11	AQ039320	AQ039320 CIT-HSP-2	1075	12	3.8	288	3	BU932309	BU932309
1003	12	3.8	262	11	AQ053655	AQ053655 RPT111-51	1076	12	3.8	288	7	AW194061	AW194061
1004	12	3.8	263	10	DW433067	DW433067 HHAGE0317	CI077	12	3.8	289	1	AA773289	AA773289
1005	12	3.8	263	11	AQ587757	AQ587757 CITBI-EI-	1078	12	3.8	289	1	AI266303	AI266303
1006	12	3.8	265	2	BF927037	BF927037 CM2-NT019	CI079	12	3.8	289	1	AA362037	AA362037
1007	12	3.8	266	8	CR529439	CR529439 DXFZp459E	CI080	12	3.8	289	2	BF843042	BF843042
1008	12	3.8	266	14	AG198085	AG198085 Pan trogl	CI081	12	3.8	289	2	BI012156	BI012156
1009	12	3.8	267	11	AQ019025	AQ019025 CIT-HSP-2	1082	12	3.8	290	2	BF836283	BF836283
1010	12	3.8	268	1	AI611902	AI611902 tL59h02.x	1083	12	3.8	290	7	AW132099	AW132099
1011	12	3.8	268	7	BE011871	BE011871 RCO-BN023	CI085	12	3.8	290	10	DR748263	DR748263
1012	12	3.8	268	11	BI51738	BI51738 CIT978SK-A-	1086	12	3.8	290	10	N87966	N87966
1013	12	3.8	268	11	AQ262717	AQ262717 CITBI-EI-	1087	12	3.8	291	4	CD105420	CD105420
1014	12	3.8	269	1	AA331804	AA331804 EST35669	1088	12	3.8	291	4	DR769182	DR769182
1015	12	3.8	269	2	BF810710	BF810710 RC3-CI016	1089	12	3.8	291	10	DW423415	DW423415
1016	12	3.8	269	10	DW431282	DW431282 HHAGE0300	1090	12	3.8	292	7	AW063449	AW063449
1017	12	3.8	269	10	DW431476	DW431476 HHAGE0302	CI090	12	3.8	292	8	CN392231	CN392231
1018	12	3.8	269	10	H93138	H93138 yt91c02.s	1091	12	3.8	292	11	AQ891008	AQ891008
1019	12	3.8	269	10	WB8906	WB8906 zh71d02.r	CI092	12	3.8	293	11	AQ101796	AQ101796
1020	12	3.8	269	11	B91507	B91507 CIT-HSP-217	1093	12	3.8	293	11	AQ261075	AQ261075
1021	12	3.8	270	1	AA303011	AA303011 EST114057	CI094	12	3.8	294	1	AI275183	AI275183
1022	12	3.8	270	7	AW806457	AW806457 MR4-UM011	1095	12	3.8	294	10	DW422368	DW422368
1023	12	3.8	270	11	AQ317737	AQ317737 RPT111-96	CI096	12	3.8	295	1	AA714073	AA714073
1024	12	3.8	271	1	AI680525	AI680525 tw82a07.x	CI097	12	3.8	295	1	AA077273	AA077273
1025	12	3.8	271	1	AI682310	AI682310 wc51e04.x	CI098	12	3.8	295	7	BE078083	BE078083
1026	12	3.8	271	7	AW817858	AW817858 PM4-ST026	CI099	12	3.8	295	10	H93386	H93386

c1100	12	3.8	295	11	AQ062628	AQ062628	CIT-HSP-2	1173	12	3.8	311	8	CV392393	CV392393	QV2-NN107
1101	12	3.8	296	1	AA889097	AA889097	am38907.8	c1174	12	3.8	311	10	F08866	F08866	HSC2TH072 n
1102	12	3.8	296	7	AW063118	AW063118	TN0255 KR	1175	12	3.8	312	1	AI733946	AI733946	qV52b11.x
1103	12	3.8	296	10	DV768403	DV768403	ILLUMIGEN	c1176	12	3.8	312	3	BQ364948	BQ364948	QV3-SN005
1104	12	3.8	296	10	DM421697	DM421697	HHAGE0214	c1177	12	3.8	312	5	CD692933	CD692933	EST9456 h
1105	12	3.8	296	10	DM421698	DM421698	HHAGE0214	c1178	12	3.8	312	10	DM415471	DM415471	HHAGE0162
1106	12	3.8	296	10	DM421748	DM421748	HHAGE0214	c1179	12	3.8	312	2	BF871412	BF871412	IL3-ET011
1107	12	3.8	297	2	BG999433	BG999433	PMO-HN007	c1180	12	3.8	313	2	BG982541	BG982541	IL3-CN006
1108	12	3.8	297	8	CN373148	CN373148	UI-H-DT1-	1181	12	3.8	313	3	BM995046	BM995046	UI-H-ED0-
1109	12	3.8	297	8	CN373148	CN373148	170005321	1182	12	3.8	313	3	DM415291	DM415291	HHAGE0160
1110	12	3.8	297	10	DM334690	DM334690	LPAGE0476	c1183	12	3.8	313	11	AQ567899	AQ567899	HS 2117 A
1111	12	3.8	297	10	DM421382	DM421382	HHAGE0211	c1184	12	3.8	314	2	BI016897	BI016897	PMO-ET025
1112	12	3.8	297	10	DM421454	DM421454	HHAGE0211	1185	12	3.8	315	3	BUS90392	BUS90392	AGENCOURT
1113	12	3.8	298	1	AA678628	AA678628	ah03f06.8	1186	12	3.8	315	10	DM414547	DM414547	HHAGE0152
1114	12	3.8	298	9	DB341814	DB341814	DE341814	1187	12	3.8	316	1	AL048199	AL048199	DKF2p586M
1115	12	3.8	298	10	DM421208	DM421208	HHAGE0209	c1188	12	3.8	316	2	BI004487	BI004487	MR4-HN005
1116	12	3.8	298	1	AA533554	AA533554	nj58h06.8	c1189	12	3.8	316	2	BI034407	BI034407	PM2-NN016
1117	12	3.8	299	7	AW271095	AW271095	xr48f06.x	c1190	12	3.8	316	3	BQ365766	BQ365766	RC4-GN008
1118	12	3.8	299	9	DA223801	DA223801	DA223801	1191	12	3.8	316	11	AQ027637	AQ027637	CIT-HSP-2
1119	12	3.8	299	11	AQ262399	AQ262399	CITBI-E1-	1192	12	3.8	317	1	AA662905	AA662905	nu32a04.8
1120	12	3.8	300	1	AA715850	AA715850	nv75b06.f	1193	12	3.8	317	1	AA416801	AA416801	zu08a03.f
1121	12	3.8	300	1	AI627970	AI627970	ty83d05.x	1194	12	3.8	317	10	T59475	T59475	yB63e03.r1
1122	12	3.8	300	3	BM688410	BM688410	UI-E-ClO-	c1195	12	3.8	317	11	AQ071396	AQ071396	HS 2265 B
1123	12	3.8	300	7	AW749329	AW749329	RC5-BT037	c1196	12	3.8	317	11	AZ521678	AZ521678	RFCI-11-1
1124	12	3.8	300	10	DM420416	DM420416	HHAGE0201	c1197	12	3.8	318	2	BF804938	BF804938	PM4-C1007
1125	12	3.8	301	1	AV710189	AV710189	AV710189	c1198	12	3.8	318	2	BF851160	BF851160	MR4-EN007
1126	12	3.8	301	1	AA515825	AA515825	nv64d05.8	1199	12	3.8	318	3	BUS35223	BUS35223	AGENCOURT
1127	12	3.8	301	10	DM420055	DM420055	HHAGE0197	c1200	12	3.8	318	7	AW855529	AW855529	CM4-CT027
1128	12	3.8	301	11	AQ052822	AQ052822	HS 3019 B	c1201	12	3.8	318	10	F00067	F00067	HSB10G061 S
1129	12	3.8	302	7	BE077822	BE077822	CM1-BT061	1202	12	3.8	318	10	F11080	F11080	HSC3FC112 n
1130	12	3.8	302	10	DM419703	DM419703	HHAGE0194	1203	12	3.8	319	5	CD520152	CD520152	AGENCOURT
1131	12	3.8	303	3	BQ712695	BQ712695	AGENCOURT	1204	12	3.8	319	5	CD520152	CD520152	AGENCOURT
1132	12	3.8	304	1	AA991824	AA991824	ot45c09.8	1205	12	3.8	320	3	BU8590349	BU8590349	AGENCOURT
1133	12	3.8	304	1	AI367948	AI367948	qm17c04.x	1206	12	3.8	320	3	BU858451	BU858451	AGENCOURT
1134	12	3.8	304	1	AI820539	AI820539	yc18f05.y	1207	12	3.8	320	10	F23285	F23285	HSP22437 H
1135	12	3.8	304	2	BF902289	BF902289	IL2-MT017	c1208	12	3.8	321	1	AI733930	AI733930	qV44b09.x
1136	12	3.8	304	2	AW302832	AW302832	xr56c02.x	c1209	12	3.8	321	2	BF990243	BF990243	MR2-BT116
1137	12	3.8	304	7	AW731919	AW731919	ba03a11.x	1210	12	3.8	321	3	BUS90349	BUS90349	AGENCOURT
1138	12	3.8	305	2	BF842823	BF842823	MR1-HT106	1211	12	3.8	321	3	BU958280	BU958280	AGENCOURT
1139	12	3.8	305	3	BQ639646	BQ639646	he18b11.y	1212	12	3.8	321	10	DM413079	DM413079	HHAGE0138
1140	12	3.8	305	10	DM417547	DM417547	HHAGE0182	1213	12	3.8	321	10	DM413099	DM413099	HHAGE0138
1141	12	3.8	305	10	DM417590	DM417590	HHAGE0183	1214	12	3.8	321	11	AQ063085	AQ063085	CIT-HSP-2
1142	12	3.8	305	11	AQ052783	AQ052783	RFC111-49	1215	12	3.8	321	11	AQ112923	AQ112923	CIT-HSP-2
1143	12	3.8	305	11	AQ071213	AQ071213	HS 5375 B	c1216	12	3.8	322	1	AI624212	AI624212	ts42d01.x
1144	12	3.8	306	1	AA229064	AA229064	nc45g08.f	c1217	12	3.8	322	1	AA319469	AA319469	EST21783
1145	12	3.8	306	1	AA321731	AA321731	EST24260	1218	12	3.8	322	2	EG985322	EG985322	PMO-CN015
1146	12	3.8	306	10	DM417380	DM417380	HHAGE0181	1219	12	3.8	323	1	AI792072	AI792072	ag60c04.y
1147	12	3.8	306	11	AQ052783	AQ052783	RFC111-49	1220	12	3.8	323	7	BF215916	BF215916	601881451
1148	12	3.8	307	1	AI440288	AI440288	tj01g08.x	1221	12	3.8	323	7	AW886014	AW886014	RC1-OT007
1149	12	3.8	307	2	BF886742	BF886742	PM4-TN017	1222	12	3.8	323	8	CN274511	CN274511	170006000
1150	12	3.8	307	2	BI051245	BI051245	CM4-GN036	1223	12	3.8	323	10	DM412593	DM412593	HHAGE0133
1151	12	3.8	307	11	AQ094249	AQ094249	HS 3022 B	c1224	12	3.8	324	2	EG008716	EG008716	RC2-GN026
1152	12	3.8	307	11	BA0578	BA0578	HS-1051-B2-	c1225	12	3.8	324	10	F08025	F08025	HSC3OC051 n
1153	12	3.8	308	1	AI284536	AI284536	qu23a07.x	1226	12	3.8	324	10	F31670	F31670	HSP230319 H
1154	12	3.8	308	1	AL699360	AL699360	DKF2p686G	1227	12	3.8	324	10	N74383	N74383	za52e08.s1
1155	12	3.8	308	1	AA65893	AA65893	EST76756	c1228	12	3.8	325	1	AI343123	AI343123	tb04e07.x
1156	12	3.8	308	2	BF884894	BF884894	PMO-ET020	1229	12	3.8	325	1	AI948984	AI948984	wq17h01.x
1157	12	3.8	308	7	AW023302	AW023302	df53a11.y	c1230	12	3.8	325	3	BUS06694	BUS06694	AGENCOURT
1158	12	3.8	308	10	DM416636	DM416636	HHAGE0173	1231	12	3.8	325	3	BF447405	BF447405	nae36607.
1159	12	3.8	308	10	DM416876	DM416876	HHAGE0176	c1232	12	3.8	325	11	B99390	B99390	CIT-HSP-228
1160	12	3.8	308	11	AZ519799	AZ519799	RFC1-11-7	c1233	12	3.8	325	11	B99390	B99390	CIT-HSP-228
1161	12	3.8	309	1	AI251563	AI251563	qv28d11.x	c1234	12	3.8	326	1	AA174141	AA174141	zp20h07.8
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1166	12	3.8	309	2	BM353513	BM353513	ig56b05.x	1239	12	3.8	327	1	AA229565	AA229565	nc15f03.s
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1168	12	3.8	309	7	AW375316	AW375316	PM1-CT015	1241	12	3.8	327	2	BI013226	BI013226	PMO-ET020
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ALIGNMENTS

RESULT 1

CR605305

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .1143

CR605305

full-length cDNA clone CS0D1022YK04 of Placent

of Homo sapiens (human)

1143 bp mRNA linear

HTC 21-JUL-2004

25-normalized

CR605305.1

GI:50486112

HTC; CNSLT_cDNA.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1143)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue

2 (bases 1 to 1143)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

Location/Qualifiers

1. .1143


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ORIGIN

Alignment Scores:
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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 85.9% Indels: 0
DB: 6 Gaps: 0

US-10-785-221-9 (1-312) x CR605305 (1-1143)
QY 1 MetAlaArgSerArgHisArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuValValAla 20
DB 224 ATGGCAGAGGAGGAGCGCCACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGCC 283
QY 21 LeuGlyTyrHisLysAlaTyrGlyPheSerAlaProLysAspGlnGlnValValThrAla 40
DB 284 CTGGGCTATCATTAAGGCTATGGGTTTCTGCCCAAGACCAACAAAGTAGTACAGCA 343
QY 41 ValGlyTyrGlnGluAlaLeuAlaCysLysThrProLysLysThrValSerSerArg 60
DB 344 GTAGAGTACCAGAGGCTATTTAGGCTGCAAAACCCCAAGAAAGACTGTTCTCCAGCA 403
QY 61 LeuGluTyrLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
DB 404 TTAGAGTGGAAAGAACTGGGTCGGAGTGCTCTCTTTGTCTACTATCAACAGACTCTTCAA 463
QY 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
DB 464 GGTGATTTTAAATTCAGCTGAGATGATAGATTTCATATCCGGATCAAAATGTGACA 523
QY 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlnAsn 120
DB 524 AGAAGTGATCGGGGAAATATCTGTAAGTTAGTGCCCATCTCGACCAAGGCCAAAC 583
QY 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
DB 584 CTGGAAGAGGATACAGTCACTCTGGAAGATTTAGTGGCTCCAGCAGTTCATCATGTGAA 643
QY 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
DB 644 GTACCCCTCTCTCTCTGAGTGGAACTGTGTGTAGAGCTACGATGTCAAGCAAGAGGG 703
QY 161 AsnProAlaProGluTyrThrTrpPheLysAspGlyIleArgLeuLeuGluAsnProArg 180
DB 704 AATCCAGCTCCTGAATACATCGTTTAAAGGATGGCATCCGTTTGTAGAAAATCCAGCA 763
QY 181 LeuGlySerGlnSerThrAsnSerSerTyrThrMetAsnThrLysThrGlyThrLeuGln 200
DB 764 CTTGGCTCCCAAGACCAACACAGCTCATACAAATGAATCAAAAACCTGGAACCTCGCAA 823
QY 201 PheAsnThrValSerLysLeuAspThrGlyGluTyrSerCysGluAlaArgAsnSerVal 220
DB 824 TTTTAACTGTTTCCAAACTGGACACTGGAGAAATATCTCTGTGAACCCCGCAATCTGTT 883
QY 221 GlyTyrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
DB 884 GGATATCGCAGGTTCTCTGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATC 943
QY 241 IleAlaAlaValValValAlaLeuValIleSerValCysGlyLeuGlyValCysTyr 260
DB 944 ATAGCAGCGTAGTAGTTGTGGCTTTAGTGATTTCCGTTTGTGGCTTGTGTATGCTAT 1003
QY 261 AlaGlnArgLysGlyTyrPheSer 268
DB 1004 GCTCAGAGGAAAGGCTACTTTTCA 1027
```

```
RESULT 2
CR618843
LOCUS
DEFINITION
CR618843 1329 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS01043YM24 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION
CR618843.1 GI:50499650
VERSION
HTC; CNSLT_CDNA.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 1329)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
REFERENCE
2 (bases 1 to 1329)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
1..1329
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS01043YM24"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 1.82e-237 Length: 1329
Score: 268.00 Matches: 268
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 85.9% Indels: 0
DB: 6 Gaps: 0

US-10-785-221-9 (1-312) x CR618843 (1-1329)
QY 1 MetAlaArgSerArgHisArgLeuLeuLeuLeuLeuLeuLeuLeuValValAla 20
DB 206 ATGGCAGAGGAGGAGCGCCACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGCC 265
QY 21 LeuGlyTyrHisLysAlaTyrGlyPheSerAlaProLysAspGlnGlnValValThrAla 40
DB 266 CTGGGCTATCATTAAGGCTATGGGTTTCTGCCCAAGACCAACAAAGTAGTACAGCA 325
QY 41 ValGluTyrGlnGluAlaIleLeuAlaCysLysThrProLysLysThrValSerSerArg 60
DB 326 GTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCCAAGAAAGACTGTTCTCTCCAGA 385
QY 61 LeuGluTyrLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
DB 386 TTAGAGTGGAGAAACTGGTCCGAGTGCTCTCTTTGTCTACTATCAACAGACTCTTCAA 445
QY 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
DB 446 GGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCATATATCCGGATCAAAATGTGACA 505
QY 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlnAsn 120
```



```
Db 506 AGAAGTGATCGGGGAAATATCGTTGTGAAGTTAGTGCCTCCCATCTGAGCAAGGCCAAAC 565
Qy 121 LeuGluGluAspThrValThrLeuGluValValValValAlaProSerCysGlu 140
Db 566 CTGGAAGAGGATACAGTCATCTCTGGAAGTATTAGTGCTCCAGCATGTTCCATCATGTGAA 625
Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
Db 626 GTACCCCTCTTCTGCTCTGAGTGAACCTGTGTAGAGTACGATGTCAAGACAAAGAAGGG 685
Qy 161 AspProAlaProGluThrThrTrpPheLysAspGlyIleArgLeuLeuGluAsnProArg 180
Db 686 AATCCAGCTCTGAATACACATGTTTAAAGATGGCATCCGTTGCTAGAAAAATCCAGA 745
Qy 181 LeuGlySerGlnSerThrAsnSerSerThrMetAsnThrLysThrGlyThrLeuGln 200
Db 746 CTTGGCTCCCAAGACCAACAGCTCATACAAATGAATACAAATACTGAACCTCTGCNA 805
Qy 201 PheAsnThrValSerLysLeuAspThrGlyGluThrSerCysGluAlaArgAsnSerVal 220
Db 806 TTTAATACTGTTTCCAACTGGACACTGGAGATATTCTGTGAGAGCCCGCAATTCGTT 865
Qy 221 GlyThrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
Db 866 GGATATCGCAGGTGCTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATC 925
Qy 241 IleAlaValValValValAlaLeuValIleSerValCysGlyLeuGlyValCysThr 260
Db 926 ATAGCAGCCGTAGTAGTTGGCCCTTAGTATTTCCGTTTGTGGCCTTGGTGTATGCTAT 985
Qy 261 AlaGlnArgLysGlyThrPheSer 268
Db 986 GCTCAGAGGAAGGCTACTTTTCA 1009

RESULT 3
CR621411
LOCUS full-length cDNA clone CS0DC022YA21 of Neuroblastoma Cot
DEFINITION 25-normalized of Homo sapiens (human).
ACCESSION CR621411.1 GI:50502218
VERSION HTC; CNSLT cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1465)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
REMARK Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1465)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1465
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC022YA21"
/tissue_type="Neuroblastoma Cot 25-normalized"
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ORIGIN
Alignment Scores: 1.99e-237 Length: 1465
Pred. No.: 268.00 Matches: 268
Score: 268.00 Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 85.9% Gaps: 0
DB: 6

US-10-785-221-9 (1-312) x CR621411 (1-1465)
Qy 1 MetAlaArgArgSerArgHisArgLeuLeuLeuLeuLeuArgTyrLeuValValAla 20
Db 423 ATGCGGAGGAGGAGCGCCACCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 482
Qy 21 LeuGlyThrHisLysAlaTyrGlyPheSerAlaProLysAspGlnGlnValValAla 40
Db 483 CTGGGCTATCATAGGCTATGCGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCGT 542
Qy 41 ValGluThrGlnGluAlaIleLeuAlaCysLysThrProLysLysThrValSerSerArg 60
Db 543 GTAGAGTACCACAGAGGCTATTTTAGCTGCAAAACCCCAAGAGAGACTGTTTCTCCAGA 602
Qy 61 LeuGluThrLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
Db 603 TTAGAGTGGAGAAACTGGGTGCGAGTGTCTCTTTGCTACTATCAACAGACTCTTCAA 662
Qy 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
Db 663 GGTGATTTTAAATAATCGAGCTGAGATGATAGATTCAATATCCGATCAAAATGTGACA 722
Qy 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlyGluAsn 120
Db 723 AGAAGTGTATCGGGGAAATATCGTTGTGAAGTTAGTGCCCATCTTGAGCAAGGCCAAAC 782
Qy 121 LeuGluGluAspThrValThrLeuGluValValLeuValAlaProAlaValProSerCysGlu 140
Db 783 CTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGCTCCAGCATGTTCCATCATGTGAA 842
Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
Db 843 GTACCCCTCTTCTGCTCTGAGTGAACCTGTGTAGAGTACGATGTCAAGCAAAAGAAGGG 902
Qy 161 AsnProAlaProGluThrThrTrpPheLysAspGlyIleArgLeuLeuGluAsnProArg 180
Db 903 AATCCAGCTCTCTGAATACACATGTTTAAAGGATGGCATCCGTTTGTGATAGAAATCCAGA 962
Qy 181 LeuGlySerGlnSerThrAsnSerSerThrMetAsnThrLysThrGlyThrLeuGln 200
Db 963 CTTGGCTCCCAAGACCAACACAGCTCATACACAAATGAATACAAATACTGGAACCTCGAA 1022
Qy 201 PheAsnThrValSerLysLeuAspThrGlyGluThrSerCysGluAlaArgAsnSerVal 220
Db 1023 TTTAATACTGTTTCCAACTGGACACTGGAGATATTCTCTGTGAAGCCCGCAATTCGTT 1082
Qy 221 GlyThrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
Db 1083 GGATATCGCAGGTGCTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATC 1142
Qy 241 IleAlaValValValValValAlaLeuValIleSerValCysGlyLeuGlyValCysThr 260
Db 1143 ATAGCAGCCGTAGTAGTTGGCCCTTAGTATTTCCGTTTGTGGCCTTGGTGTATGCTAT 1202
Qy 261 AlaGlnArgLysGlyThrPheSer 268
Db 1203 GCTCAGAGGAAGGCTACTTTTCA 1226

RESULT 4
CR599894
LOCUS full-length cDNA clone CS0D1025YK19 of Placenta Cot 25-normalized
DEFINITION
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```
Score: 268.00 Matches: 268
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 85.9% Indels: 0
DB: 6 Gaps: 0

US-10-785-221-9 (1-312) x CR621227 (1-1511)

Qy 1 MetAlaArgArgSerArgHisArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuValAla 20
Db 395 ATGCGAGGAGGAGCGCCGCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 454

Qy 21 LeuGlyTyrHisLysAlaTyrGlyPheSerAlaProLysAspGlnGlnValAlaThrAla 40
Db 455 CTGGCTATCATAGGCTATGCGTTTCTGCCCAAAAGACCAACCAAGTAGTCACAGCA 514

Qy 41 ValGluTyrGlnGluAlaLeuAlaCysLysThrProLysLysThrValSerSerArg 60
Db 515 GTAGAGTACCAAGAGGCTATTTTACCTGCAAAACCCCAAGAGACTGTTTCTCCAGCA 574

Qy 61 LeuGluTyrLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
Db 575 TTAGAGTGGGAAGAACTGGGTCGAGTGTCTCTTGTCTACTATCAACAGACTCTTCAA 634

Qy 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgIleLysAsnValThr 100
Db 635 GGTGATTTTAAATATCAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 694

Qy 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlnGln 120
Db 695 AGAAGTGTATCGGGGAATATATCGTTGTGAAGTTAGTGCCTATCGCAAGGCAAAAC 754

Qy 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
Db 755 CTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCATCATGTGAA 814

Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
Db 815 GTACCTCTCTCTGCTGAGTGGAACTGTGTAGAGTACGATGTCAAGCAAGAGGG 874

Qy 161 AsnProAlaProGluTyrThrTyrPheLysAspGlyIleArgLeuLeuGluAsnProArg 180
Db 875 AATCCAGCTCTGTAATACATGCTTTAAGGATGGCATCCGTTTGTCTAGAAAAATCCAGCA 934

Qy 181 LeuGlySerGlnSerThrAsnSerSerTyrThrMetAsnThrLysThrGlyThrLeuGln 200
Db 935 CTGGCTCCCAAGACCAACAGCTCATACAAATGAATACAAAACTGGAACCTCTGCAA 994

Qy 201 PheAsnThrValSerLysLeuAspThrGlyGluTyrSerCysGluAlaArgAsnSerVal 220
Db 995 TTTAATACTGTTTCCAACTGGACACTGGAGATATTCTCTGTGAGGCCCGCAATCTGTT 1054

Qy 221 GlyTyrArgArgCysProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIle 240
Db 1055 GGATATCGCAGGTGCTCTGGGAACGAATCAAGTAGATGATCTCAACATAAGTGGCATC 1114

Qy 241 IleAlaValValValValValAlaLeuValIleSerValCysGlyLeuGlyValCysTyr 260
Db 1115 ATAGCAGCCGTAGTGTGTGGCCTTAGTATTTCCGTTTGTGGCCTTGGTGTATGCTAT 1174

Qy 261 AlaGlnArgLysGlyTyrPheSer 268
Db 1175 GCTCAGAGGAAGGCTACTTTTCA 1198

RESULT 6
CR610497
LOCUS CR610497 full-length cDNA clone CSODI078Y002 of Placenta Cot 25-normalized
DEFINITION Of Homo sapiens (human).
ACCESSION CR610497
VERSION CR610497.1 GI:50491304
KEYWORDS HTC; cNSLT cDNA.
SOURCE Homo sapiens (human)
```


Qy 161 AsnProAlaProGluTyrThrTrpPheLysAspGlyLeuArgLeuLeuGluAenProArg 180
 Db 971 AATCCAGCTCCTGAATACATGTTTAAAGATGGCATCCGTTTGTAGAAAATCCAGA 1030
 Qy 181 LeuGlySerGlnSerThrAenSerSerTyrThrMetAenThrLysThrGlyThrLeuGln 200
 Db 1031 CTGGCTCCCAAGCACCACAGCTCATACACATGAATACAAAACCTGGAATCTGCAA 1090
 Qy 201 PheAenThrValSerLysLeuAspThrGlyGluTyrSerCysGluAlaArgAenSerVal 220
 Db 1091 TTTAATACTGTTTCCAACTGGACATCGGAGATATTCCTGTGAAGCCGCAATTCGTT 1150
 Qy 221 GlyTyrArgCysProGlyLysArgMetGlnValAspLeuAenLysSerGlyLeu 240
 Db 1151 GGATATCGCAGGTCTCTGGGAACGAATGCAAGTAGATGATCTCAACATAAGTGGGATC 1210
 Qy 241 IleAlaAlaValValValValAlaLeuValLysValCysGlyLeuGlyValCysTyr 260
 Db 1211 ATAGCAGCCGTAGTAGTTGGCTTAGTGATTTCCGTTTGTGGCTTGTGTATGCTAT 1270
 Qy 261 AlaGlnArgLysGlyTyrPheSer 268
 Db 1271 GCTCAGAGGAAGGCTACTTTTCA 1294

RESULT 7
 BX089477
 LOCUS
 DEFINITION BX089477 Soares NHPu S1 Homo sapiens cDNA clone IMAGE998E031852 ;
 IMAGE:753386, mRNA sequence;
 ACCESSION BX089477
 VERSION BX089477.1 GI:27825974
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 678)
 Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
 Radloff,U., Schneider,D. and Korn,B.
 Human UnigeneSet - RZPD3
 Unpublished (2003)
 Contact: Ina Rofls
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGE998E031852.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human UnigeneSet - RZPD3 (RZPDLIB No.972)
 http://www.rzpd.de/CloneCards/cgi-
 bin/showlib.pl.cgi/responsefileNo=972 Contact: Ina Rofls
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTCAACAGGAACAGCTATGAC.

FEATURES
 source
 1..678
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE998E031852 ; IMAGE:753386"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /clone_lib="Soares,NHPu S1"
 /notes="Organ: mixed (see below); Vector: pT7T3D-Paci;
 Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid
 DNA from three normalized libraries (melanocyte 2NbHM,
 pregnant uterus NbHPU, and fetal heart NbHH19W) were

mixed, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subclonative
 hybridization reaction. The driver was PCR-amplified cDNAs
 from pools of 5,000 clones made from the same 3 libraries.
 The pools consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

ORIGIN

Alignment Scores:
 Pred. No.: 2,49e-179 Length: 678
 Score: 205.00 Matches: 205
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 65.7% Indels: 0
 DB: 4 Gaps: 0

US-10-785-221-9 (1-312) x BX089477 (1-678)

Qy 84 LysAenAtqAlaGluMetIleAspPheAenIleArgIleLysAenValThrArgSerAsp 103
 Db 2 AAAATCGAGCTGAGATAGATTTCAATATCCGATCAAAAATGTGACAGAAGTAT 61
 Qy 104 AlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlyGlnAenLeuGlu 123
 Db 62 GCGGGGAATATCGTTTGTGAAGTTAGTCCCATCTGAGCAAGGCCAAACCTGGAAGAG 121
 Qy 124 AspThrValThrLeuGluValValAlaProAlaValProSerCysGluValProSer 143
 Db 122 GATACAGTCACCTCTGGAAGTATTAGTGGCTCCAGCATTCATGTGAAGTACCTCT 181
 Qy 144 SerAlaLeuSerGlyThrValValGluLeuAryCysGlnAspLysGluGlyAenProAla 163
 Db 182 TCTGCTCTGAGTGGAACTGTGTAGAGCTACGATGTCAAGACAAAGAGGGAAATCCAGCT 241
 Qy 164 ProGluTyrThrTrpPheLysAspGlyIleArgLeuLeuGluAenProArgLeuGlySer 183
 Db 242 CCTGAATACACATGGTTTAAAGATGGCATCCGTTTGTAGAAAATCCAGACTTGGCTCC 301
 Qy 184 GlnSerThrAenSerSerTyrThrMetAenThrLysThrGlyThrLeuGlnPheAenThr 203
 Db 302 CAAAGCACCACAGCTCATACACAATGAATACAAAACCTGGAACCTGCAATTTAATACT 361
 Qy 204 ValSerLysLeuAspThrGlyGluTyrSerCysGluAlaArgAenSerValGlyTyrArg 223
 Db 362 GTTTCAAACTGGACACTGGAGAAATATCTCTGTGAAGCCCGCAATTTCTGTGATATCGC 421
 Qy 224 ArgCysProGlyLysArgMetGlnValAspAspLeuAenLysSerGlyIleLeuAla 243
 Db 422 AGGTGTCTCTGGGAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATATAGCAGCC 481
 Qy 244 ValValValAlaLeuValLysSerValCysGlyLeuGlyValCysTyrAlaGlnArg 263
 Db 482 GTAGTAGTTGTGGCTTGTAGTATTTCCGTTTGTGGCTTGTGTATGCTATGCTCAGAG 541
 Qy 264 LysGlyTyrPheSerLysGluThrSerPheGlnLysSerAenSerSerSerLysAlaThr 283
 Db 542 AAAGGCTACTTTTCAAAAGAAACCTCTTCCAGAGAGATATTTCTTCACTTAAGCCACG 601
 Qy 284 ThrMetSerGluAen 288
 Db 602 ACAATGAGTGAAT 616

RESULT 8
 BM704815
 LOCUS
 DEFINITION BM704815 648 bp mRNA linear EST 28-FEB-2002
 UI-E-C11-afp-o-07-0-UI-r2 UI-E-C11 Homo sapiens cDNA clone
 UI-E-C11-afp-o-07-0-UI 5', mRNA sequence.
 BM704815
 ACCESSION BM704815
 VERSION GI:19018073
 KEYWORDS Homo sapiens (human)
 SOURCE EST.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 6,53e-172 Length: 681
Score: 197.00 Matches: 197
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 63.1% Indels: 0
DB: 2 Gaps: 0

US-10-785-221-9 (1-312) x B1916904 (1-681)

```
Qy 1 MetAlaArgArgSerArgHisArgLeuLeuLeuLeuLeuLeuLeuLeuLeuValAla 20
Db 89 ATGGCGAGGAGGAGCGCCACCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
Qy 21 LeuGlyTyrHisLysAlaTyrGlyPheSerAlaProLysAspGlnGlnValValThra 40
Db 149 CTGGCTATCATAGGCTATGGCTTTCTGCCCAAAAGACCAACAAGTAGTCACAGCA 208
Qy 41 ValGluTyrGlnGluAlaLeuAlaCysLysThrProLysLysThrValSerSerArg 60
Db 209 GTGGAGTACCAGAGGCTATTTAGCCTGCAAAACCCCAAGAGACTGTTCTCCAGA 268
Qy 61 LeuGluTyrLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80
Db 269 TTAGAGTGGGAAGAACTGGGCTCGGAGTGCTCTCTTTGCTACTATCAACAGACTCTTCAA 328
Qy 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgLysAsnValThr 100
Db 329 GGTGATTTTAAATCAGCTGAGATGATAGATTTCAATATCCGATCAAAATGTGACA 388
Qy 101 ArgSerAspLagLysTyrArgCysGluValSerAlaProSerGluGlnGlnAsn 120
Db 389 AGAAGTGATCGGGGAATAATCGTTGTGAAGTTAGTGCCCACTCTGAGCAAGGCCAAAC 448
Qy 121 LeuGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140
Db 449 CTGGAGAGGATACAGTCACTCTGGAGATTTAGTGGCTCCAGACTTCCATCATGTGAA 508
Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
Db 509 GTACCTCTCTGCTCTGAGTGAACCTGTGTGAGAGCTACGATGTCAAGACAAAGAAGG 568
Qy 161 AsnProAlaProGluTyrThrTrpPheLysAspGlyIleArgLeuLeuGluAsnProArg 180
Db 569 AATCCAGCTCTCGAATACACATCGTTTAAGGATGGCATCGTTTGTGTAGAAATCCAGA 628
Qy 181 LeuGlySerGlnSerThrAsnSerSerTyrThrMetAsnThrLysThrGly 197
Db 629 CTGGCTCCCAAGACCAACAGCTCATACACATGAACAAACTGGA 679
```

RESULT 10

CB992775
LOCUS CB992775
DEFINITION AGENCOURT 13511610 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30334613 5', mRNA sequence.

ACCESSION CB992775

VERSION CB992775.1

KEYWORDS GI:30287295

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 811)

NIH-MGC <http://mgi.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM355 row: c column: 06
High quality sequence stop: 673.
Location/Qualifiers

FEATURES

source

1..811

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30334613"

/tissue_type="pre-eclampic placenta"

/lab_host="DH10B Tona"

/clone_lib="NIH_MGC_148"

/note="Organ: placenta; Vector: pBluescriptR; Site:1;

all-XhoI; Site 2: BamH; Library is oligo-dT primed and

directionally cloned using primer

5'-TTTTTTTCTTTTNN-3', size-selected for average insert

size 2.3 kb and normalized to ROT 5. This is a primary

library enriched for full-length clones and constructed

using the Cap-trapper method (Carninci, in preparation).

Library constructed by M. Brownstein (NHGRI/NHGRI,

National Institutes of Health). Note: this is a NIH_MGC

Library."

ORIGIN

Alignment Scores:

Pred. No.: 7,7e-172 Length: 811
Score: 197.00 Matches: 197
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 63.1% Indels: 0
DB: 4 Gaps: 0

US-10-785-221-9 (1-312) x CB992775 (1-811)

Qy 1 MetAlaArgArgSerArgHisArgLeuLeuLeuLeuLeuLeuLeuValAla 20

Db 137 ATGGCGAGGAGGAGCGCCACCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTG 196

Qy 21 LeuGlyTyrHisLysAlaTyrGlyPheSerAlaProLysAspGlnGlnValThra 40

Db 197 CTGGGCTATCATAGGCTATGGGTTTCTGCCCAAAAGACCAACAAGTAGTCACAGCA 256

Qy 41 ValGluTyrGlnGluAlaIleLeuAlaCysLysThrProLysLysThrValSerSerArg 60

Db 257 GTAGAGTACCAGAGGCTATTTAGCCTGCAAAACCCCAAGAGACTGTTCTCCAGA 316

Qy 61 LeuGluTyrLysLysLeuGlyArgSerValSerPheValTyrTyrGlnGlnThrLeuGln 80

Db 317 TTAGAGTGAAGAAACTGGGTCGGAGTGTCTCTTTTGTCTACTATCAACAGACTCTTCAA 376

Qy 81 GlyAspPheLysAsnArgAlaGluMetIleAspPheAsnIleArgLysLysValThr 100

Db 377 GGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCGATCAAAATGTGACA 436

Qy 101 ArgSerAspAlaGlyLysTyrArgCysGluValSerAlaProSerGluGlnGlnAsn 120

Db 437 AGAAGTGTATCGGGGAATATCGTTGTGAAGTTAGTGGCTCCAGCAGTTCATCATGTGAA 496

Qy 121 LeuGluGluAspThrValThrLeuGluValLeuValAlaProAlaValProSerCysGlu 140

Db 497 CTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCATCATGTGAA 556

Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuLeuArgCysGlnAspLysGluGly 160


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Qy 121 LeuGluGluAspThrValThrLeuGluValValAlaProAlaValProSerCysGlu 140
    |||||
Db 568 CTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCCATCATGTGAA 627

Qy 141 ValProSerSerAlaLeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGly 160
    |||||
Db 628 GTACCCCTTCTGCTCTGAGTGGAACTGTGTAGAGCTACGATGTCAGAGCAAAAGAGGG 687

Qy 161 AsnProAlaProGluTyrThrTTPPhelYsAspGlyLeuArgLeuLeuGluAsnProArg 180
    |||||
Db 688 AATCCAGCTCTGANTACATGTTTAAAGATGGCATCCGTTTGCTAGAAAAATCCCGA 747

Qy 181 LeuGlySerGlnSer 185
    |||||
Db 748 CTTGGCTCCCAAGC 762

RESULT 14
CK004092
LOCUS
DEFINITION
AGENCOURT 16379762 NIH MGC 228 Homo sapiens cDNA clone
IMAGE:30719346 5', mRNA sequence.
CK004092
CK004092.1 GI:38530134
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 623)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: csapbs-r@mail.nih.gov
Tissue Procurement: Professor Miklos Palkovits
cDNA Library Preparation: Michael Brownstein / Ted Usdin
Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM264 row: a column: 19
High quality sequence stop: 546.
FEATURES
source
1..623
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30719346"
/tissue_type="Human Brain - Cerebellar Cortex"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_228"
/notes="Organ: brain/CNS; Vector: pDNR-LIB; Site 1: SfII
(directional); Site 2: SfII (directional); Library is
oligo-dr primed and directionally cloned.5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGACGATGGCATTCAGCGCGG-3'5'-ATTCTAGAGG
CCGAGCGCGGCATG-d(T)3N-IN-3. Full-length enriched
library was constructed using the Clontech Creator SMART
kit and size-selected for >0.5kb with an average insert
size of 1.2kb Library created in the laboratory of
Jonathan Kuo and Ted Usdin."
ORIGIN
Alignment Scores:
Pred. No.: 623 Length: 623
Score: 184.00 Matches: 184

```

```

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 59.0% Indels: 0
DB: 5 Gaps: 0

US-10-785-221-9 (1-312) x CK004092 (1-623)

Qy 87 AlaGluMetIleAspPheAenIleAArgIleYsAsnValThrArgSerAspAlaGlyLys 106
    |||||
Db 5 GCTGAGATGATAGATTTCATATCCGGATCAAAATGTGCAAGAGTGTGCGGGAAA 64

Qy 107 TyrArgCysGluValSerAlaProSerGluGlnGlyGlnAsnLeuGluAspThrVal 126
    |||||
Db 65 TATCGTTGTGAAGTTAGTGGCCCATCTGAGCAAGGCCAAACCTGGGAAGAGGTACAGTC 124

Qy 127 ThrLeuGluValLeuValAlaProAlaValProSerCysGluValProSerSerAlaLeu 146
    |||||
Db 125 ACTCTGGAAGTATTAGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCGCTCTG 184

Qy 147 SerGlyThrValValGluLeuArgCysGlnAspLysGluGlyAsnProAlaProGluTyr 166
    |||||
Db 185 AGTGGAACTGTGTAGAGCTACGATGTCAGACAAAGAGGAATCCAGCTCCTGNAATAC 244

Qy 167 ThrTTPPhelYsAspGlyLeuArgLeuLeuGluAsnProArgLeuGlySerGlnSerThr 186
    |||||
Db 245 ACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAAAATCCAGACTTGGCTCCCAAGCACC 304

Qy 187 AsnSerSerTyrThrMetAenThrLysThrGlyThrLeuGlnPheAenThrValSerLys 206
    |||||
Db 305 AACAGCTCATACACAATGAATACAAAACCTGGAACTCTGCAATTTAATACTGTTCCAAA 364

Qy 207 LeuAspThrGlyGluTyrSerCysGluAlaArgAsnSerValGlyTyrArgArgCysPro 226
    |||||
Db 365 CTGGACACTGGAGAAATATTCCTGTGAAGCCCGCAATCTGTTGGATATCGCAGGTGCT 424

Qy 227 GlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIleLeuAlaValValVal 246
    |||||
Db 425 GGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCATCATAGCAGCGGTAGTAGTT 484

Qy 247 ValAlaLeuValIleSerValCysGlyLeuGlyValCysTyrAlaGlnArgLysGlyTyr 266
    |||||
Db 485 GTGCGCTTGTAGTATTCGCTTTGCGCTTGGTGTATGTCTATGCTCAGAGAAAGGCTAC 544

Qy 267 PheSerLysGlu 270
    |||||
Db 545 TTTTCAAAAGAA 556

RESULT 15
BU730372/c
LOCUS
DEFINITION
BU730372
BU730372.1 GI:23654193
VERSION
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 727)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
PUBMED
JOURNAL
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu

```


Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA sequence: 1-40, >AT-richLow_complexity
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

Location/Qualifiers
 1..727
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-C11-afp-o-07-0-UI"
 /tissue_type="RPE and Choroid"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-C11"
 /notes="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-C11 is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
 TAG_TISSUE=RPE and Choroid
 TAG_LIB=UI-E-C11
 TAG_SEQ=ACCTA"

ORIGIN

Alignment Scores:
 Pred. No.: 6 64e-159 Length: 727
 Score: 183.00 Matches: 183
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 58.7% Indels: 0
 DB: 3 Gaps: 0

US-10-785-221-9 (1-312) x BU730372 (1-727)

Qy	106	LysTyrArgCysGluValSerAlaProSerGluGlnGlyClnAsnLeuGluGluAspThr	125
Db	667	AAATATCGTTGTGAAGTTAGTGCCCATCTGAGCAAGGCCAAACCTGGAAGAGGATACA	608
Qy	126	ValThrLeuGluValLeuValAlaProAlaValProSerCysGluValProSerSerAla	145
Db	607	GTCACTCTGGAAGTATAGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCCTCTCTGCT	548
Qy	146	LeuSerGlyThrValValGluLeuArgCysGlnAspLysGluGlyValAsnProAlaProGlu	165
Db	547	CTGAGTGGAACTGTGTAGAGCTACCATGTCAAGACAAGAGGGAAATCCAGCTCTTGAA	488
Qy	166	TyrThrTrpPheLysAspGlyIleArgLeuLeuGluAsnProArgLeuGlySerGlnSer	185
Db	487	TACACATGGTTTAAGGATGGCATCGCTTGCTAGAAAAATCCCAGACTTGGCTCCCAAGC	428
Qy	186	ThrAsnSerSerTyrThrMetAsnThrLysThrGlyThrLeuGlnPheAsnThrValSer	205
Db	427	ACCAACAGCTCATACACAAATGAATACAAAACTGGAACTCTGCAATTTAATACTGTTTCC	368
Qy	206	LysLeuAspThrGlyGluTyrSerCysGluAlaArgAsnSerValGlyTyrArgArgCys	225

Db	367	AAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTTCTTGGATATCGAGGTGT	308
Qy	226	ProGlyLysArgMetGlnValAspAspLeuAsnIleSerGlyIleIleAlaValVal	245
Db	307	CCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAAGTGGCATCATAGCAGCCGTAGTA	248
Qy	246	ValValAlaLeuValIleSerValCysGlyLeuGlyValCysTyrAlaGlnArgLysGly	265
Db	247	GTGTGGCCCTTAGTGATTTCCGTTTGTGGCCCTTGGTGTATGCTATGCTCAGAGGAAGGC	188
Qy	266	TyrPheSerLysGluThrSerPheGlnLysSerAsnSerSerLysAlaThrThrMet	285
Db	187	TACTTTTCAAAAGAAACCTCTTCCAGAGAGAGTAATTTCTTCATCTAAAGCCACGACAATG	128
Qy	286	SerGluAsn	288
Db	127	AGTGAAAAAT	119

Search completed: May 17, 2006, 19:06:49
 Job time : 5442 secs